

# SEARCH REQUEST FORM

Requestor's Name: \_\_\_\_\_ Serial Number: \_\_\_\_\_  
Date: \_\_\_\_\_ Phone: \_\_\_\_\_ Art Unit: \_\_\_\_\_

## Search Topic:

Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevant citations, authors, keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevant claim(s).

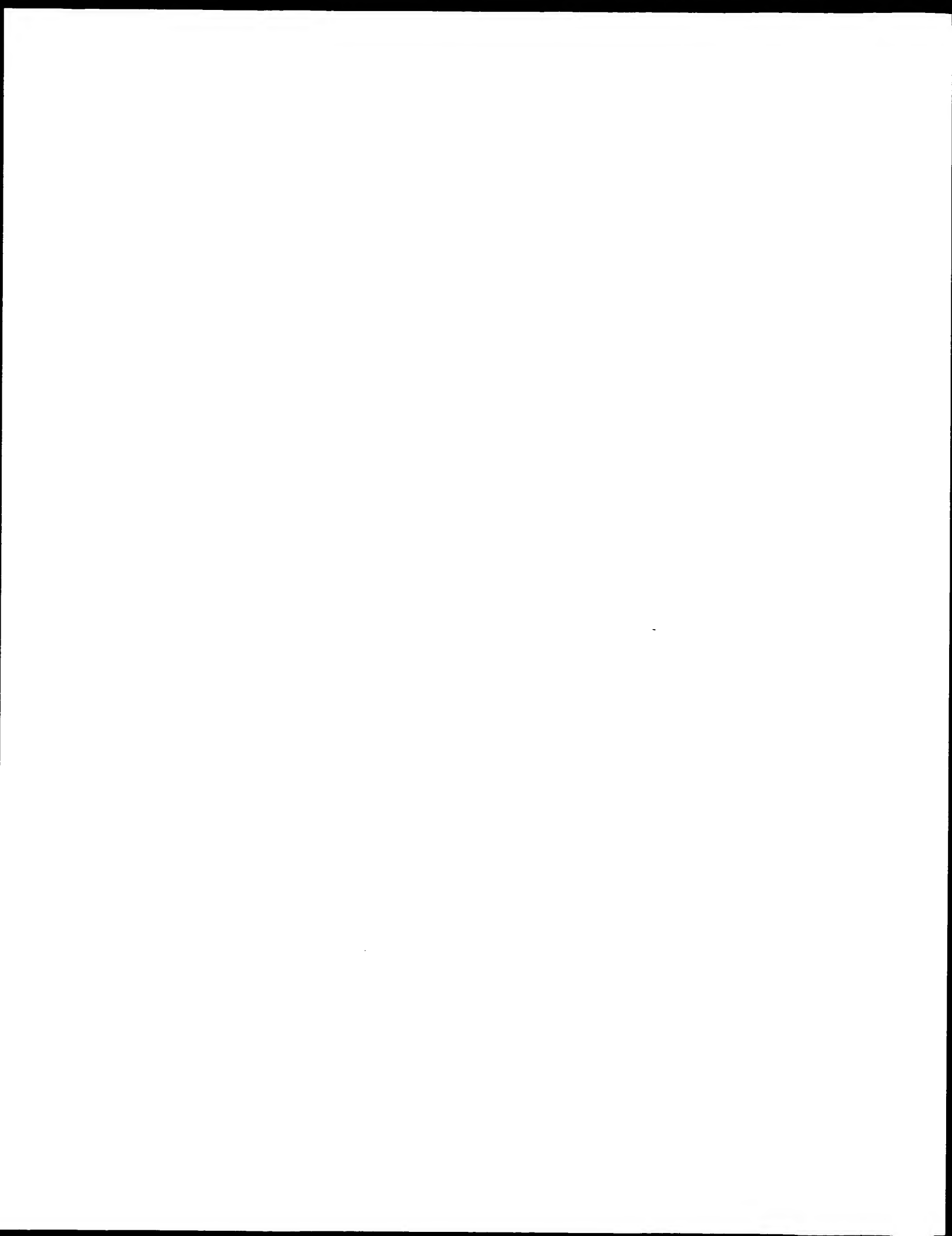
BEST AVAILABLE COPY

## STAFF USE ONLY

Date completed: 12-17-02  
Searcher: Beverly C 4999  
Terminal time: 20  
Elapsed time: \_\_\_\_\_  
CPU time: \_\_\_\_\_  
Total time: 25  
Number of Searches: \_\_\_\_\_  
Number of Databases: 1

Search Site  
\_\_\_\_ STIC  
\_\_\_\_ CM-1  
\_\_\_\_ Pre-S  
Type of Search  
\_\_\_\_ N.A. Sequence  
\_\_\_\_ A.A. Sequence  
\_\_\_\_ Structure  
\_\_\_\_ Bibliographic

Vendors  
\_\_\_\_ IG  
\_\_\_\_ STN  
\_\_\_\_ Dialog  
\_\_\_\_ APS  
\_\_\_\_ Geninfo  
\_\_\_\_ SDC  
\_\_\_\_ DARC/Questel  
☒ Other CGN





```
PR 25-MAR-1998; 98US-0079294.
PR 26-MAR-1998; 98US-0079656.
PR 27-MAR-1998; 98US-0079663.
PR 27-MAR-1998; 98US-0079664.
PR 27-MAR-1998; 98US-0079689.
PR 27-MAR-1998; 98US-0079728.
PR 27-MAR-1998; 98US-0079786.
PR 30-MAR-1998; 98US-0079920.
PR 30-MAR-1998; 98US-0079923.
PR 31-MAR-1998; 98US-0080105.
PR 31-MAR-1998; 98US-0080107.
PR 31-MAR-1998; 98US-0080165.
PR 31-MAR-1998; 98US-0080194.
PR 01-APR-1998; 98US-0080327.
PR 01-APR-1998; 98US-0080328.
PR 01-APR-1998; 98US-0080333.
PR 01-APR-1998; 98US-0080334.
PR 08-APR-1998; 98US-0081049.
PR 08-APR-1998; 98US-0081070.
PR 08-APR-1998; 98US-0081071.
PR 09-APR-1998; 98US-0081195.
PR 09-APR-1998; 98US-0081203.
PR 09-APR-1998; 98US-0081209.
PR 15-APR-1998; 98US-0081229.
PR 15-APR-1998; 98US-0081817.
PR 15-APR-1998; 98US-0081838.
PR 15-APR-1998; 98US-0081952.
PR 15-APR-1998; 98US-0081958.
PR 15-APR-1998; 98US-0082568.
PR 21-APR-1998; 98US-0082569.
PR 22-APR-1998; 98US-0082700.
PR 22-APR-1998; 98US-0082704.
PR 22-APR-1998; 98US-0082804.
PR 22-APR-1998; 98US-0082767.
PR 23-APR-1998; 98US-0082796.
PR 27-APR-1998; 98US-0083336.
PR 28-APR-1998; 98US-0083322.
PR 29-APR-1998; 98US-0083392.
PR 29-APR-1998; 98US-0083495.
PR 29-APR-1998; 98US-0083496.
PR 29-APR-1998; 98US-0083499.
PR 29-APR-1998; 98US-0083500.
PR 29-APR-1998; 98US-0083545.
PR 29-APR-1998; 98US-0083554.
PR 29-APR-1998; 98US-0083558.
PR 29-APR-1998; 98US-0083559.
PR 30-APR-1998; 98US-0083742.
PR 05-MAY-1998; 98US-0084366.
PR 06-MAY-1998; 98US-0084414.
PR 06-MAY-1998; 98US-0084441.
PR 07-MAY-1998; 98US-0084598.
PR 07-MAY-1998; 98US-0084600.
PR 07-MAY-1998; 98US-0084627.
PR 07-MAY-1998; 98US-0084637.
PR 07-MAY-1998; 98US-0084639.
PR 07-MAY-1998; 98US-0084640.
PR 07-MAY-1998; 98US-0084643.
PR 13-MAY-1998; 98US-0085323.
PR 13-MAY-1998; 98US-0085338.
PR 13-MAY-1998; 98US-0085339.
PR 15-MAY-1998; 98US-0085573.
PR 15-MAY-1998; 98US-0085579.
PR 15-MAY-1998; 98US-0085580.
PR 15-MAY-1998; 98US-0085582.
PR 15-MAY-1998; 98US-0085689.
PR 15-MAY-1998; 98US-0085697.
PR 15-MAY-1998; 98US-0085700.
PR 15-MAY-1998; 98US-0085704.
PR 18-MAY-1998; 98US-0086023.
PR 22-MAY-1998; 98US-0086392.
PR 22-MAY-1998; 98US-0086414.
PR 22-MAY-1998; 98US-0086430.
PR 22-MAY-1998; 98US-0086486.
PR 28-MAY-1998; 98US-0087098.

PR 28-MAY-1998; 98US-0087106.
PR 28-MAY-1998; 98US-0087208.
PR 30-JUL-1998; 98US-0094651.
PR 11-SEP-1998; 98US-0100038.
XX (GETH ) GENENTECH INC.
XX Wood WI, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;
XX WPI; 1999-551358/46.
XX N-PSDB; AAZ34313.
XX New secreted and transmembrane polypeptides and their polynucleotides,
XX useful for treating blood coagulation disorders, cancers and cellular
XX adhesion disorders -
XX Claim 12; Fig 217; 530pp; English.
XX The present invention describes secreted and transmembrane polypeptides
XX and their polynucleotides. The nucleotide sequences are useful as
XX sources of probes, primers, for chromosome mapping, and for generation
XX of antisense sequences. They can also be used to create transgenic
XX animals. The proteins can be used to treat a variety of diseases and
XX disorders depending on their function. Diseases that may be treated
XX include blood coagulation disorders, cancers and cellular adhesion
XX disorders. They may also be used to raise antibodies. AAZ33891 to
XX AAZ34338, and AAY41685 to AAY41774 represent polynucleotide and
XX polypeptide sequence given in the exemplification of the present
XX invention.
XX Sequence 273 AA;

Query Match 100.0%; Score 1505; DB 20; Length 273;
Best Local Similarity 100.0%; Pred. No. 1e-94;
Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEGSQEVLIMLLVLAVGTEHAYRPPRRVCAVRAHGDVPSFVQRYVQPLTTCGHR 60
DB 1 MEGSQEVLIMLLVLAVGTEHAYRPPRRVCAVRAHGDVPSFVQRYVQPLTTCGHR 60
QY 61 ACSTYRTIYRTAYRRSPGLAPRPRYACCPGWKRTSLPGACGAAICOPPCRNNGSCVQP 120
DB 61 ACSTYRTIYRTAYRRSPGLAPRPRYACCPGWKRTSLPGACGAAICOPPCRNNGSCVQP 120
QY 121 GRCPCPAGWRGDTQSDVDECSARRGGCPQRCVNTAGSYWCQCEHSHLSADGTLCPKPG 180
DB 121 GRCPCPAGWRGDTQSDVDECSARRGGCPQRCVNTAGSYWCQCEHSHLSADGTLCPKPG 180
QY 181 GPRVAPNPTGVDSAMKEEVQRLQSRVDLLEKQLVLAPLHLSAQLHGLPDPGSL 240
DB 181 GPRVAPNPTGVDSAMKEEVQRLQSRVDLLEKQLVLAPLHLSAQLHGLPDPGSL 240
QY 241 VHSFQQLGRIDSLSEQLSFLERQLGSCCKKDS 273
DB 241 VHSFQQLGRIDSLSEQLSFLERQLGSCCKKDS 273

RESULT 2
AAW88181
ID AAW8838 standard; Protein; 273 AA.
XX AAW88981;
AC AAW88981;
XX
XX 26-APR-1999 (first entry)
XX Human neuro-growth factor-like protein Zneul.
XX Zneu-1; neuro-growth factor-like protein; human; breast cancer;
XX Glioblastoma; pituitary adenoma; Alzheimer's disease; therapy;
XX nerve regeneration; haematopoiesis; fertility; contraception;
XX antibody.
XX Homo sapiens.
OS
```



XX Key Location/Qualifiers  
 FH Peptide 1..19  
 FT /note= "putative signal peptide"  
 FT Protein 20..273  
 FT /note= "mature protein"  
 FT Domain 20..104  
 FT /note= "hydrophilic domain (HSM1), homologous to an HSMC3W5A domain"  
 FT Domain 105..135  
 FT /note= "epidermal growth factor-like domain 1"  
 FT Domain 136..177  
 FT /note= "epidermal growth factor-like domain 2"  
 FT Domain 178..273  
 FT /note= "domain HSM2 homologous to an HSMC3W5A domain"  
 PN MO9857983-AZ.  
 XX 23-DEC-1998.  
 XX 18-FEB-1998; 98MO-US12763.  
 XX 18-JUN-1997; 97US-0878322.  
 PR 18-JUN-1997; 97US-0050143.  
 XX (ZYMO) ZYMOGENETICS INC.  
 XX Blumberg H, Jelinek LJ, Lehner JM, Sheppard PO; Whitmore TE;  
 XX WPI, 1999-095324/08.  
 DR N-PSDB; AAV84341.  
 XX New mammalian Zneul polypeptides - used to, e.g. treat Alzheimer's disease, cancer and to repopulate blood cells  
 PT Claim 6; Page 47-48; 70pp; English.  
 XX This polypeptide comprises human Zneul, a new neuro-growth factor-like protein. Its amino acid sequence was deduced from the cDNA sequence (see AAV84341) of a cDNA clone isolated from a brain cDNA library. Zneul's closest human homologous is HSMC3W5A, a gene in the HLA class III region, which is contained in a cosmid which contains Notch 4. Zneul is also homologous to Notch 4 in its BGF-like domains and may be involved in EGF receptor pathways.  
 CC Zneul is widely expressed in adult tissues, with high expression in heart, placenta, spleen, testis, thymoid, spinal cord and lymph node. Zneul polypeptide can be used as a growth, maintenance, or differentiation factor in the spinal cord, heart, spleen, testis, thymoid and lymph nodes. It may also play a role in breast cancer, glioblastomas, and pituitary adenomas. Zneul may be used to treat Alzheimer's disease, cancer, to repopulate blood cells after chemotherapy, to stimulate myofibroblast proliferation, stimulate or inhibit growth factors made in the placenta, in fertility and contraception, or to regenerate nerves. Claimed Zneul polypeptides (see also AAV88382-97), including specific domains of Zneul and epitope-bearing portions of Zneul, can be used to raise specific antibodies for use e.g. in diagnostic assays.  
 XX Sequence 273 AA;  
 Query Match 100.0%; Score 1505; DB 20; Length 273;  
 Best Local Similarity 100.0%; Pred. NO. 1e-94;  
 Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 121 GRCRCPAGRGDTTCQSDVDDEC SARGGCGPCRCVNTAGSYWCQMEGSLADGTLCPVKG 180  
 DB 121 GRCRCPAGRGDTTCQSDVDDEC SARGGCGPCRCVNTAGSYWCQMEGSLADGTLCPVKG 180  
 QY 181 GPRVAPNPPTGVDSAMKEEVORLQSRVDLLEKQLVLAAPHLSASQALEHGLPDPSSL 240  
 DB 181 GPRVAPNPPTGVDSAMKEEVORLQSRVDLLEKQLVLAAPHLSASQALEHGLPDPSSL 240  
 QY 241 VHSFOQLGRIDSLSEQLSFLSEQLGSCGCKKDS 273  
 DB 241 VHSFOQLGRIDSLSEQLSFLSEQLGSCGCKKDS 273  
 RESULT 3  
 AAB44327  
 ID AAB44327 standard; Protein: 273 AA.  
 AC AAB44327;  
 DT 08-FEB-2001 (first entry)  
 DE Human PRO1449 protein sequence SRQ ID NO:510.  
 XX Human, secreted protein; transmembrane protein; PRO; EST; cytosolic;  
 KW expressed sequence tag; detection; cancer.  
 XX Homo sapiens.  
 XX MO200053756-AZ.  
 XX 14-SEP-2000.  
 XX 18-FEB-2000; 2000MO-US04341.  
 PF 18-FEB-2000; 2000MO-US04341.  
 XX 08-MAR-1999; 99MO-US05028.  
 PR 12-MAR-1999; 99US-0123957.  
 PR 29-MAR-1999; 99US-0126773.  
 PR 21-APR-1999; 99US-0130232.  
 PR 28-APR-1999; 99US-0131445.  
 PR 14-MAY-1999; 99US-0134287.  
 PR 23-JUN-1999; 99US-0141037.  
 PR 26-JUL-1999; 99US-0145698.  
 PR 29-OCT-1999; 99US-0162506.  
 PR 30-NOV-1999; 99MO-US28313.  
 PR 02-DEC-1999; 99MO-US28551.  
 PR 16-DEC-1999; 99MO-US28565.  
 PR 30-DEC-1999; 99MO-US31243.  
 PR 05-JAN-2000; 99MO-US31274.  
 PR 05-JAN-2000; 2000MO-US00219.  
 PR 06-JAN-2000; 2000MO-US00277.  
 PR 06-JAN-2000; 2000MO-US00376.  
 XX (GENTH) GENENTECH INC.  
 PA Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;  
 PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;  
 PI Goddard A, Godowski FO, Grimaldi CJ, Gurney AU, Hillan KJ;  
 PI Kljavin LJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA;  
 PI Shelton DL, Stewart TA, Tumas D, Williams PM, Wood WI;  
 XX WPI, 2000-611443/58.  
 DR N-PSDB; AAC78587.  
 FT Novel PRO polypeptides and polynucleotides used in detection methods,  
 FT to target bioactive molecules to specific cells, and to modulate  
 FT cellular activities -  
 PS Claim 12; Fig 217; 636pp; English.  
 XX AAC78458 to AAC78599 represent polynucleotide and EST (expressed  
 CC sequence tag) sequences which encode secreted or transmembrane PRO

CC polypeptides. The PRO polynucleotides and polypeptides have cytostatic  
 CC activity. The polynucleotides and polypeptides can be used for detecting  
 CC the presence of PRO polypeptides in samples, for linking bioactive  
 CC molecules to cells and for modulating biological activities of cells,  
 CC using the polypeptides for specific targeting. The polypeptide targeting  
 CC can be used to kill the target cells, e.g. for the treatment of cancers.  
 CC The polypeptide pairs provide specific targeting of bioactive molecules  
 CC to cells. AAC78600 to AAC78987 represent PCR primers and probes used in  
 CC the isolation of the PRO polynucleotide sequences.

XX SQ Sequence 273 AA;

Query Match 100.0%; Score 1505; DB 21; Length 273;  
 Best Local Similarity 100.0%; Pred. No. 1e-94;  
 Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRGSEVLLMWLLVAVGGTEHAYRPGRRVCAVRAHGDVSESVQRYQPFLLTCDGHR 60

Db 1 MRGSEVLLMWLLVAVGGTEHAYRPGRRVCAVRAHGDVSESVQRYQPFLLTCDGHR 60

QY 61 ACSTYRTIYTRAYRRSPGLAPARYACCPGWKRTSGLPACGAAICOPPCRNNGSCVQP 120

Db 61 ACSTYRTIYTRAYRRSPGLAPARYACCPGWKRTSGLPACGAAICOPPCRNNGSCVQP 120

QY 121 GRCRPAGWRGDTCSQDVDECSARRGCGPQRCVNTAGSYWCQWEGHSLSGADGTLCPVK 180

Db 121 GRCRPAGWRGDTCSQDVDECSARRGCGPQRCVNTAGSYWCQWEGHSLSGADGTLCPVK 180

QY 181 GPPRVAPNPTGVDSAMKEEVQRLQSRVDLLEKQLVLAPLHSLASQALEHGLPDPGSL 240

Db 181 GPPRVAPNPTGVDSAMKEEVQRLQSRVDLLEKQLVLAPLHSLASQALEHGLPDPGSL 240

QY 241 VHSFQQLGRIDSLSQISFLEELGSCCKXDS 273

Db 241 VHSFQQLGRIDSLSQISFLEELGSCCKXDS 273

RESULT 4

AAB18675

ID AAB18675 standard; Protein; 273 AA.

AC AAB18675;

DT 22-JAN-2001 (first entry)

DE Amino acid sequence of a human a PRO1449 polypeptide.

KW Notch 4 homologue; PRO320; PRO938; PRO1031; PRO296; PRO213; PRO1449;  
 KW angiogenesis; cardiovascularisation; PRO1330; cardiovascular disorder;  
 KW endothelial disorder; angiogenic disorder; cancer; trauma; wound;  
 KW arteriosclerosis; cardiac hypertrophy.

XX Homo sapiens.

XX FH Key Location/Qualifiers

FT Peptide 1..19

FT Modified-site /note= "signal sequence"

FT Modified-site 19..25 /note= "N-myristoylation site"

FT Modified-site 26..30 /note= "amidation site"

FT Modified-site 78..84 /note= "N-myristoylation site"

FT Modified-site 93..97 /note= "N-myristoylation site"

FT Modified-site /note= "cAMP- and cGMP-dependent protein kinase phosphorylation site"

FT Modified-site 97..103 /note= "N-myristoylation site"

FT Modified-site 100..106 /note= "N-myristoylation site"

FT Modified-site 103..109 /note= "N-myristoylation site"

FT Modified-site 123..135 /note= "N-myristoylation site"

FT Region

FT Region /note= "EGF-like domain cysteine pattern signature"  
 FT 130..133  
 FT Modified-site /note= "cell attachment sequence"  
 FT 152..164  
 FT Modified-site /note= "aspartic acid and asparagine hydroxylation site"  
 FT 157..163  
 FT Modified-site /note= "N-myristoylation site"  
 FT 191..197  
 FT Modified-site /note= "N-myristoylation site"  
 FT 265..271  
 FT Modified-site /note= "N-myristoylation site"

XX W0200053752-A2.

XX 14-SEP-2000.

XX 30-DEC-1999; 99WO-US31274.

XX 08-MAR-1999; 99WO-US05028.

XX 21-APR-1999; 99US-0130232.

XX 26-APR-1999; 99US-0131022.

XX 28-APR-1999; 99US-0131445.

XX 14-MAY-1999; 99US-0134287.

XX 02-DEC-1999; 99WO-US28565.

XX (GETH ) GENENTECH INC.

XX Baker KP, Ferrara N, Goddard A, Gurney AL, Hillan KJ, Williams PM;

XX Wood WI;

XX WPI: 2000-638138/61.

XX N-PSDB; AAA75704.

XX A composition useful for treatment and diagnosis of a cardiovascular,  
 PT endothelial or angiogenic disorder, especially cancer, comprises (an  
 PT agonist or antagonist of) a PRO320, PRO938, PRO1031, PRO296, PRO213,  
 PT PRO1330 or PRO1449 polypeptide -

XX Claim 67; Fig 14; 152pp; English.

XX The present sequence represents PRO1449, a human notch 4 homologue.  
 CC The specification describes PRO320, PRO938, PRO1031, PRO296, PRO213,  
 CC PRO1330 and PRO1449 polypeptides. The polypeptides promoter or  
 CC inhibit angiogenesis and cardiovascularisation in mammals. The  
 CC polypeptides are used for the treatment and diagnosis of a  
 CC cardiovascular, endothelial or angiogenic disorder, especially  
 CC cancer. Disorders that can be diagnosed, treated or prevented by  
 CC the polypeptides of the invention include trauma such as wounds,  
 CC arteriosclerosis, and cardiac hypertrophy.

XX Sequence 273 AA;

Query Match 100.0%; Score 1505; DB 21; Length 273;  
 Best Local Similarity 100.0%; Pred. No. 1e-94;  
 Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRGSEVLLMWLLVAVGGTEHAYRPGRRVCAVRAHGDVSESVQRYQPFLLTCDGHR 60

Db 1 MRGSEVLLMWLLVAVGGTEHAYRPGRRVCAVRAHGDVSESVQRYQPFLLTCDGHR 60

QY 61 ACSTYRTIYTRAYRRSPGLAPARYACCPGWKRTSGLPACGAAICOPPCRNNGSCVQP 120

Db 61 ACSTYRTIYTRAYRRSPGLAPARYACCPGWKRTSGLPACGAAICOPPCRNNGSCVQP 120

QY 121 GRCRPAGWRGDTCSQDVDECSARRGCGPQRCVNTAGSYWCQWEGHSLSGADGTLCPVK 180

Db 121 GRCRPAGWRGDTCSQDVDECSARRGCGPQRCVNTAGSYWCQWEGHSLSGADGTLCPVK 180

QY 181 GPPRVAPNPTGVDSAMKEEVQRLQSRVDLLEKQLVLAPLHSLASQALEHGLPDPGSL 240

Db 181 GPPRVAPNPTGVDSAMKEEVQRLQSRVDLLEKQLVLAPLHSLASQALEHGLPDPGSL 240

QY 241 VHSFQQLGRIDSLSQISFLEELGSCCKXDS 273

Db 241 VHSFQQLGRIDSLSEQLSFLERQLGSCCKDS 273

# RESULT 5

AA024044 standard; Protein; 273 AA.

AA024044;

25-JAN-2001 (first entry)

Human PRO1449 protein sequence SEQ ID NO:8.

Human; tumour; diagnosis; neoplastic disease; identification; cancer; tumorigenesis; detection; neoplastic cell growth; proliferation; cytotoxic; anti-inflammatory; immunomodulatory; inflammatory disorder; immunological disorder.

OS Homo sapiens.

PN WO200053754-A1.

PD 14-SEP-2000.

PF 06-JAN-2000; 2000WO-US00277.

PR 08-MAR-1999; 99WO-US05028.

PR 12-MAR-1999; 99US-0123957.

PR 29-MAR-1999; 99US-0126773.

PR 21-APR-1999; 99US-0130232.

PR 28-APR-1999; 99US-0131445.

PR 05-OCT-1999; 99WO-US23089.

PR 30-NOV-1999; 99WO-US28313.

PR 02-DEC-1999; 99WO-US28551.

PR 02-DEC-1999; 99WO-US28564.

PR 30-DEC-1999; 99WO-US31243.

PR 30-DEC-1999; 99WO-US31274.

PA (GETH) GENENTECH INC.

PI Baker KP, Desauvage FJ, Goddard A, Gurney AL, Klein RD, Roy MA;

PI Wood WJ;

DR WPI; 2000-572269/53.

DR N-PSDB; AAC58228.

XX New isolated antibody for use in compositions and methods for the

PT diagnosis and treatment of neoplastic cell growth and proliferation in

PT mammals, including humans, and in monitoring tumor treatment -

XX Claim 61; Fig 8; 195pp; English.

PS The present invention describes an isolated antibody (Ab) that binds to

XX one of the human proteins (P) designated PRO213, PRO1330, PRO1449,

CC PRO337, PRO324, PRO351, PRO615, PRO331, PRO538, PRO664, PRO618,

CC PRO772, PRO703, PRO792 or PRO474. The Ab can be used in compositions

CC and methods for the diagnosis and treatment of neoplastic cell growth

CC and proliferation in mammals, including humans. Genes and polypeptides

CC encoded by them, that are amplified in the genome of a tumor cell, can

CC be identified and are useful targets for the treatment and prevention of

CC certain cancers and may be used to monitor tumor treatment. Compounds

CC that inhibit the expression or activity of the identified polypeptides

CC can be identified and used as antagonists. Benign or malignant tumours,

CC inflammatory disorders and immunological disorders can be treated.

CC AAC58123 to AAC58224 represent hybridisation probes and PCR primers used

CC in the isolation of the human PRO sequences. AAC58225 to AAC58241 and

CC AAC24041 to AAC24056 represent human PRO polynucleotide and protein

CC sequences given in the exemplification of the present invention.

XX Sequence 273 AA;

SQ Query Match 100.0%; Score 1505; DB 21; Length 273;

Best Local Similarity 100.0%; Pred. No. 1e-94; Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRSGQEVLLMMLVLAAGTEHAYRPPGRVCAVRAHGDVSESVQVYQPFLLTDCGR 60

Db 1 MRSGQEVLLMMLVLAAGTEHAYRPPGRVCAVRAHGDVSESVQVYQPFLLTDCGR 60

QY 61 ACSTYRTTYRTRAVRSFGALPAPPRYACCPGWRKTSGLPACGAALCPPCRNSSCVOP 120

Db 61 ACSTYRTTYRTRAVRSFGALPAPPRYACCPGWRKTSGLPACGAALCPPCRNSSCVOP 120

QY 121 GRCPGPAWGRGDTQSSVBCSARGGCPQRCNTAGSYWCQWEGHSLSADGTLCPVPG 180

Db 121 GRCPGPAWGRGDTQSSVBCSARGGCPQRCNTAGSYWCQWEGHSLSADGTLCPVPG 180

QY 181 GPRVAPNPVGSAMKEEYQRLQSRVDLLEKQLVLAFLHSLAQALEHGLPDPGSL 240

Db 181 GPRVAPNPVGSAMKEEYQRLQSRVDLLEKQLVLAFLHSLAQALEHGLPDPGSL 240

QY 241 VHSFQQLGRIDSLSEQLSFLERQLGSCCKDS 273

Db 241 VHSFQQLGRIDSLSEQLSFLERQLGSCCKDS 273

RESULT 6

AA01376 standard; Protein; 273 AA.

AA01376;

20-OCT-2000 (first entry)

Neuron-associated protein.

Neuron associated protein; NEUP; neurological disorder; epilepsy;

ischemic cerebrovascular disease; stroke; cerebral neoplasm;

Alzheimer's disease; Pick's disease; Huntington's disease;

dementia; Parkinson's disease; demyelinating disease; meningitis;

prión disease; Xuru; Creutzfeldt-Jakob disease; neurofibromatosis;

cerebral palsy; muscular dystrophy; central nervous system; CNS;

peripheral nervous system; PNS; myopathy; schizophrenia;

atrophic keratosis; arteriosclerosis; atherosclerosis; bursitis;

cataracts; hepatitis; mixed connective tissue disease; MCTD;

myelofibrosis; paroxysmal nocturnal haemoglobinuria; cancer;

autoimmune disease; inflammation; acquired immunodeficiency syndrome;

AIDS; Addison's disease; adult respiratory distress syndrome;

allergy; ankylosing spondylitis; amyloidosis; anaemia; asthma;

Werner syndrome; trauma; human.

Homo sapiens.

Key Location/Qualifiers

Peptide 1..19

Modified-site 54

Modified-site 64

Modified-site 96

Modified-site 107..134

Modified-site 130..132

Modified-site 136

Domain 141..176

Region 142

Modified-site 152..163

Modified-site 190

FT Modified-site /note= "Potential phosphorylation site"  
205  
FT Modified-site /note= "Potential phosphorylation site"  
252  
FT Modified-site /note= "Potential phosphorylation site"  
258  
FT Modified-site /note= "Potential phosphorylation site"  
268  
FT Modified-site /note= "Potential phosphorylation site"  
273  
FT Modified-site /note= "Potential phosphorylation site"  
273  
XX WO200034477-A2.  
XX 15-JUN-2000.  
XX 10-DEC-1999; 99WO-US30408.  
XX 11-DEC-1998; 98US-0210083.  
XX 11-DEC-1998; 98US-9123456.  
XX 09-FEB-1999; 99US-0119365.  
XX 16-MAR-1999; 99US-0124687.  
XX (INCY-) INCYTE PHARM INC.  
XX Tang YT, Yue H, Baughn MR, Hillman JL, Lal P, Au-young J, Yang J;  
PI Lu DAM, Azimzai Y;  
PI WPI; 2000-423423/36.  
DR N-PSDB; AAA47417.  
XX New human neuron-associated proteins and polynucleotides encoding them,  
PT useful for diagnosis, treatment and prevention of cell proliferative  
PT disorders including cancer, neuronal and neurological disorders  
XX Claim 1; Page 97; 145pp; English.  
XX Human neuron-associated proteins (NEUAP) can be used for for  
XX treating or preventing a disorder associated with decreased  
XX expression or activity of NEUAP. Antagonists of NEUAP are useful for  
XX treating or preventing disorder associated with increased expression  
XX or activity of NEUAP. NEUAP or their fragments or derivatives are  
XX useful for treating neurological disorder such as epilepsy, ischemic  
XX cerebrovascular disease, stroke, cerebral neoplasms, Alzheimer's  
XX disease, Pick's disease, Huntington's disease, dementia and  
XX Parkinson's disease. NEUAPs are also useful for treating other  
XX demyelinating diseases, bacterial and viral meningitis, prion  
XX diseases including kuru, Creutzfeldt-Jakob disease, nutritional and  
XX metabolic diseases of the nervous system, neurofibromatosis, other  
XX developmental disorders of the central nervous system, cerebral  
XX palsy, neuroskeletal disorders, autonomic nervous system disorders,  
XX cranial nerve disorders, spinal cord diseases, muscular dystrophy and  
XX other neuromuscular disorders, peripheral nervous system disorders,  
XX inherited, metabolic, endocrine, and toxic myopathies, mental  
XX disorders including mood, anxiety and schizophrenic disorders, a cell  
XX proliferative disorder such as actinic keratosis, arteriosclerosis,  
XX atherosclerosis, bursitis, cirrhosis, hepatitis, mixed connective  
XX tissue disease (MCTD), myelofibrosis, paroxysmal nocturnal  
XX haemoglobinuria, cancers of the adrenal gland, bladder, bone,  
XX bone marrow, brain, breast, cervix, and an autoimmune/inflammatory  
XX disorder such as acquired immunodeficiency syndrome (AIDS), Addison's  
XX disease, adult respiratory distress syndrome, allergies, ankylosing  
XX spondylitis, amyloidosis, anemia, asthma, Werner syndrome,  
XX complications of cancer, hemodialysis, and extracorporeal circulation,  
XX viral, bacterial, fungal parasitic, protozoal, and helminthic  
XX infections, and trauma. This protein was given the Incyte ID no.  
XX 829443CD1.  
XX Sequence 273 AA;  
XX Query Match 100.0%; Score 1505; DB 21; Length 273;  
XX Best Local Similarity 100.0%; Pred. No. 1e-94;  
XX Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRGSEVLLMLLLVAVGTEHAYRPRRVCARAHGDPVSESFVQRYVQPLTTCDGHR 60  
DB 1 MRGSEVLLMLLLVAVGTEHAYRPRRVCARAHGDPVSESFVQRYVQPLTTCDGHR 60  
QY 61 ACSTYRTIYRTYRRSPGLAPARPRYACPGWKRTSGLPAGCAAIACOPPCRNNGSCVQP 120  
DB 61 ACSTYRTIYRTYRRSPGLAPARPRYACPGWKRTSGLPAGCAAIACOPPCRNNGSCVQP 120  
QY 121 GRCRCFAGWRGDTCSQSDVDECSARRGGCPQRCVNTAGSYWCOCWEGHSLSDAGTLCVPKG 180  
DB 121 GRCRCFAGWRGDTCSQSDVDECSARRGGCPQRCVNTAGSYWCOCWEGHSLSDAGTLCVPKG 180  
QY 181 GPRVAPNPTGVDSAMKEEVQRLQSRVDLLEKLOLVLAHLHSLASQALEHGLPDPGSL 240  
DB 181 GPRVAPNPTGVDSAMKEEVQRLQSRVDLLEKLOLVLAHLHSLASQALEHGLPDPGSL 240  
QY 241 VHSFQOLGRIDSLSEIOISFLEELGSCCKKDS 273  
DB 241 VHSFQOLGRIDSLSEIOISFLEELGSCCKKDS 273  
RESULT 7  
ID AAM23991 standard; Protein; 273 AA.  
XX AAM23991  
XX AC AAM23991;  
XX 12-OCT-2001 (first entry)  
XX Human EST encoded protein SEQ ID NO: 1516.  
XX Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;  
XX tomato; monkey; dog; sea urchin; expressed sequence tag; EST;  
XX diagnostic; forensic test; gene mapping; genetic disorder;  
XX biodiversity; gene therapy; nutrition.  
XX Homo sapiens.  
XX WO200154477-A2  
XX 02-AUG-2001  
XX 25-JAN-2001; 2001WO-US02687.  
XX 25-JAN-2000; 2000US-0491404.  
XX 17-JUL-2000; 2000US-0617746.  
XX 03-AUG-2000; 2000US-0631451.  
XX 15-SEP-2000; 2000US-0663870.  
XX (HYSB-) HYSEQ INC.  
XX Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;  
XX Cao Y, Drmanac RA, Zhang J, Werhman T;  
XX WPI; 2001-476164/51.  
XX N-PSDB; AAH98650.  
XX Isolated polypeptide for treatment of diseases, diagnostics, raising  
XX antibodies and research use -  
XX Claim 20; Page 1046-1047; 1275pp; English.  
XX The present invention provides the protein and coding sequences of novel  
XX proteins from a variety of organisms, including human, dog, cat, horse,  
XX cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea  
XX urchin and tomato. These were derived from expressed sequence tags (ESTs)  
XX from the organism of interest. They can be used in diagnostics,  
XX forensics, gene mapping, identification of mutations, to assess  
XX biodiversity and for nutritional purposes. The present sequence is a  
XX protein of the invention.  
XX Sequence 273 AA;

Query Match 100.0%; Score 1505; DB 22; Length 273;  
 Best Local Similarity 100.0%; Pred. No. 1e-94;  
 Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC 1 MRSGEVLMMVLVLAAGTEHAHPRGRVCAVRAHGDVPSSEFVQRYVOPFLITCDGHR 60  
 CC 1 MRSGEVLMMVLVLAAGTEHAHPRGRVCAVRAHGDVPSSEFVQRYVOPFLITCDGHR 60  
 DB 1 MRSGEVLMMVLVLAAGTEHAHPRGRVCAVRAHGDVPSSEFVQRYVOPFLITCDGHR 60

QY 61 ACSTYRTYRTAYRRSPGLAPARPRVACCPGMRKTSGLPACGAAICQPPCRNGSCVQ 120  
 DB 61 ACSTYRTYRTAYRRSPGLAPARPRVACCPGMRKTSGLPACGAAICQPPCRNGSCVQ 120  
 QY 121 GRRCPCAGMGDTQSDVDDECSARRGCCPQRCVNTAGSYWCQCEGHSLSADGTLCPVK 180  
 DB 121 GRRCPCAGMGDTQSDVDDECSARRGCCPQRCVNTAGSYWCQCEGHSLSADGTLCPVK 180  
 QY 181 GPRVAPNPPTGVDSAMKEEVQRLQSRVDLLEKQLVLAFLHSLASQALHGLPDPGSL 240  
 DB 181 GPRVAPNPPTGVDSAMKEEVQRLQSRVDLLEKQLVLAFLHSLASQALHGLPDPGSL 240

QY 241 VHSFQQLGRIDLSLEQISFLEEQIGSCCKKDS 273  
 DB 241 VHSFQQLGRIDLSLEQISFLEEQIGSCCKKDS 273

RESULT 8  
 AAB61609  
 ID AAB61609 standard; Protein; 273 AA.  
 XX AAB61609;  
 AC AAB61609;  
 XX 05-APR-2001 (first entry)  
 DT 05-APR-2001 (first entry)  
 XX Human protein HP03375.  
 DE Human protein HP03375.  
 XX Human; hydrophobic domain; immune deficiency; autoimmune disorder;  
 KW allergy; tissue growth; regeneration; wound healing; burn; tumour;  
 KW periodontal disease; thrombolytic condition; haemostatic condition;  
 KW infection.  
 XX Homo-sapiens.  
 OS Homo-sapiens.  
 AC MO200102563-A2.  
 XX 11-JAN-2001.  
 PD 11-JAN-2001.  
 XX 16-JUN-2000; 2000MO-JP03948.  
 PF 16-JUN-2000; 2000MO-JP03948.  
 XX 02-JUL-1999; 99UP-0188835.  
 PR 02-JUL-1999; 99UP-0188835.  
 XX (SAGA) SAGAMI CHEM RES CENT  
 PA (SAGA) SAGAMI CHEM RES CENT  
 XX (PROT-) PROTEGENE INC.  
 PI Kato S, Kimura T;  
 XX Kato S, Kimura T;  
 XX MPI; 2001-071581/08.  
 DR MPI; 2001-071581/08.  
 XX N-PSDB; AAF28680, AAF28690.  
 DR N-PSDB; AAF28680, AAF28690.  
 XX New human proteins with hydrophobic domains, useful for the treatment  
 PT of immune disorders, tumors, allergic conditions, thrombosis and  
 XX microbial infection -  
 XX Claim 1; Pages 97-98; 153p; English.  
 PS The present invention relates to human proteins (AAB61608-AAB61617) and  
 CC their coding sequences (AAF28679-AAF28698). The proteins of the present  
 CC invention have hydrophobic domains and can be used for the treatment of  
 CC various immune deficiencies and disorders, such as severe combined  
 CC immunodeficiency (SCID), multiple sclerosis, rheumatoid arthritis,  
 CC autoimmune pulmonary inflammation, graft-versus-host disease and  
 CC Guillain-Barre syndrome. The proteins may also be useful in the treatment  
 CC of allergic reactions and conditions, such as asthma and in regulation of

CC haematopoiesis or lymphoid cell deficiencies. The proteins may also have  
 CC utility in compositions used for bone, cartilage, tendon and/or nerve  
 CC tissue growth or regeneration as well as wound healing and in the  
 CC treatment of burns. The proteins may be used in the treatment of  
 CC periodontal disease and in other tooth repair processes. Other uses  
 CC include treatment of thrombolytic and haemostatic conditions, treatment  
 CC or prevention of tumours and inhibiting infection by bacteria, viruses,  
 CC fungi and other parasites.

CC Sequence 273 AA;  
 SQ Sequence 273 AA;  
 Query Match 100.0%; Score 1505; DB 22; Length 273;  
 Best Local Similarity 100.0%; Pred. No. 1e-94;  
 Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRSGEVLMMVLVLAAGTEHAHPRGRVCAVRAHGDVPSSEFVQRYVOPFLITCDGHR 60  
 DB 1 MRSGEVLMMVLVLAAGTEHAHPRGRVCAVRAHGDVPSSEFVQRYVOPFLITCDGHR 60  
 QY 61 ACSTYRTYRTAYRRSPGLAPARPRVACCPGMRKTSGLPACGAAICQPPCRNGSCVQ 120  
 DB 61 ACSTYRTYRTAYRRSPGLAPARPRVACCPGMRKTSGLPACGAAICQPPCRNGSCVQ 120  
 QY 121 GRRCPCAGMGDTQSDVDDECSARRGCCPQRCVNTAGSYWCQCEGHSLSADGTLCPVK 180  
 DB 121 GRRCPCAGMGDTQSDVDDECSARRGCCPQRCVNTAGSYWCQCEGHSLSADGTLCPVK 180  
 QY 181 GPRVAPNPPTGVDSAMKEEVQRLQSRVDLLEKQLVLAFLHSLASQALHGLPDPGSL 240  
 DB 181 GPRVAPNPPTGVDSAMKEEVQRLQSRVDLLEKQLVLAFLHSLASQALHGLPDPGSL 240

QY 241 VHSFQQLGRIDLSLEQISFLEEQIGSCCKKDS 273  
 DB 241 VHSFQQLGRIDLSLEQISFLEEQIGSCCKKDS 273

RESULT 9  
 AAY41769  
 ID AAY41769 standard; Protein; 273 AA.  
 XX AAY41769;  
 AC AAY41769;  
 XX 07-DEC-1999 (first entry)  
 DT 07-DEC-1999 (first entry)  
 XX Human PRO213-1 protein sequence.  
 DE Human PRO213-1 protein sequence.  
 XX Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation;  
 KW probe; blood coagulation disorder; cancer; cellular adhesion disorder;  
 KW secreted protein; transmembrane protein.  
 XX Homo-sapiens.  
 OS Homo-sapiens.  
 AC MO9946281-A2.  
 XX MO9946281-A2.  
 XX 16-SEP-1999.  
 PD 16-SEP-1999.  
 XX 08-MAR-1999; 99MO-US05028.  
 PR 08-MAR-1999; 99MO-US05028.  
 XX 10-MAR-1998; 98US-0077450.  
 PR 10-MAR-1998; 98US-0077450.  
 XX 11-MAR-1998; 98US-0077632.  
 PR 11-MAR-1998; 98US-0077632.  
 XX 11-MAR-1998; 98US-0077641.  
 PR 11-MAR-1998; 98US-0077641.  
 XX 12-MAR-1998; 98US-0077791.  
 PR 12-MAR-1998; 98US-0077791.  
 XX 13-MAR-1998; 98US-0078004.  
 PR 13-MAR-1998; 98US-0078004.  
 XX 17-MAR-1998; 98US-0040220.  
 PR 17-MAR-1998; 98US-0040220.  
 XX 20-MAR-1998; 98US-0078886.  
 PR 20-MAR-1998; 98US-0078886.  
 XX 20-MAR-1998; 98US-0078910.  
 PR 20-MAR-1998; 98US-0078910.  
 XX 20-MAR-1998; 98US-0078936.  
 PR 20-MAR-1998; 98US-0078936.  
 XX 25-MAR-1998; 98US-0079294.  
 PR 25-MAR-1998; 98US-0079294.  
 XX 26-MAR-1998; 98US-0079656.  
 PR 26-MAR-1998; 98US-0079656.  
 XX 27-MAR-1998; 98US-0079663.  
 PR 27-MAR-1998; 98US-0079663.  
 XX 27-MAR-1998; 98US-0079664.  
 PR 27-MAR-1998; 98US-0079664.





Tue Dec 17 14:03:46 2002

```

XX
AC AAB44325;
XX
XX 08-FEB-2001 (first entry)
XX
DE Human PRO213-1 protein sequence SEQ ID NO:506.
XX
XX Human; secreted protein; transmembrane protein; PRO; EST; cytostatic;
XX expressed sequence tag; detection; cancer.
XX
XX Homo sapiens.
XX
XX WO200053756-A2.
XX
XX 14-SEP-2000.
XX
XX 18-FEB-2000; 2000WO-US04341.
XX
XX 08-MAR-1999; 99WO-US05028.
XX 12-MAR-1999; 99US-0123957.
XX 29-MAR-1999; 99US-0126773.
XX 21-APR-1999; 99US-0130232.
XX 28-APR-1999; 99US-0131445.
XX 14-MAY-1999; 99US-0134287.
XX 23-JUN-1999; 99US-0141037.
XX 26-JUL-1999; 99US-0145698.
XX 29-OCT-1999; 99US-0162506.
XX 30-NOV-1999; 99WO-US28313.
XX 02-DEC-1999; 99WO-US28551.
XX 16-DEC-1999; 99WO-US30095.
XX 30-DEC-1999; 99WO-US31243.
XX 30-DEC-1999; 99WO-US31274.
XX 05-JAN-2000; 2000WO-US00219.
XX 06-JAN-2000; 2000WO-US00277.
XX 06-JAN-2000; 2000WO-US00376.
XX
XX (GETH ) GENENTECH INC.
XX
XX Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
XX Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
XX Goddard A, Godowski PJ, Grimaldi CU, Gurney AL, Hillan KJ;
XX Kljavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA;
XX Shelton DL, Stewart TA, Tumas D, Williams PM, Wood WI;
XX
XX WPI; 2000-611443/58.
XX N-PSDB; AAC78585.
XX
XX Novel PRO polypeptides and polynucleotides used in detection methods,
XX to target bioactive molecules to specific cells, and to modulate
XX cellular activities -
XX
XX Claim 12; Fig 213; 636pp; English.
XX
XX AAC78458 to AAC78599 represent polynucleotide and EST (expressed
XX sequence tag) sequences which encode secreted or transmembrane PRO
XX polypeptides. The PRO polynucleotides and polypeptides have cytostatic
XX activity. The polynucleotides and polypeptides can be used for detecting
XX the presence of PRO polypeptides in samples, for linking bioactive
XX molecules to cells and for modulating biological activities of cells,
XX using the polypeptides for specific targeting. The polypeptide targeting
XX can be used to kill the target cells, e.g. for the treatment of cancers.
XX The polypeptide pairs provide specific targeting of bioactive molecules
XX to cells. AAC78600 to AAC78987 represent PCR primers and probes used in
XX the isolation of the PRO polynucleotide sequences.
XX
XX Sequence 273 AA:
XX
XX Query Match 99.9%; Score 1504; DB 21; Length 273;
XX Best Local Similarity 99.6%; Pred. No. 1.2e-94;
XX Matches 272; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 MRGSEVLLMVLAVGTEHAYRPGRRVCAVRAHGDVSEFVQRYQFLLTTCGDHR 60

```

QY



PT cellular activities -  
 XX  
 PS Claim 12; Fig 215; 636pp; English.  
 XX  
 CC AAC78458 to AAC78599 represent polynucleotide and EST (expressed  
 CC sequence tag) sequences which encode secreted or transmembrane PRO  
 CC polypeptides. The PRO polynucleotides and polypeptides have cytostatic  
 CC activity. The polynucleotides and polypeptides can be used for detecting  
 CC the presence of PRO polypeptides in samples, for linking bioactive  
 CC molecules to cells and for modulating biological activities of cells,  
 CC using the polypeptides for specific targeting. The polypeptide targeting  
 CC can be used to kill the target cells, e.g. for the treatment of cancers.  
 CC The polypeptide pairs provide specific targeting of bioactive molecules  
 CC to cells. AAC78600 to AAC78987 represent PCR primers and probes used in  
 CC the isolation of the PRO polynucleotide sequences.

SO Sequence 273 AA;

Query Match 99.9%; Score 1504; DB 21; Length 273;  
 Best Local Similarity 99.6%; Pred. No. 1.2e-94;  
 Matches 272; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRGSEVLLMVLAVGTEHAYRPGRRVCAVRAHGDVSESFVORYOPLTTCDGHR 60  
 DB 1 MRGSEVLLMVLAVGTEHAYRPGRRVCAVRAHGDVSESFVORYOPLTTCDGHR 60  
 QY 61 ACSTYRTIYRTAYRSPGLAPRPRVACCPGKRTSGLPAGCAAIICPPCRNGSCVOP 120  
 DB 61 ACSTYRTIYRTAYRSPGLAPRPRVACCPGKRTSGLPAGCAAIICPPCRNGSCVOP 120  
 QY 121 GRGCRPAGWRGDTCCSDVDECSARRGCGPCRCVNTAGSYWCQCEGHSLSADGTLCPVKG 180  
 DB 121 GRGCRPAGWRGDTCCSDVDECSARRGCGPCRCVNTAGSYWCQCEGHSLSADGTLCPVKG 180  
 QY 181 GPPRYAPNPTGVDASMKKEVQRLQSRVLLBEKQLVLAPLHSLASQALEKLPDPSSL 240  
 DB 181 GPPRYAPNPTGVDASMKKEVQRLQSRVLLBEKQLVLAPLHSLASQALEKLPDPSSL 240  
 QY 241 VHSFOQLGRIDSLSEQISFLEROLSCSCCKDSS 273  
 DB 241 VHSFOQLGRIDSLSEQISFLEROLSCSCCKDSS 273

RESULT 13

AAB18673  
 ID AAB18673 standard; Protein; 273 AA.

AC AAB18673;

DT 22-JAN-2001 (first entry)

XX Amino acid sequence of a human a PRO213 polypeptide.

KW Growth arrest-specific gene 6 protein homologue; PRO320; PRO938; PRO1031;  
 KW PRO296; PRO213; PRO1449; angiogenesis; cardiovascularisation; PRO1330;  
 KW cardiovascular disorder; endothelial disorder; angiogenic disorder;  
 KW cancer; trauma; wound; atherosclerosis; cardiac hypertrophy.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 1..19

FT Modified-site /note= "signal sequence"

FT Modified-site /note= "N-myristoylation site"

FT Modified-site /note= "amidation site"

FT Modified-site /note= "N-myristoylation site"

FT Modified-site /note= "CAMP- and GMP-dependent protein kinase phosphorylation site"

FT Modified-site 97..103

FT FT /note= "N-myristoylation site"  
 FT 100..106  
 FT FT /note= "N-myristoylation site"  
 FT 103..109  
 FT FT /note= "N-myristoylation site"  
 FT 123..135  
 FT FT /note= "EGF-like domain cysteine pattern signature"  
 FT 130..133  
 FT FT /note= "cell attachment sequence"  
 FT 152..164  
 FT FT /note= "aspartic acid and asparagine hydroxylation site"  
 FT 157..163  
 FT FT /note= "N-myristoylation site"  
 FT 191..197  
 FT FT /note= "N-myristoylation site"  
 FT 265..271  
 FT FT /note= "N-myristoylation site"

PN WO200053752-A2.

XX 14-SEP-2000.

XX 30-DEC-1999; 99WO-US31274.

XX 08-MAR-1999; 99WO-US05028.

XX 21-APR-1999; 99US-0130232.

XX 26-APR-1999; 99US-0131022.

XX 28-APR-1999; 99US-0131445.

XX 02-DEC-1999; 99US-0134287.

XX 02-DEC-1999; 99WO-US28565.

XX (GETH ) GENENTECH INC.

XX Baker KP, Ferrara N, Goddard A, Gurney AL, Hillan KJ, Williams PM;

XX Wood WT;

XX WPI; 2000-638138/61.

XX N-PSDB; AAA75702.

XX A composition useful for treatment and diagnosis of a cardiovascular,

XX endothelial or angiogenic disorder, especially cancer, comprises (an

XX agonist or antagonist of) a PRO320, PRO938, PRO1031, PRO296, PRO213,

XX PRO1330 or PRO1449 polypeptide -

XX Claim 67; Fig 10; 152pp; English.

XX The present sequence represents PRO213, a human growth arrest-specific

XX gene 6 protein homologue. The specification describes PRO320, PRO938,

XX PRO1031, PRO296, PRO213, and PRO1449 polypeptides. The

XX polypeptides promoter or inhibit angiogenesis and cardiovascularisation

XX in mammals. The polypeptides are used for the treatment and diagnosis

XX of a cardiovascular, endothelial or angiogenic disorder, especially

XX cancer. Disorders that can be diagnosed, treated or prevented by

XX the polypeptides of the invention include trauma such as wounds,

XX atherosclerosis, and cardiac hypertrophy.

SO Sequence 273 AA;

Query Match 99.9%; Score 1504; DB 21; Length 273;  
 Best Local Similarity 99.6%; Pred. No. 1.2e-94;  
 Matches 272; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRGSEVLLMVLAVGTEHAYRPGRRVCAVRAHGDVSESFVORYOPLTTCDGHR 60

DB 1 MRGSEVLLMVLAVGTEHAYRPGRRVCAVRAHGDVSESFVORYOPLTTCDGHR 60

QY 61 ACSTYRTIYRTAYRSPGLAPRPRVACCPGKRTSGLPAGCAAIICPPCRNGSCVOP 120

DB 61 ACSTYRTIYRTAYRSPGLAPRPRVACCPGKRTSGLPAGCAAIICPPCRNGSCVOP 120

QY 121 GRGCRPAGWRGDTCCSDVDECSARRGCGPCRCVNTAGSYWCQCEGHSLSADGTLCPVKG 180

DB 121 GRGCRPAGWRGDTCCSDVDECSARRGCGPCRCVNTAGSYWCQCEGHSLSADGTLCPVKG 180

Tue Dec 17 14:03:46 2002

PI Baker KP, Ferrara N, Goddard A, Gurney AL, Hillan KJ, Williams PM;  
PI Wood WI;  
XX  
XX  
DR WPI: 2000-638138/61.  
DR N-PSDB; AAA75703.  
XX  
XX  
XX A composition useful for treatment and diagnosis of a cardiovascular,  
XX endothelial or angiogenic disorder, especially cancer, comprises (an  
XX agonist or antagonist of) a PRO1320, PRO938, PRO1031, PRO296, PRO213,  
XX PRO1330 or PRO1449 polypeptide -  
XX  
XX  
XX Claim 67; Fig 12; 152pp; English.

XX The present sequence represents PRO1330, a human notch 4 homologue.  
XX The specification describes PRO1320, PRO938, PRO1031, PRO296, PRO213,  
XX PRO1330 and PRO1449 polypeptides. The polypeptides promoter or  
XX inhibit angiogenesis and cardiovascularisation in mammals. The  
XX polypeptides are used for the treatment and diagnosis of a  
XX cardiovascular, endothelial or angiogenic disorder, especially  
XX cancer. Disorders that can be diagnosed, treated or prevented by  
XX the polypeptides of the invention include trauma such as wounds,  
XX atherosclerosis, and cardiac hypertrophy.  
XX  
XX  
XX Sequence 273 AA;

Query Match 99.9%; Score 1504; DB 21; Length 273;  
Best Local Similarity 99.6%; Pred No. 1.2e-94;  
Matches 272; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRGQEVLLMVLAVGGTEHAYRFRVCAVRAHGDVPSFVQVYQPLTTCDGHR 60  
Db 1 MRGQEVLLMVLAVGGTEHAYRFRVCAVRAHGDVPSFVQVYQPLTTCDGHR 60  
QY 61 ACSTYRTIYTAIRRSPLAPAPRYACCPGWKRTSLGACGAAICQPPCRNGSCVQP 120  
Db 61 ACSTYRTIYTAIRRSPLAPAPRYACCPGWKRTSLGACGAAICQPPCRNGSCVQP 120  
QY 121 GRCPAGWRGDTCSQSDVDECSARRGGCPQRCVNTAGSYWCQWEGHSLSDGTLCPVKG 180  
Db 121 GRCPAGWRGDTCSQSDVDECSARRGGCPQRCVNTAGSYWCQWEGHSLSDGTLCPVKG 180  
QY 181 GPPRVAPNPTGVDSAMKEEVQRLQSRVDLLEKQLVLAPLHSLASQALEHGLPDPGSL 240  
Db 181 GPPRVAPNPTGVDSAMKEEVQRLQSRVDLLEKQLVLAPLHSLASQALEHGLPDPGSL 240  
QY 241 VHSFOQLGRIDSLSEQISFLEEQLGSCCKDS 273  
Db 241 VHSFOQLGRIDSLSEQISFLEEQLGSCCKDS 273

RESULT 15  
AAB24042

ID AAB24042 standard; Protein; 273 AA.

XX  
XX  
AC AAB24042;  
XX  
DT 25-JAN-2001 (first entry)  
XX  
XX  
DE Human PRO213 protein sequence SEQ ID NO:4.

XX Human; tumour; diagnosis; neoplastic disease; identification; cancer;  
XX tumorigenesis; detection; neoplastic cell growth; proliferation;  
XX cytostatic; antiinflammatory; immunomodulatory; inflammatory disorder;  
XX immunological disorder.  
XX  
XX Homo sapiens.  
XX  
XX WO200053754-A1.  
XX  
XX 14-SEP-2000.  
XX  
XX 06-JAN-2000; 2000WO-US00277.

QY 181 GPPRVAPNPTGVDSAMKEEVQRLQSRVDLLEKQLVLAPLHSLASQALEHGLPDPGSL 240  
Db 181 GPPRVAPNPTGVDSAMKEEVQRLQSRVDLLEKQLVLAPLHSLASQALEHGLPDPGSL 240  
QY 241 VHSFOQLGRIDSLSEQISFLEEQLGSCCKDS 273  
Db 241 VHSFOQLGRIDSLSEQISFLEEQLGSCCKDS 273

RESULT 14

AAB18674  
ID AAB18674 standard; Protein; 273 AA.

XX  
XX  
AC AAB18674;  
XX  
DT 22-JAN-2001 (first entry)  
XX  
XX Amino acid sequence of a human PRO1330 polypeptide.

XX Notch 4 homologue; PRO320; PRO938; PRO1031; PRO296; PRO1449;  
XX angiogenesis; cardiovascularisation; PRO1330; cardiovascular disorder;  
XX endothelial disorder; angiogenic disorder; cancer; trauma; wound;  
XX atherosclerosis; cardiac hypertrophy.  
XX  
XX  
XX Homo sapiens.

OS  
XX

Key Location/Qualifiers

FT Peptide 1..19  
FT /note= "signal sequence"  
FT Modified-site 19..25  
FT /note= "N-myristoylation site"  
FT Modified-site 26..30  
FT /note= "amidation site"  
FT Modified-site 78..84  
FT /note= "N-myristoylation site"  
FT Modified-site 93..97  
FT /note= "cAMP- and cGMP-dependent protein kinase phosphorylation site"  
FT Modified-site 97..103  
FT /note= "N-myristoylation site"  
FT Modified-site 100..106  
FT /note= "N-myristoylation site"  
FT Modified-site 103..109  
FT /note= "N-myristoylation site"  
FT Region 123..135  
FT /note= "EGF-like domain cysteine pattern signature"  
FT Region 130..133  
FT /note= "cell attachment sequence"  
FT Modified-site 152..164  
FT /note= "aspartic acid and asparagine hydroxylation site"  
FT Modified-site 157..163  
FT /note= "N-myristoylation site"  
FT Modified-site 191..197  
FT /note= "N-myristoylation site"  
FT Modified-site 265..271  
FT /note= "N-myristoylation site"

XX WO200053752-A2.

XX  
XX  
PD 14-SEP-2000.  
XX  
XX  
XX 30-DEC-1999; 99WO-US31274.  
XX  
XX 08-MAR-1999; 99WO-US05028.  
XX 21-APR-1999; 99US-0130232.  
XX 26-APR-1999; 99US-0131022.  
XX 28-APR-1999; 99US-0131445.  
XX 14-MAY-1999; 99US-0134287.  
XX 02-DEC-1999; 99WO-US28565.  
XX  
XX (GETH ) GENENTECH INC.

PR 08-MAR-1999; 99WO-US05028.  
PR 12-MAR-1999; 99US-0123957.  
PR 29-MAR-1999; 98US-0126773.  
PR 21-APR-1999; 99US-0130232.  
PR 28-APR-1999; 99US-0131445.  
PR 05-OCT-1999; 99WO-US23089.  
PR 30-NOV-1999; 99WO-US28313.  
PR 02-DEC-1999; 99WO-US28551.  
PR 30-DEC-1999; 99WO-US28564.  
PR 30-DEC-1999; 99WO-US31243.  
PR 30-DEC-1999; 99WO-US31274.

XX (GETH ) GENENTECH INC.

XX Baker KP, Desauvage FT, Goddard A, Gurney AL, Klein RD, Roy MA,  
PI Wood WJ;

XX WPI; 2000-572269/53.  
DR N-PSDB; AAC58226.

XX New isolated antibody for use in compositions and methods for the  
PT diagnosis and treatment of neoplastic cell growth and proliferation in  
PT mammals, including humans, and in monitoring tumor treatment -

XX Claim 61; Fig 4; 195pp; English.

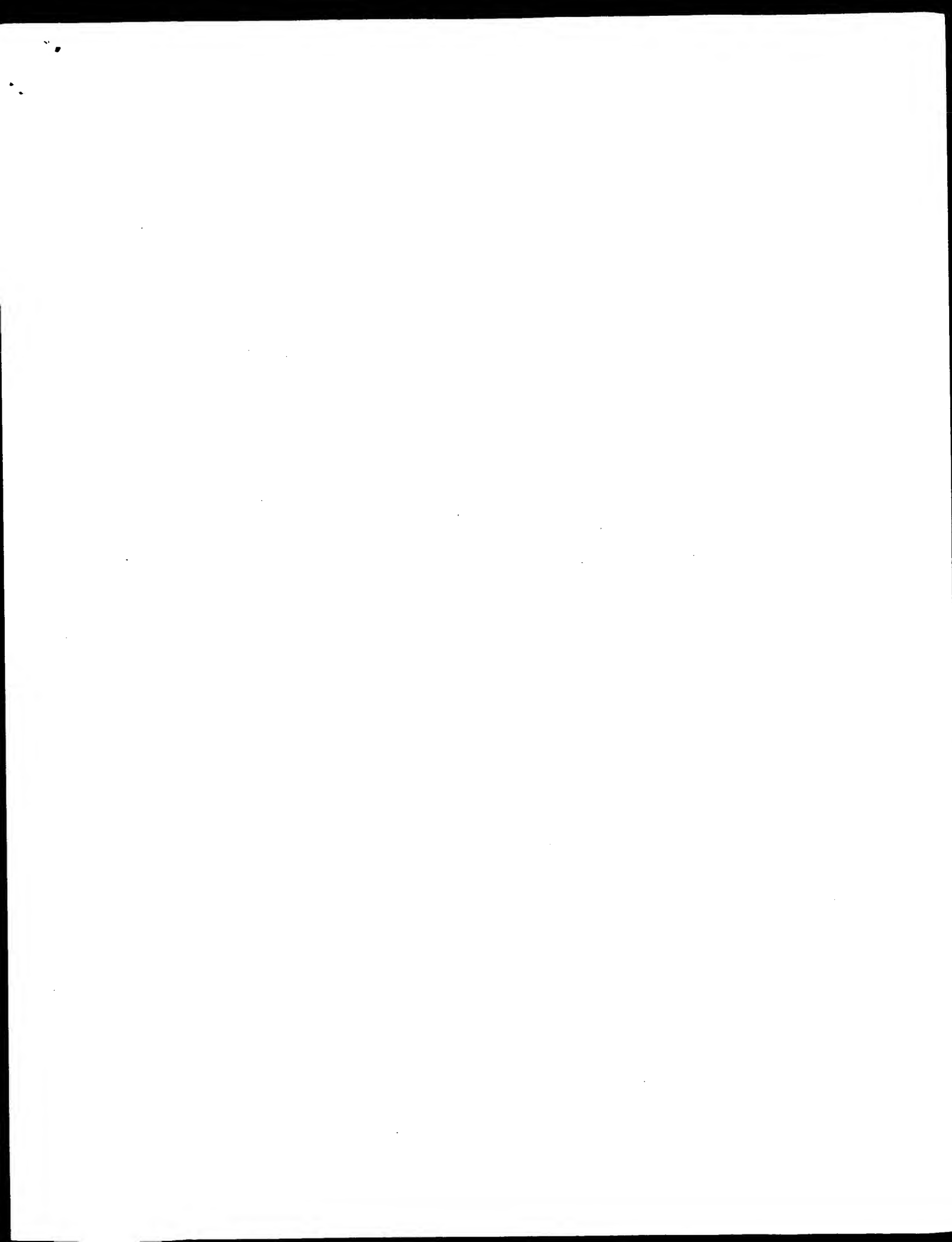
XX The present invention describes an isolated antibody (Ab) that binds to  
CC one of the human proteins (P) designated PRO213, PRO1310, PRO1449,  
CC PRO237, PRO324, PRO351, PRO362, PRO615, PRO531, PRO364, PRO618,  
CC PRO772, PRO703, PRO792 or PRO474. The Ab can be used in compositions  
CC and methods for the diagnosis and treatment of neoplastic cell growth  
CC and proliferation in mammals, including humans. Genes and polypeptides  
CC encoded by them, that are amplified in the genome of a tumour cell, can  
CC be identified and are useful targets for the treatment and prevention of  
CC certain cancers and may be used to monitor tumour treatment. Compounds  
CC that inhibit the expression or activity of the identified polypeptides  
CC can be identified and used as antagonists. Benign or malignant tumours,  
CC inflammatory disorders and immunological disorders can be treated.  
CC AAC58123 to AAC58224 represent hybridisation probes and PCR primers used  
CC in the isolation of the human PRO sequences. AAC58225 to AAC58241 and  
CC AAB24041 to AAB24056 represent human PRO polynucleotide and protein  
CC sequences given in the exemplification of the present invention.

XX Sequence 273 AA;

XX Query Match 99.9%; Score 1504; DB 21; Length 273;

XX Best Local Similarity 99.6%; Pred. No. 1.2e-94;  
Matches 272; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRGSOEVLMLVLAAGTEHAHVRGRRVCAVRAHGDVSESFVQRYVQPFLLTCDGHR 60  
DB 1 MRGSOEVLMLVLAAGTEHAHVRGRRVCAVRAHGDVSESFVQRYVQPFLLTCDGHR 60  
QY 61 ACSTYRTIYTAHRSRPGAPAPRRYACCPGWRKTSGLPGACGAACIQPCRNAGSCVOP 120  
DB 61 ACSTYRTIYTAHRSRPGAPAPRRYACCPGWRKTSGLPGACGAACIQPCRNAGSCVOP 120  
QY 121 GRRCPCAGMGRDTCOSDVDECSARRGGCPQRCVNTAGSTWCCMGHSLSADGTLCPK 180  
DB 121 GRRCPCAGMGRDTCOSDVDECSARRGGCPQRCVNTAGSTWCCMGHSLSADGTLCPK 180  
QY 181 GPPRVAHPNPTGVDSAMKEEVORLQSRVDLEERKQLVLAFLHSLASQALEHGLPDPSLL 240  
DB 181 GPPRVAHPNPTGVDSAMKEEVORLQSRVDLEERKQLVLAFLHSLASQALEHGLPDPSLL 240  
QY 241 VHSFQOLGRIDSLSEQISFLERQLSGSCCKDS 273  
DB 241 VHSFQOLGRIDSLSEQISFLERQLSGSCCKDS 273



GenCore version 5.1.3  
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 17, 2002, 10:00:46 ; Search time 13.4687 Seconds  
(without alignments)  
596.380 Million cell updates/sec

Title: US-09-852-472-2

Perfect score: 1505  
Sequence: 1 MRGSEVLLMMLVLA VSGT.....SEQISFLEQLGSCCKKD 273

Scoring table:  
Gapop 10.0, Gapext 0.5

Searched: 262574 seqs, 2942292 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database:

1: /cgn2\_6/ptodata/1/1aa/5A.COMB.pdp.\*  
2: /cgn2\_6/ptodata/1/1aa/5B.COMB.pdp.\*  
3: /cgn2\_6/ptodata/1/1aa/6A.COMB.pdp.\*  
4: /cgn2\_6/ptodata/1/1aa/6B.COMB.pdp.\*  
5: /cgn2\_6/ptodata/1/1aa/PTUS.COMB.pdp.\*  
6: /cgn2\_6/ptodata/1/1aa/backfile1.pdp.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	1181	78.5	4 US-09-724-864-52	Sequence 52, Appl
2	255.5	17.0	4 US-09-249-697A-6	Sequence 6, Appl
3	255.5	17.0	4 US-09-363-316B-6	Sequence 6, Appl
4	252.5	16.8	4 US-09-249-697A-19	Sequence 19, Appl
5	252.5	16.8	4 US-09-363-316B-24	Sequence 24, Appl
6	217.5	14.5	4 US-09-363-316B-18	Sequence 18, Appl
7	217.5	14.5	4 US-09-249-697A-4	Sequence 4, Appl
8	217.5	14.5	4 US-09-363-316B-4	Sequence 4, Appl
9	216.5	14.4	4 US-09-249-697A-3	Sequence 3, Appl
10	216.5	14.4	4 US-09-363-316B-3	Sequence 3, Appl
11	195	13.0	4 US-09-467-997-1	Sequence 1, Appl
12	189	12.6	4 US-08-282-141-2	Sequence 2, Appl
13	189	12.6	4 US-08-435-434-2	Sequence 2, Appl
14	189	12.6	4 US-08-435-436-2	Sequence 2, Appl
15	189	12.6	4 US-08-438-863-2	Sequence 2, Appl
16	189	12.6	4 US-08-438-864-2	Sequence 2, Appl
17	189	12.6	4 US-08-438-862-2	Sequence 2, Appl
18	189	12.6	4 US-08-628-747-2	Sequence 2, Appl
19	189	12.6	4 US-08-402-253-2	Sequence 2, Appl
20	189	12.6	4 US-08-443-866B-2	Sequence 2, Appl
21	184	12.2	4 US-08-282-141-3	Sequence 3, Appl
22	184	12.2	4 US-08-435-434-1	Sequence 1, Appl
23	184	12.2	4 US-08-435-436-1	Sequence 1, Appl
24	184	12.2	4 US-08-438-863-1	Sequence 1, Appl
25	184	12.2	4 US-08-438-864-1	Sequence 1, Appl
26	184	12.2	4 US-08-438-862-1	Sequence 1, Appl
27	184	12.2	4 US-08-628-747-1	Sequence 1, Appl

28	184	12.2	673	4 US-08-402-253-1	Sequence 1, Appl
29	184	12.2	673	4 US-08-443-866B-1	Sequence 1, Appl
30	183	12.2	810	3 US-08-820-170A-34	Sequence 34, Appl
31	183	12.2	810	3 US-09-055-699-34	Sequence 34, Appl
32	183	12.2	810	4 US-09-273-565-34	Sequence 34, Appl
33	183	12.2	810	4 US-09-565-538-34	Sequence 34, Appl
34	183	12.2	810	4 US-09-661-468-34	Sequence 34, Appl
35	181.5	12.1	816	2 US-08-820-170A-37	Sequence 37, Appl
36	181.5	12.1	816	3 US-09-055-699-37	Sequence 37, Appl
37	181.5	12.1	816	4 US-09-273-565-37	Sequence 37, Appl
38	181.5	12.1	816	4 US-09-565-538-37	Sequence 37, Appl
39	181.5	12.1	816	4 US-09-661-468-37	Sequence 37, Appl
40	176	11.7	652	2 US-08-751-305-2	Sequence 2, Appl
41	176	11.7	2703	1 US-08-185-432-19	Sequence 19, Appl
42	176	11.7	2703	4 US-08-899-232-4	Sequence 2, Appl
43	173.5	11.5	1833	3 US-08-479-722B-2	Sequence 2, Appl
44	173.5	11.5	1833	5 PCT-US95-02251-18	Sequence 18, Appl
45	169	11.2	830	3 US-08-872-855-11	Sequence 11, Appl

## ALIGNMENTS

RESULT 1  
US-09-724-864-52  
Sequence 52, Application US/09724864  
Patent No. 6380362  
GENERAL INFORMATION:  
APPLICANT: Watson, James D.  
TITLE OF INVENTION: Polynucleotides, polypeptides expressed  
TITLE OF INVENTION: By the polynucleotides and methods for their use.  
FILE REFERENCE: 11000, 105001  
CURRENT APPLICATION NUMBER: US/09/724,864  
CURRENT FILING DATE: 2000-11-28  
PRIOR APPLICATION NUMBER: U.S. No. 6380362 60/171,678  
NUMBER OF SEQ ID NOS: 2  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 52  
LENGTH: 278  
TYPE: PRT  
ORGANISM: Mouse  
US-09-724-864-52

Query Match 78.5%; Score 1181; DB 4; Length 278;  
Best Local Similarity 78.1%; Pred. No. 8.1e-87;

Matches 214; Conservative 18; Mismatches 40; Indels 2; Gaps 2;

QY 1 MRGSEVLLMMLVLA VSG-TEHAYRPGRRVCAVAHAGDPVSESFVORVOPFLTTCGH 59  
DB 4 MMSGSLVLA WLVLAADOTTHVYRPSRVCTVIGISGSISETIVQRYOPLTTCGH 63  
QY 60 RACSTYRTTYRATYRPSRGLAPARPRVACCPGKRTSGIPGACGAIICOPPRNGSCVQ 119  
DB 64 RACSTYRTTYRATYRPSRGLAPARPRVACCPGKRTSGIPGACGAIICOPPRNGSCVQ 123  
QY 120 PRCPCPGWRSDTQOSVDECSARGGCPQRCVNTTASVYCCQCHGSLADGTLCPK 179  
DB 124 PRCPCPGWRSDTQOSVDECSARGGCPQRCVNTTASVYCCQCHGSLADGTLCPK 183  
QY 180 GSPRPVAPNT-GVDSAMKEEYORLQSHVLDLEKLCVLA PLHSLSAQLHGLPDPGS 238  
DB 184 EGPSPVAPNTGVDVSMAREEYVRLQARVVDLEKLCVLA PLHSLSAQLHGLPDPGS 243  
QY 233 LLVHSFOQLGRIDSLEQISFLEQLGSCCKD 272  
DB 244 LLVHSFOQLGRIDSLEQISFLEQLGSCCKD 277

RESULT 2  
US-09-249-697A-6  
Sequence 6, Application US/09249697A



```
; PRIOR APPLICATION NUMBER: US 08/966,800
; PRIOR FILING DATE: 1997-11-22
; NUMBER OF SEQ ID NOS : 19
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 537
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(537)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-249-697A-4

Query Match          14.5%; Score 217.5; DB 4; Length 537;
Best Local Similarity 40.2%; Pred. No. 9.ee-10;
Matches   49; Conservative    9; Mismatches  35; Indels   29; Gaps        6;

QY      91 GWKRTSGLDGACGAATICOPPCRNCGSCVQPGRCRCPAGWRBGDTQQSDVDCECSARRGCPQ 150
Db       1 GWRRNS--KGVC-EATTCERGCK-FEECVGNPKRCRCPFYTGTCTOSQDVNECGMKPRPCH 56
               |||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
QY     151 RCNVTAGSYWCOCWEHSHLSADGITLV-----PKGGPP---RVAA 186
Db      57 RCVNTGSIXKCFLCGLSGHMLMPDAT-CVNSTRICAMINCQYSCEPTTBSPQCCLPSSSLRLIA 115
              |||||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
```

```

RESULT 8
US-09-363-316B-4
: Sequence 4, Application US/09363316B
: Patent No. 6392019
: GENERAL INFORMATION:
: APPLICANT: Ford, John
: APPLICANT: Yeung, George
: TITLE OF INVENTION: EGF MOTIF PROTEIN MATERIALS AND METHODS
: FILE REFERENCE: 28110/35852
: CURRENT APPLICATION NUMBER: US/09/363,316B
: CURRENT FILING DATE: 1999-07-28
: PRIOR APPLICATION NUMBER: US 09/249,697
: PRIOR FILING DATE: 1999-02-12
: PRIOR APPLICATION NUMBER: US 08/968,800
: PRIOR FILING DATE: 1997-11-22
: NUMBER OF SEQ ID NOS: 24
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 4
: LENGTH: 537
: TYPE: PRT
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (503)
: OTHER INFORMATION: Xaa = any amino acid
US-09-363-316B-4

Query Match          14.5%, Score 217.5, DB 4, Length 537;
Best Local Similarity 40.2%, Pred. No. 9, 6e-10;
Matches 49; Conservative 9; Mismatches 35; Indels 29; Gaps 6;

QY  GMRKSTGLGAGAGAIICDPCCRNNGSCVQPGRCRCPCAGMRGDPICQSDVDCEASRAGGCPQ 150
Db  1 GMRKRS-KGVC-EATCEPGCK-RFECVGPWKRCFPFGITGKICSDVDCEGMRKRPQCH 56
QY  RCVNTAGSYWCQCEWGHSLISADGTLCV-----PKGGPP-----RVA 186
Db  57 RCVNTAGSYKCCFLSGHMLMPDAR-CVNSRTCAMINCQYECDEPTBEGPQCLCPSSGLRLA 115
QY  187 EN 188
Db  116 EN 117

```

## RESULT 9

US-09-249-697A-3

; Sequence 3, Application US/09249697A

; Patent No. 6392018

; GENERAL INFORMATION:

; APPLICANT: Ford, John

; TITLE OF INVENTION: NOVEL EGF MOTIF PROTEIN OBTAINED FROM A CDNA LIBRARY OF FETAL

; FILE REFERENCE: 24011-727

; CURRENT APPLICATION NUMBER: US/09/249,697A

; CURRENT FILING DATE: 1999-02-12

; PRIOR APPLICATION NUMBER: US 08/968,800

; PRIOR FILING DATE: 1997-11-22

; NUMBER OF SEQ ID NOS: 19

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 3

; LENGTH: 100

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-249-697A-3

## Query Match

Best Local Similarity 14.4%; Score 216.5; DB 4; Length 100;

Matches 43; Conservative 7; Mismatches 32; Indels 5; Gaps 4;

Qy 91 GWKRTSGLPGACGAAICOPPCRNCGSCVQPCRCPCAGWRGDTQSDVDECSARRGGCPQ 150

Db 1 GWRNRS--KGVC-EATCEPGCK-FGECVGNKCRCFPGYTGKTCSDVNECGMKPRPCQH 56

Qy 151 RCVNTAGSYWCQCEGHSLSDGTLV 177

Db 57 RCVNTAGSYKCFCLSGHMLMPDAT-CV 82

## RESULT 10

US-09-363-316B-3

; Sequence 3, Application US/09363316B

; Patent No. 6392019

; GENERAL INFORMATION:

; APPLICANT: Ford, John

; TITLE OF INVENTION: EGF MOTIF PROTEIN MATERIALS AND METHODS

; FILE REFERENCE: 28110/35852

; CURRENT APPLICATION NUMBER: US/09/363,316B

; CURRENT FILING DATE: 1999-07-28

; PRIOR APPLICATION NUMBER: US 09/249,697

; PRIOR FILING DATE: 1999-02-12

; PRIOR APPLICATION NUMBER: US 08/968,800

; PRIOR FILING DATE: 1997-11-22

; NUMBER OF SEQ ID NOS: 24

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 3

; LENGTH: 100

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-363-316B-3

## Query Match

Best Local Similarity 14.4%; Score 216.5; DB 4; Length 100;

Matches 43; Conservative 7; Mismatches 32; Indels 5; Gaps 4;

Qy 91 GWKRTSGLPGACGAAICOPPCRNCGSCVQPCRCPCAGWRGDTQSDVDECSARRGGCPQ 150

Db 1 GWRNRS--KGVC-EATCEPGCK-FGECVGNKCRCFPGYTGKTCSDVNECGMKPRPCQH 56

Qy 151 RCVNTAGSYWCQCEGHSLSDGTLV 177

Db 57 RCVNTAGSYKCFCLSGHMLMPDAT-CV 82

## RESULT 11

US-09-467-997-1

; Sequence 1, Application US/09467997

; Patent No. 6379925

; GENERAL INFORMATION:

; APPLICANT: Kitajewski, Jan

; APPLICANT: Uyttendaele, Hendrik

; TITLE OF INVENTION: ANGIOGENIC MODULATION BY NOTCH SIGNAL TRANSDUCTION

; FILE REFERENCE: 53863-A-PCT-US

; CURRENT APPLICATION NUMBER: US/09/467,997

; CURRENT FILING DATE: 1999-12-20

; NUMBER OF SEQ ID NOS: 10

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 1

; LENGTH: 1964

; TYPE: PRT

; ORGANISM: mouse

US-09-467-997-1

## Query Match

Best Local Similarity 13.0%; Score 196; DB 4; Length 1964;

Matches 50; Conservative 12; Mismatches 54; Indels 30; Gaps 7;

Qy 80 AFAPRYVACCPGWK-RTSGLPGACGAAICOPPCRNCGSCVQPG---RCRCPCAGWRGDTQ 135

Db 134 ASGRFQCCEPWTGECQLRDFCSA----NPCANGGVCLATYFQIQCRCPFGEGHTCE 189

Qy 136 SDVDECSARRGGCPQ--RCVNTAGSYWCQ---WEGHSLSDGTLVCP---KGGPRVA 186

Db 190 RDINECFLEPGFCPGTSGHNTLGSYQCLFVQGGPQCKLRKKGACPPGSLNGGTCLV 249

Qy 187 PNP-----TGVDSAMKEE 199

Db 250 PEGHSTFHLCLCPGFTGLDCEMNP 275

## RESULT 12

US-08-282-141-2

; Sequence 2, Application US/08282141

; Patent No. 5538861

; GENERAL INFORMATION:

; APPLICANT: Schneider, Claudio

; APPLICANT: Varnum, Brian

; APPLICANT: Avanzi, Giancarlo

; APPLICANT: Brancolini, Claudio

; TITLE OF INVENTION: Stimulating Factor for the AXL Receptor

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Amgen Inc.

; STREET: 1840 DeHavilland Drive

; CITY: Thousand Oaks

; STATE: California

; COUNTRY: United States

; ZIP: 91320-1789

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/282,141

; FILING DATE:

; CLASSIFICATION: 435

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 678 amino acids

; TYPE: amino acid

; STRANDEDNESS: unknown

; TOPOLOGY: unknown

; MOLECULE TYPE: protein

US-08-282-141-2



Query Match 12.6%; Score 189; DB 1; Length 678;  
Best Local Similarity 34.2%; Pred. No. 2.3e-07;  
Matches 53; Conservative 8; Mismatches 64; Indels 30; Gaps 8;

QY 46 QRYVPEFLTCDG-----RACSTYRTYRTAYRSPGLAPRPYAC-----PGWK 93  
DB 47 RRAQVFEBAKQHLERECVELCS--REARAEVENDPETDYFPRYLDCKINKYSPYT 104  
QY 94 RTSG-----LPACGAATCQPPC-RNGGSCVOP--GR--CRCPAGWRGDTQSDVDEC 141  
DB 105 KNSGFATCVQNLDPQC-----TPNFCDRKGTQACQDLMGNFCLCKAGWGRLCDKDVNEC 160  
QY 142 SARRGCPQRCVNTAGSYWCQWEGHSLADGTLIC 176  
DB 161 SQENGGLQICHNKPGRSFHCSHGFEISDGRTC 195

## RESULT 13

US-08-435-434-2  
Sequence 2, Application US/08435434  
Patent No. 5714385  
GENERAL INFORMATION:  
APPLICANT: Mather, Jennie P.  
APPLICANT: Li, Ronghao  
APPLICANT: Chen, Jian  
TITLE OF INVENTION: ISOLATING AND CULTURING SCHWANN CELLS  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: patin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/435,434  
FILING DATE: 10-MAY-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Lee, Wendy M.  
REGISTRATION NUMBER: 00,000  
REFERENCE/DOCKET NUMBER: 946-2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/225-1994  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 678 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-435-434-2

Query Match 12.6%; Score 189; DB 1; Length 678;  
Best Local Similarity 34.2%; Pred. No. 2.3e-07;  
Matches 53; Conservative 8; Mismatches 64; Indels 30; Gaps 8;

QY 46 QRYVPEFLTCDG-----RACSTYRTYRTAYRSPGLAPRPYAC-----PGWK 93  
DB 47 RRAQVFEBAKQHLERECVELCS--REARAEVENDPETDYFPRYLDCKINKYSPYT 104  
QY 94 RTSG-----LPACGAATCQPPC-RNGGSCVOP--GR--CRCPAGWRGDTQSDVDEC 141  
DB 105 KNSGFATCVQNLDPQC-----TPNFCDRKGTQACQDLMGNFCLCKAGWGRLCDKDVNEC 160

QY 142 SARRGCPQRCVNTAGSYWCQWEGHSLADGTLIC 176  
DB 161 SQENGGLQICHNKPGRSFHCSHGFEISDGRTC 195

## RESULT 14

US-08-435-436-2  
Sequence 2, Application US/08435436  
Patent No. 5721139  
GENERAL INFORMATION:  
APPLICANT: Mather, Jennie P.  
APPLICANT: Li, Ronghao  
APPLICANT: Chen, Jian  
TITLE OF INVENTION: ISOLATING AND CULTURING SCHWANN CELLS  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: patin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/435,436  
FILING DATE: 10-MAY-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Lee, Wendy M.  
REGISTRATION NUMBER: 00,000  
REFERENCE/DOCKET NUMBER: 946-3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/225-1994  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 678 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-435-436-2

Query Match 12.6%; Score 189; DB 1; Length 678;  
Best Local Similarity 34.2%; Pred. No. 2.3e-07;  
Matches 53; Conservative 8; Mismatches 64; Indels 30; Gaps 8;

QY 46 QRYVPEFLTCDG-----RACSTYRTYRTAYRSPGLAPRPYAC-----PGWK 93  
DB 47 RRAQVFEBAKQHLERECVELCS--REARAEVENDPETDYFPRYLDCKINKYSPYT 104  
QY 94 RTSG-----LPACGAATCQPPC-RNGGSCVOP--GR--CRCPAGWRGDTQSDVDEC 141  
DB 105 KNSGFATCVQNLDPQC-----TPNFCDRKGTQACQDLMGNFCLCKAGWGRLCDKDVNEC 160  
QY 142 SARRGCPQRCVNTAGSYWCQWEGHSLADGTLIC 176  
DB 161 SQENGGLQICHNKPGRSFHCSHGFEISDGRTC 195

## RESULT 15

US-08-438-863-2  
Sequence 2, Application US/08438863  
Patent No. 5849585  
GENERAL INFORMATION:  
APPLICANT: Mather, Jennie P.  
APPLICANT: Ronghao Li



GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 17, 2002, 10:03:07 ; Search time 8.80645 Seconds  
(without alignments)  
516.533 Million cell updates/sec

Title: US-09-852-472-2  
Perfect score: 1505  
Sequence: 1 MRSQEVLMILVAVGCT.....SEQISFLEQLGSCCKKDS 273

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 105981 segs, 16662342 residues  
Total number of hits satisfying chosen parameters: 105981

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA.\*  
1: /cgn2\_6/ptodata/2/pubppaa/US08\_NEW\_PUB.pep.\*  
2: /cgn2\_6/ptodata/2/pubppaa/PCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/2/pubppaa/US06\_NEW\_PUB.pep.\*  
4: /cgn2\_6/ptodata/2/pubppaa/US07\_NEW\_PUB.pep.\*  
5: /cgn2\_6/ptodata/2/pubppaa/US07\_PUBCOMB.pep.\*  
6: /cgn2\_6/ptodata/2/pubppaa/US07\_PUBCOMB.pep.\*  
7: /cgn2\_6/ptodata/2/pubppaa/PCTUS\_PUBCOMB.pep.\*  
8: /cgn2\_6/ptodata/2/pubppaa/US08\_PUBCOMB.pep.\*  
9: /cgn2\_6/ptodata/2/pubppaa/US09\_PUBCOMB.pep.\*  
10: /cgn2\_6/ptodata/2/pubppaa/US10\_NEW\_PUB.pep.\*  
11: /cgn2\_6/ptodata/2/pubppaa/US10\_PUBCOMB.pep.\*  
12: /cgn2\_6/ptodata/2/pubppaa/US60\_PUBCOMB.pep.\*  
13: /cgn2\_6/ptodata/2/pubppaa/US60\_PUBCOMB.pep.\*  
14: /cgn2\_6/ptodata/2/pubppaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1505	100.0	273	US-09-978-295A-510	Sequence 510, App
2	1505	100.0	273	US-09-978-697-510	Sequence 510, App
3	1505	100.0	273	US-09-978-192A-510	Sequence 510, App
4	1504	99.9	273	US-09-978-295A-506	Sequence 506, App
5	1504	99.9	273	US-09-978-295A-508	Sequence 508, App
6	1504	99.9	273	US-09-978-697-506	Sequence 506, App
7	1504	99.9	273	US-09-978-697-508	Sequence 508, App
8	1504	99.9	273	US-09-978-192A-506	Sequence 508, App
9	1504	99.9	273	US-09-978-192A-508	Sequence 508, App
10	1504	99.9	273	US-09-978-192A-508	Sequence 508, App
11	1392	92.5	251	US-09-790-264-10	Sequence 10, Appl
12	1340.5	89.1	295	US-09-978-295A-2	Sequence 12, Appl
13	1340.5	89.1	295	US-09-978-697-2	Sequence 2, Appl
14	1340.5	89.1	295	US-09-978-192A-2	Sequence 2, Appl
15	1181	78.5	275	US-09-790-264-15	Sequence 15, Appl
16	945.5	62.8	287	US-09-764-898-218	Sequence 218, App
17	945.5	62.8	288	US-09-764-853-841	Sequence 841, App
18	945.5	62.8	288	US-09-764-898-290	Sequence 290, App
19	945.5	62.8	314	US-09-764-853-670	Sequence 670, App

20	919.5	61.1	247	10	US-09-790-264-20	Sequence 20, Appl
21	255.5	17.0	533	9	US-09-981-649A-6	Sequence 6, Appl
22	252.5	16.8	338	9	US-09-978-295A-119	Sequence 119, App
23	252.5	16.8	338	9	US-09-978-697-119	Sequence 119, App
24	252.5	16.8	338	9	US-09-978-192A-119	Sequence 119, App
25	252.5	16.8	553	10	US-09-981-649A-24	Sequence 24, Appl
26	252.5	16.8	554	10	US-09-981-649A-32	Sequence 32, Appl
27	250.5	16.6	554	10	US-09-981-649A-30	Sequence 30, Appl
28	250.5	16.6	559	9	US-09-981-649A-28	Sequence 28, Appl
29	223	14.8	509	10	US-09-905-291A-315	Sequence 315, App
30	223	14.8	509	10	US-09-909-320-315	Sequence 315, App
31	223	14.8	509	10	US-09-909-088B-315	Sequence 315, App
32	223	14.8	509	12	US-10-052-598A-52	Sequence 52, Appl
33	217.5	14.5	502	10	US-09-981-649A-18	Sequence 18, Appl
34	217.5	14.5	537	10	US-09-981-649A-4	Sequence 4, Appl
35	216.5	14.4	100	10	US-09-981-649A-3	Sequence 3, Appl
36	207	13.8	201	10	US-09-764-853-797	Sequence 797, App
37	207	13.8	201	10	US-09-764-898-270	Sequence 270, App
38	184	12.2	652	10	US-09-789-919-96	Sequence 96, Appl
39	183	12.2	810	10	US-09-976-165-34	Sequence 34, Appl
40	181.5	12.1	816	10	US-09-976-165-37	Sequence 37, Appl
41	173.5	11.5	1246	10	US-09-919-497-85	Sequence 85, Appl
42	172	11.4	534	10	US-09-804-156-14	Sequence 14, Appl
43	172	11.4	534	10	US-09-946-633-6	Sequence 6, Appl
44	169	11.2	1055	10	US-09-855-722-2	Sequence 2, Appl
45	166	11.0	1212	10	US-09-855-722-3	Sequence 3, Appl

## ALIGNMENTS

RESULT 1  
US-09-978-295A-510  
; Sequence 510, Application US/09978295A  
; Patent No. US20020156006A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Bocstein, David  
; APPLICANT: Deamoysers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gottlieb, Mary E.  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Shelton, David L.  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2630P1C11  
; CURRENT FILING DATE: US/09/978, 295A  
; PRIOR APPLICATION NUMBER: 2001-10-15  
; PRIOR FILING DATE: 2001-07-30  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/064249

;	PRIOR APPLICATION NUMBER: 60/081817
;	PRIOR FILING DATE: 1998-04-15
;	PRIOR APPLICATION NUMBER: 60/081819
;	PRIOR FILING DATE: 1998-04-15
;	PRIOR APPLICATION NUMBER: 60/081952
;	PRIOR FILING DATE: 1998-04-15
;	PRIOR APPLICATION NUMBER: 60/081838
;	PRIOR FILING DATE: 1998-04-15
;	PRIOR APPLICATION NUMBER: 60/082568
;	PRIOR FILING DATE: 1998-04-21
;	PRIOR APPLICATION NUMBER: 60/082569
;	PRIOR FILING DATE: 1998-04-21
;	PRIOR APPLICATION NUMBER: 60/082704
;	PRIOR FILING DATE: 1998-04-22
;	PRIOR APPLICATION NUMBER: 60/082804
;	PRIOR FILING DATE: 1998-04-22
;	PRIOR APPLICATION NUMBER: 60/082700
;	PRIOR FILING DATE: 1998-04-22
;	PRIOR APPLICATION NUMBER: 60/082799
;	PRIOR FILING DATE: 1998-04-22
;	PRIOR APPLICATION NUMBER: 60/082796
;	PRIOR FILING DATE: 1998-04-23
;	PRIOR APPLICATION NUMBER: 60/083336
;	PRIOR FILING DATE: 1998-04-27
;	PRIOR APPLICATION NUMBER: 60/083322
;	PRIOR FILING DATE: 1998-04-28
;	PRIOR APPLICATION NUMBER: 60/083392
;	PRIOR FILING DATE: 1998-04-29
;	PRIOR APPLICATION NUMBER: 60/083495
;	PRIOR FILING DATE: 1998-04-29
;	PRIOR APPLICATION NUMBER: 60/083496
;	PRIOR FILING DATE: 1998-04-29
;	PRIOR APPLICATION NUMBER: 60/083499
;	PRIOR FILING DATE: 1998-04-29
;	PRIOR APPLICATION NUMBER: 60/083545
;	PRIOR FILING DATE: 1998-04-29
;	PRIOR APPLICATION NUMBER: 60/083554
;	PRIOR FILING DATE: 1998-04-29
;	PRIOR APPLICATION NUMBER: 60/083558
;	PRIOR FILING DATE: 1998-04-29
;	PRIOR APPLICATION NUMBER: 60/083559
;	PRIOR FILING DATE: 1998-04-29
;	PRIOR APPLICATION NUMBER: 60/083500
;	PRIOR FILING DATE: 1998-04-29
;	PRIOR APPLICATION NUMBER: 60/083742
;	PRIOR FILING DATE: 1998-04-30
;	PRIOR APPLICATION NUMBER: 60/084366
;	PRIOR FILING DATE: 1998-05-05
;	PRIOR APPLICATION NUMBER: 60/084414
;	PRIOR FILING DATE: 1998-05-06
;	PRIOR APPLICATION NUMBER: 60/084441
;	PRIOR FILING DATE: 1998-05-06
;	PRIOR APPLICATION NUMBER: 60/084637
;	PRIOR FILING DATE: 1998-05-07
;	PRIOR APPLICATION NUMBER: 60/084639
;	PRIOR FILING DATE: 1998-05-07
;	PRIOR APPLICATION NUMBER: 60/084640
;	PRIOR FILING DATE: 1998-05-07
;	PRIOR APPLICATION NUMBER: 60/084598
;	PRIOR FILING DATE: 1998-05-07
;	PRIOR APPLICATION NUMBER: 60/084600
;	PRIOR FILING DATE: 1998-05-07
;	PRIOR APPLICATION NUMBER: 60/084627
;	PRIOR FILING DATE: 1998-05-07
;	PRIOR APPLICATION NUMBER: 60/084643
;	PRIOR FILING DATE: 1998-05-07
;	PRIOR APPLICATION NUMBER: 60/085339
;	PRIOR FILING DATE: 1998-05-13
;	PRIOR APPLICATION NUMBER: 60/085338
;	PRIOR FILING DATE: 1998-05-13
;	PRIOR APPLICATION NUMBER: 60/085323
;	PRIOR FILING DATE: 1998-05-13
;	PRIOR APPLICATION NUMBER: 60/085582

PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085700  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085689  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085579  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085580  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085573  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085704  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 1505; DB 9; Length 273;  
Best Local Similarity 100.0%; Pred. No. 1,2e+100;  
Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRSGOEVLMMVLVAVGTEHAYRGRVCANRAHGDVPSBSFVQRYQPTTCDGHR 60  
DB 1 MRSGOEVLMMVLVAVGTEHAYRGRVCANRAHGDVPSBSFVQRYQPTTCDGHR 60  
QY 61 ACSTYRTYATVARSFGLAPARPRYACCPGMRKTSGLPGACGAIICOPPCRRGSSCVQ 120  
DB 61 ACSTYRTYATVARSFGLAPARPRYACCPGMRKTSGLPGACGAIICOPPCRRGSSCVQ 120  
QY 121 GRRCPCAGWBDTCOSDVDECSARRGCPQRCVNTAGSYWCQCEHSHLSADDTLCVPGK 180  
DB 121 GRRCPCAGWBDTCOSDVDECSARRGCPQRCVNTAGSYWCQCEHSHLSADDTLCVPGK 180  
QY 181 GPRVAVNPFGVSNAMKEEVQRLQSRVDLLEKQLVLAHSLASQALHEGLPDPGSL 240  
DB 181 GPRVAVNPFGVSNAMKEEVQRLQSRVDLLEKQLVLAHSLASQALHEGLPDPGSL 240  
QY 241 VHSFOQLGRIDLSSEQISFLEQLGSCCKDS 273  
DB 241 VHSFOQLGRIDLSSEQISFLEQLGSCCKDS 273

RESULT 2  
US-09-978-697-510  
Sequence 510, Application US/09978697  
Patent No. US20020169284A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnovers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerlitsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2630PIC27  
CURRENT APPLICATION NUMBER: US/09/978,697  
CURRENT FILING DATE: 2001-10-16  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/064249  
PRIOR FILING DATE: 1997-11-03  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/066364  
PRIOR FILING DATE: 1997-11-21  
PRIOR APPLICATION NUMBER: 60/077450  
PRIOR FILING DATE: 1998-03-10  
PRIOR APPLICATION NUMBER: 60/077632  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077641  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077649  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077791  
PRIOR FILING DATE: 1998-03-12  
PRIOR APPLICATION NUMBER: 60/078004  
PRIOR FILING DATE: 1998-03-13  
PRIOR APPLICATION NUMBER: 60/078886  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/078936  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/078910  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/078939  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/079224  
PRIOR FILING DATE: 1998-03-25  
PRIOR APPLICATION NUMBER: 60/079656  
PRIOR FILING DATE: 1998-03-26  
PRIOR APPLICATION NUMBER: 60/079664  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/079689  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/079663  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/079728  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/079786  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/079920  
PRIOR FILING DATE: 1998-03-30  
PRIOR APPLICATION NUMBER: 60/079923  
PRIOR FILING DATE: 1998-03-30  
PRIOR APPLICATION NUMBER: 60/080105  
PRIOR FILING DATE: 1998-03-31  
PRIOR APPLICATION NUMBER: 60/080107  
PRIOR FILING DATE: 1998-03-31  
PRIOR APPLICATION NUMBER: 60/080165  
PRIOR FILING DATE: 1998-03-31  
PRIOR APPLICATION NUMBER: 60/080194  
PRIOR FILING DATE: 1998-03-31  
PRIOR APPLICATION NUMBER: 60/080327  
PRIOR FILING DATE: 1998-04-01  
PRIOR APPLICATION NUMBER: 60/080328  
PRIOR FILING DATE: 1998-04-01  
PRIOR APPLICATION NUMBER: 60/080333  
PRIOR FILING DATE: 1998-04-01  
PRIOR APPLICATION NUMBER: 60/080334  
PRIOR FILING DATE: 1998-04-01  
PRIOR APPLICATION NUMBER: 60/081070  
PRIOR FILING DATE: 1998-04-08  
PRIOR APPLICATION NUMBER: 60/081049  
PRIOR FILING DATE: 1998-04-08  
PRIOR APPLICATION NUMBER: 60/081071

PRIOR FILING DATE:	1998-04-08
PRIOR APPLICATION NUMBER:	60/081195
PRIOR FILING DATE:	1998-04-08
PRIOR APPLICATION NUMBER:	60/081203
PRIOR FILING DATE:	1998-04-09
PRIOR APPLICATION NUMBER:	60/081229
PRIOR FILING DATE:	1998-04-09
PRIOR APPLICATION NUMBER:	60/081955
PRIOR FILING DATE:	1998-04-15
PRIOR APPLICATION NUMBER:	60/081817
PRIOR FILING DATE:	1998-04-15
PRIOR APPLICATION NUMBER:	60/081819
PRIOR FILING DATE:	1998-04-15
PRIOR APPLICATION NUMBER:	60/081952
PRIOR FILING DATE:	1998-04-15
PRIOR APPLICATION NUMBER:	60/081838
PRIOR FILING DATE:	1998-04-15
PRIOR APPLICATION NUMBER:	60/082568
PRIOR FILING DATE:	1998-04-21
PRIOR APPLICATION NUMBER:	60/082569
PRIOR FILING DATE:	1998-04-21
PRIOR APPLICATION NUMBER:	60/082704
PRIOR FILING DATE:	1998-04-22
PRIOR APPLICATION NUMBER:	60/082804
PRIOR FILING DATE:	1998-04-22
PRIOR APPLICATION NUMBER:	60/082700
PRIOR FILING DATE:	1998-04-22
PRIOR APPLICATION NUMBER:	60/082797
PRIOR FILING DATE:	1998-04-22
PRIOR APPLICATION NUMBER:	60/082796
PRIOR FILING DATE:	1998-04-23
PRIOR APPLICATION NUMBER:	60/083336
PRIOR FILING DATE:	1998-04-27
PRIOR APPLICATION NUMBER:	60/083322
PRIOR FILING DATE:	1998-04-28
PRIOR APPLICATION NUMBER:	60/083392
PRIOR FILING DATE:	1998-04-29
PRIOR APPLICATION NUMBER:	60/083495
PRIOR FILING DATE:	1998-04-29
PRIOR APPLICATION NUMBER:	60/083496
PRIOR FILING DATE:	1998-04-29
PRIOR APPLICATION NUMBER:	60/083499
PRIOR FILING DATE:	1998-04-29
PRIOR APPLICATION NUMBER:	60/083545
PRIOR FILING DATE:	1998-04-29
PRIOR APPLICATION NUMBER:	60/083554
PRIOR FILING DATE:	1998-04-29
PRIOR APPLICATION NUMBER:	60/083558
PRIOR FILING DATE:	1998-04-29
PRIOR APPLICATION NUMBER:	60/083559
PRIOR FILING DATE:	1998-04-29
PRIOR APPLICATION NUMBER:	60/083500
PRIOR FILING DATE:	1998-04-29
PRIOR APPLICATION NUMBER:	60/083742
PRIOR FILING DATE:	1998-04-30
PRIOR APPLICATION NUMBER:	60/084366
PRIOR FILING DATE:	1998-05-05
PRIOR APPLICATION NUMBER:	60/084414
PRIOR FILING DATE:	1998-05-06
PRIOR APPLICATION NUMBER:	60/084441
PRIOR FILING DATE:	1998-05-06
PRIOR APPLICATION NUMBER:	60/084637
PRIOR FILING DATE:	1998-05-07
PRIOR APPLICATION NUMBER:	60/084639
PRIOR FILING DATE:	1998-05-07
PRIOR APPLICATION NUMBER:	60/084640
PRIOR FILING DATE:	1998-05-07
PRIOR APPLICATION NUMBER:	60/084598
PRIOR FILING DATE:	1998-05-07
PRIOR APPLICATION NUMBER:	60/084600
PRIOR FILING DATE:	1998-5-07
PRIOR APPLICATION NUMBER:	60/084627
PRIOR FILING DATE:	1998-05-07

;	PRIOR APPLICATION NUMBER: 60/084643	
;	PRIOR FILING DATE: 1998-05-07	
;	PRIOR APPLICATION NUMBER: 60/085339	
;	PRIOR FILING DATE: 1998-05-13	
;	PRIOR APPLICATION NUMBER: 60/085338	
;	PRIOR FILING DATE: 1998-05-13	
;	PRIOR APPLICATION NUMBER: 60/085323	
;	PRIOR FILING DATE: 1998-05-13	
;	PRIOR APPLICATION NUMBER: 60/085582	
;	PRIOR FILING DATE: 1998-05-15	
;	PRIOR APPLICATION NUMBER: 60/085700	
;	PRIOR FILING DATE: 1998-05-15	
;	PRIOR APPLICATION NUMBER: 60/085689	
;	PRIOR FILING DATE: 1998-05-15	
;	PRIOR APPLICATION NUMBER: 60/085579	
;	PRIOR FILING DATE: 1998-05-15	
;	PRIOR APPLICATION NUMBER: 60/085580	
;	PRIOR FILING DATE: 1998-05-15	
;	PRIOR APPLICATION NUMBER: 60/085573	
;	PRIOR FILING DATE: 1998-05-15	
;	PRIOR APPLICATION NUMBER: 60/085704	
;	PRIOR FILING DATE: 1998-05-15	
;	PRIOR APPLICATION NUMBER: 60/085697	
;		
Qy	Query Match	100.0%; Score 1505;
	Best Local Similarity	100.0%; Pred. No. 1.
	Matches	273; Conservative 0; Mismatches
Db	1 MRGQEVLLMMLLVLAAGTGHAYRPPGRVCAVRAHG	
Db	1 MRGQEVLLMMLLVLAAGTGHAYRPPGRVCAVRAHG	
Qy	61 ACSTVTTIYRTAYRRSPGLAPRYPYACCPGKWRTSGL	
Db	61 ACSTVTTIYRTAYRRSPGLAPRYPYACCPGKWRTSGL	
Qy	121 GRCCPAGRWGDTQCSVDDECSARRGGGPQR CVNTAG	
Db	121 GRCCPAGRWGDTQCSVDDECSARRGGGPQR CVNTAG	
Qy	181 GPPRVAPNPTGVDSAMKEVQRLOQRVDLLEEKQLV	
Db	181 GPPRVAPNPTGVDSAMKEVQRLOQRVDLLEEKQLV	
Qy	241 VHSFOQLGRIDSLSQISFLEEQLGSCSCCKDS	273
Db	241 VHSFOQLGRIDSLSQISFLEEQLGSCSCCKDS	273

### RESULT 3

```

US-09-378-192A-510
; Sequence 510, Application US/09978192A
;
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Paton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.

```

APPLICANT: Pan, James;  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: Acids Encoding the Same  
CURRENT APPLICATION NUMBER: P2630P1C9  
CURRENT FILING DATE: 2001-10-15  
PRIOR APPLICATION NUMBER: 09/916585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/064249  
PRIOR FILING DATE: 1997-11-03  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/066364  
PRIOR FILING DATE: 1997-11-21  
PRIOR APPLICATION NUMBER: 60/077450  
PRIOR FILING DATE: 1998-03-10  
PRIOR APPLICATION NUMBER: 60/077632  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077641  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077649  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077791  
PRIOR FILING DATE: 1998-03-12  
PRIOR APPLICATION NUMBER: 60/078004  
PRIOR FILING DATE: 1998-03-13  
PRIOR APPLICATION NUMBER: 60/078886  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/078936  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/078910  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/078939  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/079294  
PRIOR FILING DATE: 1998-03-25  
PRIOR APPLICATION NUMBER: 60/079656  
PRIOR FILING DATE: 1998-03-26  
PRIOR APPLICATION NUMBER: 60/079664  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/079689  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/079663  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/079728  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/079786  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/079920  
PRIOR FILING DATE: 1998-03-30  
PRIOR APPLICATION NUMBER: 60/079923  
PRIOR FILING DATE: 1998-03-30  
PRIOR APPLICATION NUMBER: 60/080105  
PRIOR FILING DATE: 1998-03-31  
PRIOR APPLICATION NUMBER: 60/080107  
PRIOR FILING DATE: 1998-03-31  
PRIOR APPLICATION NUMBER: 60/080165  
PRIOR FILING DATE: 1998-03-31  
PRIOR APPLICATION NUMBER: 60/080194  
PRIOR FILING DATE: 1998-03-31  
PRIOR APPLICATION NUMBER: 60/080327  
PRIOR FILING DATE: 1998-04-01  
PRIOR APPLICATION NUMBER: 60/080328  
PRIOR FILING DATE: 1998-04-01

PRIOR APPLICATION NUMBER: 60/080333  
PRIOR FILING DATE: 1998-04-01  
PRIOR APPLICATION NUMBER: 60/080334  
PRIOR FILING DATE: 1998-04-01  
PRIOR APPLICATION NUMBER: 60/081070  
PRIOR FILING DATE: 1998-04-08  
PRIOR APPLICATION NUMBER: 60/081049  
PRIOR FILING DATE: 1998-04-08  
PRIOR APPLICATION NUMBER: 60/081071  
PRIOR FILING DATE: 1998-04-08  
PRIOR APPLICATION NUMBER: 60/081195  
PRIOR FILING DATE: 1998-04-08  
PRIOR APPLICATION NUMBER: 60/081203  
PRIOR FILING DATE: 1998-04-09  
PRIOR APPLICATION NUMBER: 60/081229  
PRIOR FILING DATE: 1998-04-09  
PRIOR APPLICATION NUMBER: 60/081955  
PRIOR FILING DATE: 1998-04-15  
PRIOR APPLICATION NUMBER: 60/081817  
PRIOR FILING DATE: 1998-04-15  
PRIOR APPLICATION NUMBER: 60/081819  
PRIOR FILING DATE: 1998-04-15  
PRIOR APPLICATION NUMBER: 60/081952  
PRIOR FILING DATE: 1998-04-15  
PRIOR APPLICATION NUMBER: 60/081838  
PRIOR FILING DATE: 1998-04-15  
PRIOR APPLICATION NUMBER: 60/082568  
PRIOR FILING DATE: 1998-04-21  
PRIOR APPLICATION NUMBER: 60/082569  
PRIOR FILING DATE: 1998-04-21  
PRIOR APPLICATION NUMBER: 60/082704  
PRIOR FILING DATE: 1998-04-22  
PRIOR APPLICATION NUMBER: 60/082804  
PRIOR FILING DATE: 1998-04-22  
PRIOR APPLICATION NUMBER: 60/082700  
PRIOR FILING DATE: 1998-04-22  
PRIOR APPLICATION NUMBER: 60/082797  
PRIOR FILING DATE: 1998-04-22  
PRIOR APPLICATION NUMBER: 60/082796  
PRIOR FILING DATE: 1998-04-23  
PRIOR APPLICATION NUMBER: 60/083336  
PRIOR FILING DATE: 1998-04-27  
PRIOR APPLICATION NUMBER: 60/083322  
PRIOR FILING DATE: 1998-04-28  
PRIOR APPLICATION NUMBER: 60/083392  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083495  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083496  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083499  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083545  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083554  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083558  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083559  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083500  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083742  
PRIOR FILING DATE: 1998-04-30  
PRIOR APPLICATION NUMBER: 60/084366  
PRIOR FILING DATE: 1998-05-05  
PRIOR APPLICATION NUMBER: 60/084414  
PRIOR FILING DATE: 1998-05-06  
PRIOR APPLICATION NUMBER: 60/084441  
PRIOR FILING DATE: 1998-05-06  
PRIOR APPLICATION NUMBER: 60/084637  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/084639

us-09-852-472-2.rapb

Tue Dec 17 14:03:48 2002

PRIOR FILING DATE: 1998-05-07  
 PRIOR APPLICATION NUMBER: 60/084640  
 PRIOR FILING DATE: 1998-05-07  
 PRIOR APPLICATION NUMBER: 60/084598  
 PRIOR FILING DATE: 1998-05-07  
 PRIOR APPLICATION NUMBER: 60/084600  
 PRIOR FILING DATE: 1998-05-07  
 PRIOR APPLICATION NUMBER: 60/084627  
 PRIOR FILING DATE: 1998-05-07  
 PRIOR APPLICATION NUMBER: 60/084643  
 PRIOR FILING DATE: 1998-05-07  
 PRIOR APPLICATION NUMBER: 60/085339  
 PRIOR FILING DATE: 1998-05-13  
 PRIOR APPLICATION NUMBER: 60/085338  
 PRIOR FILING DATE: 1998-05-13  
 PRIOR APPLICATION NUMBER: 60/085323  
 PRIOR FILING DATE: 1998-05-13  
 PRIOR APPLICATION NUMBER: 60/085582  
 PRIOR FILING DATE: 1998-05-15  
 PRIOR APPLICATION NUMBER: 60/085700  
 PRIOR FILING DATE: 1998-05-15  
 PRIOR APPLICATION NUMBER: 60/085689  
 PRIOR FILING DATE: 1998-05-15  
 PRIOR APPLICATION NUMBER: 60/085579  
 PRIOR FILING DATE: 1998-05-15  
 PRIOR APPLICATION NUMBER: 60/085580  
 PRIOR FILING DATE: 1998-05-15  
 PRIOR APPLICATION NUMBER: 60/085573  
 PRIOR FILING DATE: 1998-05-15  
 PRIOR APPLICATION NUMBER: 60/085704  
 PRIOR FILING DATE: 1998-05-15  
 PRIOR APPLICATION NUMBER: 60/085697  
 PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 1505; DB 9; Length 273;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-100;  
 Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRGSEVLLMLLVAVGCTGHAYRPGRRVCAVRAHGDVPVSEFVQVQPLTTCDGHR 60  
 DB 1 MRGSEVLLMLLVAVGCTGHAYRPGRRVCAVRAHGDVPVSEFVQVQPLTTCDGHR 60  
 QY 61 ACSTYRTIYTRAYRSPGLAPARYACCPGWKRTSLPGACGAACIQQPCRNNGSCVOP 120  
 DB 61 ACSTYRTIYTRAYRSPGLAPARYACCPGWKRTSLPGACGAACIQQPCRNNGSCVOP 120  
 QY 121 GRCPAGWGDTCQSDVDECSARRGGCPQRCVNTAGSYWCQWEGHSLADGTLCPVKG 180  
 DB 121 GRCPAGWGDTCQSDVDECSARRGGCPQRCVNTAGSYWCQWEGHSLADGTLCPVKG 180  
 QY 181 GPRVAPNPTGVDSAMKEEVQRLQSRVDLLEKLQVLAPLHSLASQALEHGLPDPGSL 240  
 DB 181 GPRVAPNPTGVDSAMKEEVQRLQSRVDLLEKLQVLAPLHSLASQALEHGLPDPGSL 240  
 QY 241 VHSFQQLGRIDLSLEQISFLEEQLGSCCKKDS 273  
 DB 241 VHSFQQLGRIDLSLEQISFLEEQLGSCCKKDS 273

RESULT 4  
 US-09-978-295A-506  
 Sequence 506 Application US/09378295A  
 Patent No. US2002015606A1  
 GENERAL INFORMATION:  
 APPLICANT: Ashkenazi, Avi  
 APPLICANT: Baker Kevin P.  
 APPLICANT: Botstein, David  
 APPLICANT: Desnoyers, Luc  
 APPLICANT: Eaton, Dan  
 APPLICANT: Fertara, Napoleon  
 APPLICANT: Filvaroff, Ellen  
 APPLICANT: Fong, Sherman  
 APPLICANT: Gao, Wei-Qiang  
 APPLICANT: Gerber, Hanspeter

APPLICANT: Gerritsen, Mary E.  
 APPLICANT: Goddard, Audrey  
 APPLICANT: Godowski, Paul J.  
 APPLICANT: Grimaldi, J. Christopher  
 APPLICANT: Gurney, Austin L.  
 APPLICANT: Hillan, Kenneth J.  
 APPLICANT: Kijavlin, Ivar J.  
 APPLICANT: Kuo, Sophia S.  
 APPLICANT: Napier, Mary A.  
 APPLICANT: Pan, James  
 APPLICANT: Paoni, Nicholas F.  
 APPLICANT: Roy, Margaret Ann  
 APPLICANT: Shelton, David L.  
 APPLICANT: Stewart, Timothy A.  
 APPLICANT: Tumas, Daniel  
 APPLICANT: Williams, P. Mickey  
 APPLICANT: Wood, William I.  
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 FILE REFERENCE: P2630FIC11  
 CURRENT FILING DATE: 2001-10-15  
 PRIOR APPLICATION NUMBER: 09/918585  
 PRIOR FILING DATE: 2001-07-30  
 PRIOR APPLICATION NUMBER: 60/062250  
 PRIOR FILING DATE: 1997-10-17  
 PRIOR APPLICATION NUMBER: 60/064249  
 PRIOR FILING DATE: 1997-11-03  
 PRIOR APPLICATION NUMBER: 60/065311  
 PRIOR FILING DATE: 1997-11-13  
 PRIOR APPLICATION NUMBER: 60/066364  
 PRIOR FILING DATE: 1997-11-21  
 PRIOR APPLICATION NUMBER: 60/077450  
 PRIOR FILING DATE: 1998-03-10  
 PRIOR APPLICATION NUMBER: 60/077632  
 PRIOR FILING DATE: 1998-03-11  
 PRIOR APPLICATION NUMBER: 60/077641  
 PRIOR FILING DATE: 1998-03-11  
 PRIOR APPLICATION NUMBER: 60/077649  
 PRIOR FILING DATE: 1998-03-11  
 PRIOR APPLICATION NUMBER: 60/077791  
 PRIOR FILING DATE: 1998-03-12  
 PRIOR APPLICATION NUMBER: 60/078004  
 PRIOR FILING DATE: 1998-03-13  
 PRIOR APPLICATION NUMBER: 60/078886  
 PRIOR FILING DATE: 1998-03-20  
 PRIOR APPLICATION NUMBER: 60/078936  
 PRIOR FILING DATE: 1998-03-20  
 PRIOR APPLICATION NUMBER: 60/078910  
 PRIOR FILING DATE: 1998-03-20  
 PRIOR APPLICATION NUMBER: 60/078939  
 PRIOR FILING DATE: 1998-03-20  
 PRIOR APPLICATION NUMBER: 60/079294  
 PRIOR FILING DATE: 1998-03-25  
 PRIOR APPLICATION NUMBER: 60/079656  
 PRIOR FILING DATE: 1998-03-26  
 PRIOR APPLICATION NUMBER: 60/079664  
 PRIOR FILING DATE: 1998-03-27  
 PRIOR APPLICATION NUMBER: 60/079689  
 PRIOR FILING DATE: 1998-03-27  
 PRIOR APPLICATION NUMBER: 60/079663  
 PRIOR FILING DATE: 1998-03-27  
 PRIOR APPLICATION NUMBER: 60/079728  
 PRIOR FILING DATE: 1998-03-27  
 PRIOR APPLICATION NUMBER: 60/079786  
 PRIOR FILING DATE: 1998-03-27  
 PRIOR APPLICATION NUMBER: 60/079920  
 PRIOR FILING DATE: 1998-03-30  
 PRIOR APPLICATION NUMBER: 60/079923  
 PRIOR FILING DATE: 1998-03-30  
 PRIOR APPLICATION NUMBER: 60/080105  
 PRIOR FILING DATE: 1998-03-31  
 PRIOR APPLICATION NUMBER: 60/080107



PRIOR FILING DATE: 1998-03-31  
 PRIOR APPLICATION NUMBER: 60/080165  
 PRIOR FILING DATE: 1998-03-31  
 PRIOR APPLICATION NUMBER: 60/080194  
 PRIOR FILING DATE: 1998-03-31  
 PRIOR APPLICATION NUMBER: 60/080327  
 PRIOR FILING DATE: 1998-04-01  
 PRIOR APPLICATION NUMBER: 60/080328  
 PRIOR FILING DATE: 1998-04-01  
 PRIOR APPLICATION NUMBER: 60/080333  
 PRIOR FILING DATE: 1998-04-01  
 PRIOR APPLICATION NUMBER: 60/080334  
 PRIOR FILING DATE: 1998-04-01  
 PRIOR APPLICATION NUMBER: 60/081070  
 PRIOR FILING DATE: 1998-04-08  
 PRIOR APPLICATION NUMBER: 60/081049  
 PRIOR FILING DATE: 1998-04-08  
 PRIOR APPLICATION NUMBER: 60/081071  
 PRIOR FILING DATE: 1998-04-08  
 PRIOR APPLICATION NUMBER: 60/081195  
 PRIOR FILING DATE: 1998-04-08  
 PRIOR APPLICATION NUMBER: 60/081203  
 PRIOR FILING DATE: 1998-04-09  
 PRIOR APPLICATION NUMBER: 60/081229  
 PRIOR FILING DATE: 1998-04-09  
 PRIOR APPLICATION NUMBER: 60/081955  
 PRIOR FILING DATE: 1998-04-15  
 PRIOR APPLICATION NUMBER: 60/081817  
 PRIOR FILING DATE: 1998-04-15  
 PRIOR APPLICATION NUMBER: 60/081819  
 PRIOR FILING DATE: 1998-04-15  
 PRIOR APPLICATION NUMBER: 60/081952  
 PRIOR FILING DATE: 1998-04-15  
 PRIOR APPLICATION NUMBER: 60/081838  
 PRIOR FILING DATE: 1998-04-15  
 PRIOR APPLICATION NUMBER: 60/082568  
 PRIOR FILING DATE: 1998-04-21  
 PRIOR APPLICATION NUMBER: 60/082559  
 PRIOR FILING DATE: 1998-04-21  
 PRIOR APPLICATION NUMBER: 60/082704  
 PRIOR FILING DATE: 1998-04-22  
 PRIOR APPLICATION NUMBER: 60/082804  
 PRIOR FILING DATE: 1998-04-22  
 PRIOR APPLICATION NUMBER: 60/082700  
 PRIOR FILING DATE: 1998-04-22  
 PRIOR APPLICATION NUMBER: 60/082797  
 PRIOR FILING DATE: 1998-04-22  
 PRIOR APPLICATION NUMBER: 60/082796  
 PRIOR FILING DATE: 1998-04-23  
 PRIOR APPLICATION NUMBER: 60/083336  
 PRIOR FILING DATE: 1998-04-27  
 PRIOR APPLICATION NUMBER: 60/083322  
 PRIOR FILING DATE: 1998-04-28  
 PRIOR APPLICATION NUMBER: 60/083392  
 PRIOR FILING DATE: 1998-04-29  
 PRIOR APPLICATION NUMBER: 60/083495  
 PRIOR FILING DATE: 1998-04-29  
 PRIOR APPLICATION NUMBER: 60/083496  
 PRIOR FILING DATE: 1998-04-29  
 PRIOR APPLICATION NUMBER: 60/083499  
 PRIOR FILING DATE: 1998-04-29  
 PRIOR APPLICATION NUMBER: 60/083545  
 PRIOR FILING DATE: 1998-04-29  
 PRIOR APPLICATION NUMBER: 60/083554  
 PRIOR FILING DATE: 1998-04-29  
 PRIOR APPLICATION NUMBER: 60/083558  
 PRIOR FILING DATE: 1998-04-29  
 PRIOR APPLICATION NUMBER: 60/083559  
 PRIOR FILING DATE: 1998-04-29  
 PRIOR APPLICATION NUMBER: 60/083500  
 PRIOR FILING DATE: 1998-04-29  
 PRIOR APPLICATION NUMBER: 60/083742  
 PRIOR FILING DATE: 1998-04-30

PRIOR APPLICATION NUMBER: 60/084366  
 PRIOR FILING DATE: 1998-05-05  
 PRIOR APPLICATION NUMBER: 60/084414  
 PRIOR FILING DATE: 1998-05-06  
 PRIOR APPLICATION NUMBER: 60/084441  
 PRIOR FILING DATE: 1998-05-06  
 PRIOR APPLICATION NUMBER: 60/084637  
 PRIOR FILING DATE: 1998-05-07  
 PRIOR APPLICATION NUMBER: 60/084639  
 PRIOR FILING DATE: 1998-05-07  
 PRIOR APPLICATION NUMBER: 60/084640  
 PRIOR FILING DATE: 1998-05-07  
 PRIOR APPLICATION NUMBER: 60/084598  
 PRIOR FILING DATE: 1998-05-07  
 PRIOR APPLICATION NUMBER: 60/084600  
 PRIOR FILING DATE: 1998-05-07  
 PRIOR APPLICATION NUMBER: 60/084627  
 PRIOR FILING DATE: 1998-05-07  
 PRIOR APPLICATION NUMBER: 60/084643  
 PRIOR FILING DATE: 1998-05-07  
 PRIOR APPLICATION NUMBER: 60/085339  
 PRIOR FILING DATE: 1998-05-13  
 PRIOR APPLICATION NUMBER: 60/085338  
 PRIOR FILING DATE: 1998-05-13  
 PRIOR APPLICATION NUMBER: 60/085323  
 PRIOR FILING DATE: 1998-05-13  
 PRIOR APPLICATION NUMBER: 60/085582  
 PRIOR FILING DATE: 1998-05-15  
 PRIOR APPLICATION NUMBER: 60/085700  
 PRIOR FILING DATE: 1998-05-15  
 PRIOR APPLICATION NUMBER: 60/085689  
 PRIOR FILING DATE: 1998-05-15  
 PRIOR APPLICATION NUMBER: 60/085579  
 PRIOR FILING DATE: 1998-05-15  
 PRIOR APPLICATION NUMBER: 60/085580  
 PRIOR FILING DATE: 1998-05-15  
 PRIOR APPLICATION NUMBER: 60/085573  
 PRIOR FILING DATE: 1998-05-15  
 PRIOR APPLICATION NUMBER: 60/085704  
 PRIOR FILING DATE: 1998-05-15  
 PRIOR APPLICATION NUMBER: 60/085697

Query Match 99.9%; Score 1504; DB 9; Length 273;  
 Best Local Similarity 99.6%; Pred. No. 1.5e-100;  
 Matches 272; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRGSOEVLMMVLA VAGSTEHAYRPGRRVCARAHGDPVSESPVORYOPELTTCCGHR 60  
 DB 1 MRGSOEVLMMVLA VAGSTEHAYRPGRRVCARAHGDPVSESPVORYOPELTTCCGHR 60  
 QY 61 ACSTYRTIYRTAYRRSPGLAPARPRYACCPMKRTSGLPAGCGAATCOPPCRRNGSCVCP 120  
 DB 61 ACSTYRTIYRTAYRRSPGLAPARPRYACCPMKRTSGLPAGCGAATCOPPCRRNGSCVCP 120  
 QY 121 GRCRCAGMRGPTCCSDVDECSARRGGCPRCVNTAGSYWCQCEHGSLSADDTLCVPPG 180  
 DB 121 GRCRCAGMRGPTCCSDVDECSARRGGCPRCVNTAGSYWCQCEHGSLSADDTLCVPPG 180  
 QY 181 GPRVAPNPPTGVDSAMKEEYORLQSRVLDLEKQLVLAFLHSLASQALEHGLPDPGSL 240  
 DB 181 GPRVAPNPPTGVDSAMKEEYORLQSRVLDLEKQLVLAFLHSLASQALEHGLPDPGSL 240  
 QY 241 VHSFOQLGRIDSLSQISFLBEQJGSCCKKDS 273  
 DB 241 VHSFOQLGRIDSLSQISFLBEQJGSCCKKDS 273

RESULT 5  
 US-09-978-295A-508  
 Sequence 508, Application US/09978295A  
 Patent No. US20020156006A1  
 GENERAL INFORMATION:  
 APPLICANT: Aethkenazi, Avi

us-09-852-472-2.rapb

Tue Dec 17 14:03:48 2002

APPLICANT: Baker Kevin P.  
 APPLICANT: Botstein, David  
 APPLICANT: Desnoyers, Luc  
 APPLICANT: Eaton, Dan  
 APPLICANT: Ferrara, Napoleon  
 APPLICANT: Filvaroff, Ellen  
 APPLICANT: Fong, Sherman  
 APPLICANT: Gao, Wei-Qiang  
 APPLICANT: Gerber, Hanspeter  
 APPLICANT: Gerritsen, Mary E.  
 APPLICANT: Goddard, Audrey  
 APPLICANT: Godowski, Paul J.  
 APPLICANT: Grimaldi, J. Christopher  
 APPLICANT: Gurney, Austin L.  
 APPLICANT: Hillan, Kenneth J.  
 APPLICANT: Kijavlin, Ivar J.  
 APPLICANT: Kuo, Sophia S.  
 APPLICANT: Napier, Mary A.  
 APPLICANT: Pan, James  
 APPLICANT: Paoni, Nicholas F.  
 APPLICANT: Roy, Margaret Ann  
 APPLICANT: Shelton, David L.  
 APPLICANT: Stewart, Timothy A.  
 APPLICANT: Tumas, Daniel  
 APPLICANT: Williams, P. Mickey  
 APPLICANT: Wood, William I.  
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 TITLE OF INVENTION: Acids Encoding the Same  
 FILE REFERENCE: P2630PIC11  
 CURRENT APPLICATION NUMBER: US/09/978,295A  
 CURRENT FILING DATE: 2001-10-15  
 PRIOR APPLICATION NUMBER: 09/918585  
 PRIOR FILING DATE: 2001-07-30  
 PRIOR APPLICATION NUMBER: 60/062250  
 PRIOR FILING DATE: 1997-10-17  
 PRIOR APPLICATION NUMBER: 60/064249  
 PRIOR FILING DATE: 1997-11-03  
 PRIOR APPLICATION NUMBER: 60/065311  
 PRIOR FILING DATE: 1997-11-13  
 PRIOR APPLICATION NUMBER: 60/066364  
 PRIOR FILING DATE: 1997-11-21  
 PRIOR APPLICATION NUMBER: 60/077450  
 PRIOR FILING DATE: 1998-03-10  
 PRIOR APPLICATION NUMBER: 60/077632  
 PRIOR FILING DATE: 1998-03-11  
 PRIOR APPLICATION NUMBER: 60/077641  
 PRIOR FILING DATE: 1998-03-11  
 PRIOR APPLICATION NUMBER: 60/077649  
 PRIOR FILING DATE: 1998-03-11  
 PRIOR APPLICATION NUMBER: 60/077791  
 PRIOR FILING DATE: 1998-03-12  
 PRIOR APPLICATION NUMBER: 60/078004  
 PRIOR FILING DATE: 1998-03-13  
 PRIOR APPLICATION NUMBER: 60/078886  
 PRIOR FILING DATE: 1998-03-20  
 PRIOR APPLICATION NUMBER: 60/078936  
 PRIOR FILING DATE: 1998-03-20  
 PRIOR APPLICATION NUMBER: 60/078910  
 PRIOR FILING DATE: 1998-03-20  
 PRIOR APPLICATION NUMBER: 60/078939  
 PRIOR FILING DATE: 1998-03-20  
 PRIOR APPLICATION NUMBER: 60/079294  
 PRIOR FILING DATE: 1998-03-25  
 PRIOR APPLICATION NUMBER: 60/079656  
 PRIOR FILING DATE: 1998-03-26  
 PRIOR APPLICATION NUMBER: 60/079664  
 PRIOR FILING DATE: 1998-03-27  
 PRIOR APPLICATION NUMBER: 60/079689  
 PRIOR FILING DATE: 1998-03-27  
 PRIOR APPLICATION NUMBER: 60/079663  
 PRIOR FILING DATE: 1998-03-27  
 PRIOR APPLICATION NUMBER: 60/079728  
 PRIOR FILING DATE: 1998-03-27  
 PRIOR APPLICATION NUMBER: 60/079786  
 PRIOR FILING DATE: 1998-03-27  
 PRIOR APPLICATION NUMBER: 60/079920  
 PRIOR FILING DATE: 1998-03-30  
 PRIOR APPLICATION NUMBER: 60/079923  
 PRIOR FILING DATE: 1998-03-30  
 PRIOR APPLICATION NUMBER: 60/080105  
 PRIOR FILING DATE: 1998-03-31  
 PRIOR APPLICATION NUMBER: 60/080107  
 PRIOR FILING DATE: 1998-03-31  
 PRIOR APPLICATION NUMBER: 60/080165  
 PRIOR FILING DATE: 1998-03-31  
 PRIOR APPLICATION NUMBER: 60/080194  
 PRIOR FILING DATE: 1998-03-31  
 PRIOR APPLICATION NUMBER: 60/080327  
 PRIOR FILING DATE: 1998-04-01  
 PRIOR APPLICATION NUMBER: 60/080328  
 PRIOR FILING DATE: 1998-04-01  
 PRIOR APPLICATION NUMBER: 60/080333  
 PRIOR FILING DATE: 1998-04-01  
 PRIOR APPLICATION NUMBER: 60/080334  
 PRIOR FILING DATE: 1998-04-01  
 PRIOR APPLICATION NUMBER: 60/081070  
 PRIOR FILING DATE: 1998-04-08  
 PRIOR APPLICATION NUMBER: 60/081049  
 PRIOR FILING DATE: 1998-04-08  
 PRIOR APPLICATION NUMBER: 60/081071  
 PRIOR FILING DATE: 1998-04-08  
 PRIOR APPLICATION NUMBER: 60/081195  
 PRIOR FILING DATE: 1998-04-08  
 PRIOR APPLICATION NUMBER: 60/081203  
 PRIOR FILING DATE: 1998-04-09  
 PRIOR APPLICATION NUMBER: 60/081229  
 PRIOR FILING DATE: 1998-04-09  
 PRIOR APPLICATION NUMBER: 60/081955  
 PRIOR FILING DATE: 1998-04-15  
 PRIOR APPLICATION NUMBER: 60/081817  
 PRIOR FILING DATE: 1998-04-15  
 PRIOR APPLICATION NUMBER: 60/081819  
 PRIOR FILING DATE: 1998-04-15  
 PRIOR APPLICATION NUMBER: 60/081952  
 PRIOR FILING DATE: 1998-04-15  
 PRIOR APPLICATION NUMBER: 60/081838  
 PRIOR FILING DATE: 1998-04-15  
 PRIOR APPLICATION NUMBER: 60/082568  
 PRIOR FILING DATE: 1998-04-21  
 PRIOR APPLICATION NUMBER: 60/082569  
 PRIOR FILING DATE: 1998-04-21  
 PRIOR APPLICATION NUMBER: 60/082704  
 PRIOR FILING DATE: 1998-04-22  
 PRIOR APPLICATION NUMBER: 60/082804  
 PRIOR FILING DATE: 1998-04-22  
 PRIOR APPLICATION NUMBER: 60/082700  
 PRIOR FILING DATE: 1998-04-22  
 PRIOR APPLICATION NUMBER: 60/082797  
 PRIOR FILING DATE: 1998-04-22  
 PRIOR APPLICATION NUMBER: 60/082796  
 PRIOR FILING DATE: 1998-04-23  
 PRIOR APPLICATION NUMBER: 60/083336  
 PRIOR FILING DATE: 1998-04-27  
 PRIOR APPLICATION NUMBER: 60/083322  
 PRIOR FILING DATE: 1998-04-28  
 PRIOR APPLICATION NUMBER: 60/083392  
 PRIOR FILING DATE: 1998-04-29  
 PRIOR APPLICATION NUMBER: 60/083495  
 PRIOR FILING DATE: 1998-04-29  
 PRIOR APPLICATION NUMBER: 60/083496  
 PRIOR FILING DATE: 1998-04-29  
 PRIOR APPLICATION NUMBER: 60/083499  
 PRIOR FILING DATE: 1998-04-29  
 PRIOR APPLICATION NUMBER: 60/083545  
 PRIOR FILING DATE: 1998-04-29  
 PRIOR APPLICATION NUMBER: 60/083554

PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083558  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083559  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083500  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083742  
PRIOR FILING DATE: 1998-04-30  
PRIOR APPLICATION NUMBER: 60/084366  
PRIOR FILING DATE: 1998-05-05  
PRIOR APPLICATION NUMBER: 60/084414  
PRIOR FILING DATE: 1998-05-06  
PRIOR APPLICATION NUMBER: 60/084441  
PRIOR FILING DATE: 1998-05-06  
PRIOR APPLICATION NUMBER: 60/084637  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/084639  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/084640  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/084627  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/084643  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/085339  
PRIOR FILING DATE: 1998-05-13  
PRIOR APPLICATION NUMBER: 60/085338  
PRIOR FILING DATE: 1998-05-13  
PRIOR APPLICATION NUMBER: 60/085323  
PRIOR FILING DATE: 1998-05-13  
PRIOR APPLICATION NUMBER: 60/085582  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085700  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085689  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085579  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085580  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085573  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085704  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085697

Query Match 99.98; Score 1504; DB 9; Length 273;

Best Local Similarity 99.64; Pred. No. 1.5e-100; Matches 272; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

1 MRGSEVILMLVAVGTEHAYRGRVCAVARAGDPVSESVQRPFLITTCGHR 60  
1 MRGSEVILMLVAVGTEHAYRGRVCAVARAGDPVSESVQRPFLITTCGHR 60  
61 ACSTYRTITRYARRSPGLAPARPRVACCPGWKRTSGLPAGCALICQPCRRGSGCVOP 120  
61 ACSTYRTITRYARRSPGLAPARPRVACCPGWKRTSGLPAGCALICQPCRRGSGCVOP 120  
121 GRGCPAGMRGDTQSDVDECSARRGCPORCVNTAGSYWCOCWEGHSLADGTLCPKG 180  
121 GRGCPAGMRGDTQSDVDECSARRGCPORCVNTAGSYWCOCWEGHSLADGTLCPKG 180  
181 GPPVAPVPTGVDASAMKEVORLQSRVLDLEKQLVLAFLHSLASQALHGLPDPGSL 240  
181 GPPVAPVPTGVDASAMKEVORLQSRVLDLEKQLVLAFLHSLASQALHGLPDPGSL 240  
241 VHSFOUIGRIDLSLSQISFLBEOLGSCSCKKDS 273  
VHSFOUIGRIDLSLSQISFLBEOLGSCSCKKDS 273

Db 241 VHSFOUIGRIDLSLSQISFLBEOLGSCSCKKDS 273

RESULT 6  
US-09-978-697-506  
Sequence 506, Application US/09978697  
Patent No. US20020169284A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnuyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Grimsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kijavini, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David U.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630FIC27  
CURRENT FILING DATE: 2001-10-16  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/064249  
PRIOR FILING DATE: 1997-11-03  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/066364  
PRIOR FILING DATE: 1997-11-21  
PRIOR APPLICATION NUMBER: 60/077450  
PRIOR FILING DATE: 1998-03-10  
PRIOR APPLICATION NUMBER: 60/077632  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077641  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077649  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077791  
PRIOR FILING DATE: 1998-03-12  
PRIOR APPLICATION NUMBER: 60/078004  
PRIOR FILING DATE: 1998-03-13  
PRIOR APPLICATION NUMBER: 60/078886  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/078936  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/078910  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/078939  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/079294  
PRIOR FILING DATE: 1998-03-25  
PRIOR APPLICATION NUMBER: 60/079656

; PRIOR FILING DATE: 1998-03-26  
; PRIOR APPLICATION NUMBER: 60/079664  
; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: 60/079689  
; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: 60/079663  
; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: 60/079728  
; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: 60/079786  
; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: 60/079920  
; PRIOR FILING DATE: 1998-03-30  
; PRIOR APPLICATION NUMBER: 60/079923  
; PRIOR FILING DATE: 1998-03-30  
; PRIOR APPLICATION NUMBER: 60/080105  
; PRIOR FILING DATE: 1998-03-31  
; PRIOR APPLICATION NUMBER: 60/080107  
; PRIOR FILING DATE: 1998-03-31  
; PRIOR APPLICATION NUMBER: 60/080165  
; PRIOR FILING DATE: 1998-03-31  
; PRIOR APPLICATION NUMBER: 60/080194  
; PRIOR FILING DATE: 1998-03-31  
; PRIOR APPLICATION NUMBER: 60/080327  
; PRIOR FILING DATE: 1998-04-01  
; PRIOR APPLICATION NUMBER: 60/080328  
; PRIOR FILING DATE: 1998-04-01  
; PRIOR APPLICATION NUMBER: 60/080333  
; PRIOR FILING DATE: 1998-04-01  
; PRIOR APPLICATION NUMBER: 60/080334  
; PRIOR FILING DATE: 1998-04-01  
; PRIOR APPLICATION NUMBER: 60/081070  
; PRIOR FILING DATE: 1998-04-08  
; PRIOR APPLICATION NUMBER: 60/081049  
; PRIOR FILING DATE: 1998-04-08  
; PRIOR APPLICATION NUMBER: 60/081071  
; PRIOR FILING DATE: 1998-04-08  
; PRIOR APPLICATION NUMBER: 60/081195  
; PRIOR FILING DATE: 1998-04-08  
; PRIOR APPLICATION NUMBER: 60/081203  
; PRIOR FILING DATE: 1998-04-09  
; PRIOR APPLICATION NUMBER: 60/081229  
; PRIOR FILING DATE: 1998-04-09  
; PRIOR APPLICATION NUMBER: 60/081955  
; PRIOR FILING DATE: 1998-04-15  
; PRIOR APPLICATION NUMBER: 60/081817  
; PRIOR FILING DATE: 1998-04-15  
; PRIOR APPLICATION NUMBER: 60/081819  
; PRIOR FILING DATE: 1998-04-15  
; PRIOR APPLICATION NUMBER: 60/081952  
; PRIOR FILING DATE: 1998-04-15  
; PRIOR APPLICATION NUMBER: 60/081838  
; PRIOR FILING DATE: 1998-04-15  
; PRIOR APPLICATION NUMBER: 60/082568  
; PRIOR FILING DATE: 1998-04-21  
; PRIOR APPLICATION NUMBER: 60/082569  
; PRIOR FILING DATE: 1998-04-21  
; PRIOR APPLICATION NUMBER: 60/082704  
; PRIOR FILING DATE: 1998-04-22  
; PRIOR APPLICATION NUMBER: 60/082804  
; PRIOR FILING DATE: 1998-04-22  
; PRIOR APPLICATION NUMBER: 60/082700  
; PRIOR FILING DATE: 1998-04-22  
; PRIOR APPLICATION NUMBER: 60/082797  
; PRIOR FILING DATE: 1998-04-22  
; PRIOR APPLICATION NUMBER: 60/082796  
; PRIOR FILING DATE: 1998-04-23  
; PRIOR APPLICATION NUMBER: 60/083336  
; PRIOR FILING DATE: 1998-04-27  
; PRIOR APPLICATION NUMBER: 60/083322  
; PRIOR FILING DATE: 1998-04-28  
; PRIOR APPLICATION NUMBER: 60/083392  
; PRIOR FILING DATE: 1998-04-29

; PRIOR APPLICATION NUMBER: 60/083495  
; PRIOR FILING DATE: 1998-04-29  
; PRIOR APPLICATION NUMBER: 60/083496  
; PRIOR FILING DATE: 1998-04-29  
; PRIOR APPLICATION NUMBER: 60/083499  
; PRIOR FILING DATE: 1998-04-29  
; PRIOR APPLICATION NUMBER: 60/083545  
; PRIOR FILING DATE: 1998-04-29  
; PRIOR APPLICATION NUMBER: 60/083554  
; PRIOR FILING DATE: 1998-04-29  
; PRIOR APPLICATION NUMBER: 60/083558  
; PRIOR FILING DATE: 1998-04-29  
; PRIOR APPLICATION NUMBER: 60/083559  
; PRIOR FILING DATE: 1998-04-29  
; PRIOR APPLICATION NUMBER: 60/083500  
; PRIOR FILING DATE: 1998-04-29  
; PRIOR APPLICATION NUMBER: 60/083742  
; PRIOR FILING DATE: 1998-04-30  
; PRIOR APPLICATION NUMBER: 60/084366  
; PRIOR FILING DATE: 1998-05-05  
; PRIOR APPLICATION NUMBER: 60/084414  
; PRIOR FILING DATE: 1998-05-06  
; PRIOR APPLICATION NUMBER: 60/084441  
; PRIOR FILING DATE: 1998-05-06  
; PRIOR APPLICATION NUMBER: 60/084637  
; PRIOR FILING DATE: 1998-05-07  
; PRIOR APPLICATION NUMBER: 60/084639  
; PRIOR FILING DATE: 1998-05-07  
; PRIOR APPLICATION NUMBER: 60/084640  
; PRIOR FILING DATE: 1998-05-07  
; PRIOR APPLICATION NUMBER: 60/084598  
; PRIOR FILING DATE: 1998-05-07  
; PRIOR APPLICATION NUMBER: 60/084600  
; PRIOR FILING DATE: 1998-05-07  
; PRIOR APPLICATION NUMBER: 60/084627  
; PRIOR FILING DATE: 1998-05-07  
; PRIOR APPLICATION NUMBER: 60/084643  
; PRIOR FILING DATE: 1998-05-07  
; PRIOR APPLICATION NUMBER: 60/085339  
; PRIOR FILING DATE: 1998-05-13  
; PRIOR APPLICATION NUMBER: 60/085338  
; PRIOR FILING DATE: 1998-05-13  
; PRIOR APPLICATION NUMBER: 60/085323  
; PRIOR FILING DATE: 1998-05-13  
; PRIOR APPLICATION NUMBER: 60/085582  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085700  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085689  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085579  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085580  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085573  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085704  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 99.9%; Score 1504; DB 9; Length 273;  
Best Local Similarity 99.6%; Pred. No. 1.5e-100;  
Matches 272; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRGSEVLLMVLAVGTEHAYRPGRRVCAVRAHGDVPVSEFVQRYVQPLTTCGDHR 60  
Db 1 MRGSEVLLMVLAVGTEHAYRPGRRVCAVRAHGDVPVSEFVQRYVQPLTTCGDHR 60  
QY 61 ACSTVRTIYRTAYRSPGLAPRPRYACCPGWKRTSGLPGACGAAICOPPCRNNGSCVQP 120  
Db 61 ACSTVRTIYRTAYRSPGLAPRPRYACCPGWKRTSGLPGACGAAICOPPCRNNGSCVQP 120  
QY 121 GRCRCFAGWRGDTCSQDVDECSARRGGCPQRCVNTAGSVWCQWEGHSLSDADTLCLVCPKG 180

Db 121 GRKCPGMDGDDTCQVDCSARRG3CCPQRCINTAGSYWCOCWEGSHISADGTLCPK 180  
QY 181 GPRVAPNPTGVDSAMKEEYORLQSRVDLLEKLOVLAPLHSLASQALHGLPPGSL 240  
Db 181 GPRVAPNPTGVDSAMKEEYORLQSRVDLLEKLOVLAPLHSLASQALHGLPPGSL 240  
QY 241 VHSFOOLGRIDLSLEQTSFLEQLGSCSCCKDS 273  
Db 241 VHSFOOLGRIDLSLEQTSFLEQLGSCSCCKDS 273

## RESULT 7

US-09-978-697-508  
Sequence 508, Application US/09978697  
Patent No. US20020169284A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnovers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gottlieb, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin J.  
APPLICANT: Hillan, Kenneth U.  
APPLICANT: Kijavich, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James;  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630P1C27  
CURRENT APPLICATION NUMBER: US/09/978,697  
PRIOR APPLICATION NUMBER: 2001-10-16  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/064249  
PRIOR FILING DATE: 1997-11-03  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/066364  
PRIOR FILING DATE: 1997-11-21  
PRIOR APPLICATION NUMBER: 60/077450  
PRIOR FILING DATE: 1998-03-10  
PRIOR APPLICATION NUMBER: 60/077632  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077641  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077649  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077791  
PRIOR FILING DATE: 1998-03-12  
PRIOR APPLICATION NUMBER: 60/078004  
PRIOR FILING DATE: 1998-03-13  
PRIOR APPLICATION NUMBER: 60/078886  
PRIOR FILING DATE: 1998-03-20

PRIOR APPLICATION NUMBER: 60/078936  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/078910  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/078939  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/079294  
PRIOR FILING DATE: 1998-03-25  
PRIOR APPLICATION NUMBER: 60/079656  
PRIOR FILING DATE: 1998-03-26  
PRIOR APPLICATION NUMBER: 60/079664  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/079689  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/079663  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/079728  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/079786  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/079920  
PRIOR FILING DATE: 1998-03-30  
PRIOR APPLICATION NUMBER: 60/079923  
PRIOR FILING DATE: 1998-03-30  
PRIOR APPLICATION NUMBER: 60/080105  
PRIOR FILING DATE: 1998-03-31  
PRIOR APPLICATION NUMBER: 60/080107  
PRIOR FILING DATE: 1998-03-31  
PRIOR APPLICATION NUMBER: 60/080165  
PRIOR FILING DATE: 1998-03-31  
PRIOR APPLICATION NUMBER: 60/080194  
PRIOR FILING DATE: 1998-03-31  
PRIOR APPLICATION NUMBER: 60/080327  
PRIOR FILING DATE: 1998-04-01  
PRIOR APPLICATION NUMBER: 60/080328  
PRIOR FILING DATE: 1998-04-01  
PRIOR APPLICATION NUMBER: 60/080333  
PRIOR FILING DATE: 1998-04-01  
PRIOR APPLICATION NUMBER: 60/080334  
PRIOR FILING DATE: 1998-04-01  
PRIOR APPLICATION NUMBER: 60/081070  
PRIOR FILING DATE: 1998-04-08  
PRIOR APPLICATION NUMBER: 60/081049  
PRIOR FILING DATE: 1998-04-08  
PRIOR APPLICATION NUMBER: 60/081071  
PRIOR FILING DATE: 1998-04-08  
PRIOR APPLICATION NUMBER: 60/081195  
PRIOR FILING DATE: 1998-04-08  
PRIOR APPLICATION NUMBER: 60/081203  
PRIOR FILING DATE: 1998-04-09  
PRIOR APPLICATION NUMBER: 60/081229  
PRIOR FILING DATE: 1998-04-09  
PRIOR APPLICATION NUMBER: 60/081955  
PRIOR FILING DATE: 1998-04-15  
PRIOR APPLICATION NUMBER: 60/081817  
PRIOR FILING DATE: 1998-04-15  
PRIOR APPLICATION NUMBER: 60/081819  
PRIOR FILING DATE: 1998-04-15  
PRIOR APPLICATION NUMBER: 60/081952  
PRIOR FILING DATE: 1998-04-15  
PRIOR APPLICATION NUMBER: 60/081838  
PRIOR FILING DATE: 1998-04-15  
PRIOR APPLICATION NUMBER: 60/082568  
PRIOR FILING DATE: 1998-04-21  
PRIOR APPLICATION NUMBER: 60/082569  
PRIOR FILING DATE: 1998-04-21  
PRIOR APPLICATION NUMBER: 60/082704  
PRIOR FILING DATE: 1998-04-22  
PRIOR APPLICATION NUMBER: 60/082804  
PRIOR FILING DATE: 1998-04-22  
PRIOR APPLICATION NUMBER: 60/082700  
PRIOR FILING DATE: 1998-04-22  
PRIOR APPLICATION NUMBER: 60/082797

Tue Dec 17 14:03:48 2002

;; PRIOR FILING DATE: 1998-04-22  
;; PRIOR APPLICATION NUMBER: 60/082796  
;; PRIOR FILING DATE: 1998-04-23  
;; PRIOR APPLICATION NUMBER: 60/083336  
;; PRIOR FILING DATE: 1998-04-27  
;; PRIOR APPLICATION NUMBER: 60/083322  
;; PRIOR FILING DATE: 1998-04-28  
;; PRIOR APPLICATION NUMBER: 60/083392  
;; PRIOR FILING DATE: 1998-04-29  
;; PRIOR APPLICATION NUMBER: 60/083495  
;; PRIOR FILING DATE: 1998-04-29  
;; PRIOR APPLICATION NUMBER: 60/083496  
;; PRIOR FILING DATE: 1998-04-29  
;; PRIOR APPLICATION NUMBER: 60/083499  
;; PRIOR FILING DATE: 1998-04-29  
;; PRIOR APPLICATION NUMBER: 60/083545  
;; PRIOR FILING DATE: 1998-04-29  
;; PRIOR APPLICATION NUMBER: 60/083554  
;; PRIOR FILING DATE: 1998-04-29  
;; PRIOR APPLICATION NUMBER: 60/083558  
;; PRIOR FILING DATE: 1998-04-29  
;; PRIOR APPLICATION NUMBER: 60/083559  
;; PRIOR FILING DATE: 1998-04-29  
;; PRIOR APPLICATION NUMBER: 60/083500  
;; PRIOR FILING DATE: 1998-04-29  
;; PRIOR APPLICATION NUMBER: 60/083742  
;; PRIOR FILING DATE: 1998-04-30  
;; PRIOR APPLICATION NUMBER: 60/084366  
;; PRIOR FILING DATE: 1998-05-05  
;; PRIOR APPLICATION NUMBER: 60/084414  
;; PRIOR FILING DATE: 1998-05-06  
;; PRIOR APPLICATION NUMBER: 60/084441  
;; PRIOR FILING DATE: 1998-05-06  
;; PRIOR APPLICATION NUMBER: 60/084637  
;; PRIOR FILING DATE: 1998-05-07  
;; PRIOR APPLICATION NUMBER: 60/084639  
;; PRIOR FILING DATE: 1998-05-07  
;; PRIOR APPLICATION NUMBER: 60/084640  
;; PRIOR FILING DATE: 1998-05-07  
;; PRIOR APPLICATION NUMBER: 60/084598  
;; PRIOR FILING DATE: 1998-05-07  
;; PRIOR APPLICATION NUMBER: 60/084600  
;; PRIOR FILING DATE: 1998-05-07  
;; PRIOR APPLICATION NUMBER: 60/084627  
;; PRIOR FILING DATE: 1998-05-07  
;; PRIOR APPLICATION NUMBER: 60/084643  
;; PRIOR FILING DATE: 1998-05-07  
;; PRIOR APPLICATION NUMBER: 60/085339  
;; PRIOR FILING DATE: 1998-05-13  
;; PRIOR APPLICATION NUMBER: 60/085338  
;; PRIOR FILING DATE: 1998-05-13  
;; PRIOR APPLICATION NUMBER: 60/085323  
;; PRIOR FILING DATE: 1998-05-13  
;; PRIOR APPLICATION NUMBER: 60/085582  
;; PRIOR FILING DATE: 1998-05-15  
;; PRIOR APPLICATION NUMBER: 60/085700  
;; PRIOR FILING DATE: 1998-05-15  
;; PRIOR APPLICATION NUMBER: 60/085689  
;; PRIOR FILING DATE: 1998-05-15  
;; PRIOR APPLICATION NUMBER: 60/085579  
;; PRIOR FILING DATE: 1998-05-15  
;; PRIOR APPLICATION NUMBER: 60/085580  
;; PRIOR FILING DATE: 1998-05-15  
;; PRIOR APPLICATION NUMBER: 60/085573  
;; PRIOR FILING DATE: 1998-05-15  
;; PRIOR APPLICATION NUMBER: 60/085704  
;; PRIOR FILING DATE: 1998-05-15  
;; PRIOR APPLICATION NUMBER: 60/085697

Query Match 99.9%; Score 1504; DB 9; Length 273;  
Best Local Similarity 99.6%; Pred. No. 1.5e-100;  
Matches 272; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRGQEVLLMVLAVGGTEHAYRPGRRVCAVRAHGDVPSSEFVQRYOPELTTCDGHR 60  
DB 1 MRGQEVLLMVLAVGGTEHAYRPGRRVCAVRAHGDVPSSEFVQRYOPELTTCDGHR 60  
QY 61 ACSTYRTYRTAYRRSPGLAPARPRYACCPGWKRTSGLPGACGAAI CQPPCRNGGSCVQP 120  
DB 61 ACSTYRTYRTAYRRSPGLAPARPRYACCPGWKRTSGLPGACGAAI CQPPCRNGGSCVQP 120  
QY 121 GRCRCFAGRGDTQSDVDECSARRGGCPQRCVNTAGSYWCQWEGHSLSDGTLCVPGK 180  
DB 121 GRCRCFAGRGDTQSDVDECSARRGGCPQRCVNTAGSYWCQWEGHSLSDGTLCVPGK 180  
QY 181 GPRVAPNPTGVDSSAMKEEVORLQSRVDLLEKQLVLAPLHSLASQALEHGLDPPGSL 240  
DB 181 GPRVAPNPTGVDSSAMKEEVORLQSRVDLLEKQLVLAPLHSLASQALEHGLDPPGSL 240  
QY 241 VHSFOQLGRIDSLSEIISFLEQLGSCSKKDS 273  
DB 241 VHSFOQLGRIDSLSEIISFLEQLGSCSKKDS 273  
RESULT 8  
US-09-978-192A-506  
; Sequence 506, Application US/09978192A  
; Patent No. US20020177553A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James;  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Shelton, David L.  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2630F1C9  
; CURRENT APPLICATION NUMBER: US/09/978,192A  
; CURRENT FILING DATE: 2001-10-15  
; PRIOR APPLICATION NUMBER: 09/918585  
; PRIOR FILING DATE: 2001-07-30  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/064249  
; PRIOR FILING DATE: 1997-11-03  
; PRIOR APPLICATION NUMBER: 60/065311  
; PRIOR FILING DATE: 1997-11-13  
; PRIOR APPLICATION NUMBER: 60/066364  
; PRIOR FILING DATE: 1997-11-21  
; PRIOR APPLICATION NUMBER: 60/077450  
; PRIOR FILING DATE: 1998-03-10  
; PRIOR APPLICATION NUMBER: 60/077632  
; PRIOR FILING DATE: 1998-03-11  
; PRIOR APPLICATION NUMBER: 60/077641

PRIOR FILING DATE:	1998-03-11
PRIOR APPLICATION NUMBER:	60/0776494
PRIOR FILING DATE:	1998-03-11
PRIOR APPLICATION NUMBER:	60/0777921
PRIOR FILING DATE:	1998-03-12
PRIOR APPLICATION NUMBER:	60/0780044
PRIOR FILING DATE:	1998-03-13
PRIOR APPLICATION NUMBER:	60/0788866
PRIOR FILING DATE:	1998-03-20
PRIOR APPLICATION NUMBER:	60/0789326
PRIOR FILING DATE:	1998-03-20
PRIOR APPLICATION NUMBER:	60/0789110
PRIOR FILING DATE:	1998-03-20
PRIOR APPLICATION NUMBER:	60/0789393
PRIOR FILING DATE:	1998-03-20
PRIOR APPLICATION NUMBER:	60/0792294
PRIOR FILING DATE:	1998-03-25
PRIOR APPLICATION NUMBER:	60/0796566
PRIOR FILING DATE:	1998-03-27
PRIOR APPLICATION NUMBER:	60/0796656
PRIOR FILING DATE:	1998-03-26
PRIOR APPLICATION NUMBER:	60/0796654
PRIOR FILING DATE:	1998-03-27
PRIOR APPLICATION NUMBER:	60/0796889
PRIOR FILING DATE:	1998-03-27
PRIOR APPLICATION NUMBER:	60/0796633
PRIOR FILING DATE:	1998-03-27
PRIOR APPLICATION NUMBER:	60/0796633
PRIOR FILING DATE:	1998-03-27
PRIOR APPLICATION NUMBER:	60/0797128
PRIOR FILING DATE:	1998-03-27
PRIOR APPLICATION NUMBER:	60/0797866
PRIOR FILING DATE:	1998-03-27
PRIOR APPLICATION NUMBER:	60/0799220
PRIOR FILING DATE:	1998-03-30
PRIOR APPLICATION NUMBER:	60/0799223
PRIOR FILING DATE:	1998-03-30
PRIOR APPLICATION NUMBER:	60/0801055
PRIOR FILING DATE:	1998-03-31
PRIOR APPLICATION NUMBER:	60/0801077
PRIOR FILING DATE:	1998-03-31
PRIOR APPLICATION NUMBER:	60/0801655
PRIOR FILING DATE:	1998-03-31
PRIOR APPLICATION NUMBER:	60/0801944
PRIOR FILING DATE:	1998-03-31
PRIOR APPLICATION NUMBER:	60/0803277
PRIOR FILING DATE:	1998-04-01
PRIOR APPLICATION NUMBER:	60/0803228
PRIOR FILING DATE:	1998-04-01
PRIOR APPLICATION NUMBER:	60/0803333
PRIOR FILING DATE:	1998-04-01
PRIOR APPLICATION NUMBER:	60/0803344
PRIOR FILING DATE:	1998-04-01
PRIOR APPLICATION NUMBER:	60/0810770
PRIOR FILING DATE:	1998-04-08
PRIOR APPLICATION NUMBER:	60/0810499
PRIOR FILING DATE:	1998-04-08
PRIOR APPLICATION NUMBER:	60/0810771
PRIOR FILING DATE:	1998-04-08
PRIOR APPLICATION NUMBER:	60/0811355
PRIOR FILING DATE:	1998-04-08
PRIOR APPLICATION NUMBER:	60/0812033
PRIOR FILING DATE:	1998-04-09
PRIOR APPLICATION NUMBER:	60/0812259
PRIOR FILING DATE:	1998-04-09
PRIOR APPLICATION NUMBER:	60/0819555
PRIOR FILING DATE:	1998-04-15
PRIOR APPLICATION NUMBER:	60/0818177
PRIOR FILING DATE:	1998-04-15
PRIOR APPLICATION NUMBER:	60/0818199
PRIOR FILING DATE:	1998-04-15
PRIOR APPLICATION NUMBER:	60/0819552
PRIOR FILING DATE:	1998-04-15
PRIOR APPLICATION NUMBER:	60/0818388
PRIOR FILING DATE:	1998-04-15
PRIOR APPLICATION NUMBER:	60/0825568
PRIOR FILING DATE:	1998-04-21

1	PRIOR APPLICATION NUMBER: 60/082556
2	PRIOR FILING DATE: 1998-04-21
3	PRIOR APPLICATION NUMBER: 60/082704
4	PRIOR FILING DATE: 1998-04-22
5	PRIOR APPLICATION NUMBER: 60/082804
6	PRIOR FILING DATE: 1998-04-22
7	PRIOR APPLICATION NUMBER: 60/082700
8	PRIOR FILING DATE: 1998-04-22
9	PRIOR APPLICATION NUMBER: 60/082797
10	PRIOR FILING DATE: 1998-04-22
11	PRIOR APPLICATION NUMBER: 60/082796
12	PRIOR FILING DATE: 1998-04-23
13	PRIOR APPLICATION NUMBER: 60/083336
14	PRIOR FILING DATE: 1998-04-27
15	PRIOR APPLICATION NUMBER: 60/083322
16	PRIOR FILING DATE: 1998-04-28
17	PRIOR APPLICATION NUMBER: 60/083392
18	PRIOR FILING DATE: 1998-04-29
19	PRIOR APPLICATION NUMBER: 60/083495
20	PRIOR FILING DATE: 1998-04-29
21	PRIOR APPLICATION NUMBER: 60/083496
22	PRIOR FILING DATE: 1998-04-29
23	PRIOR APPLICATION NUMBER: 60/083499
24	PRIOR FILING DATE: 1998-04-29
25	PRIOR APPLICATION NUMBER: 60/083545
26	PRIOR FILING DATE: 1998-04-29
27	PRIOR APPLICATION NUMBER: 60/083554
28	PRIOR FILING DATE: 1998-04-29
29	PRIOR APPLICATION NUMBER: 60/083558
30	PRIOR FILING DATE: 1998-04-29
31	PRIOR APPLICATION NUMBER: 60/083559
32	PRIOR FILING DATE: 1998-04-29
33	PRIOR APPLICATION NUMBER: 60/083500
34	PRIOR FILING DATE: 1998-04-29
35	PRIOR APPLICATION NUMBER: 60/083742
36	PRIOR FILING DATE: 1998-04-30
37	PRIOR APPLICATION NUMBER: 60/083366
38	PRIOR FILING DATE: 1998-05-05
39	PRIOR APPLICATION NUMBER: 60/084414
40	PRIOR FILING DATE: 1998-05-06
41	PRIOR APPLICATION NUMBER: 60/084441
42	PRIOR FILING DATE: 1998-05-06
43	PRIOR APPLICATION NUMBER: 60/084637
44	PRIOR FILING DATE: 1998-05-07
45	PRIOR APPLICATION NUMBER: 60/084639
46	PRIOR FILING DATE: 1998-05-07
47	PRIOR APPLICATION NUMBER: 60/084640
48	PRIOR FILING DATE: 1998-05-07
49	PRIOR APPLICATION NUMBER: 60/084598
50	PRIOR FILING DATE: 1998-05-07
51	PRIOR APPLICATION NUMBER: 60/084600
52	PRIOR FILING DATE: 1998-05-07
53	PRIOR APPLICATION NUMBER: 60/084627
54	PRIOR FILING DATE: 1998-05-07
55	PRIOR APPLICATION NUMBER: 60/084643
56	PRIOR FILING DATE: 1998-05-07
57	PRIOR APPLICATION NUMBER: 60/085339
58	PRIOR FILING DATE: 1998-05-13
59	PRIOR APPLICATION NUMBER: 60/085338
60	PRIOR FILING DATE: 1998-05-13
61	PRIOR APPLICATION NUMBER: 60/085323
62	PRIOR FILING DATE: 1998-05-13
63	PRIOR APPLICATION NUMBER: 60/085582
64	PRIOR FILING DATE: 1998-05-15
65	PRIOR APPLICATION NUMBER: 60/085700
66	PRIOR FILING DATE: 1998-05-15
67	PRIOR APPLICATION NUMBER: 60/085669
68	PRIOR FILING DATE: 1998-05-15
69	PRIOR APPLICATION NUMBER: 60/085579
70	PRIOR FILING DATE: 1998-05-15
71	PRIOR APPLICATION NUMBER: 60/085580
72	PRIOR FILING DATE: 1998-05-15
73	PRIOR APPLICATION NUMBER: 60/085573

Tue Dec 17 14:03:48 2002

; PRIOR FILING DATE: 1998-05-15  
 ; PRIOR APPLICATION NUMBER: 60/085704  
 ; PRIOR FILING DATE: 1998-05-15  
 ; PRIOR APPLICATION NUMBER: 60/085697

Query Match 99.9%; Score 1504; DB 9; Length 273;  
 Best Local Similarity 99.8%; Pred. No. 1.5e-100;  
 Matches 272; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MRGSOEVLMLVLA	VGGTEHAYRPGRRVCAVRAHGD	PVSSFVORVQPF	LTTC	CDGHR	60
Db	1	MRGSOEVLMLVLA	VGGTEHAYRPGRRVCAVRAHGD	PVSSFVORVQPF	LTTC	CDGHR	60
Qy	61	ACSTYRTTYR	YRSPGLAPRPRYACCPGWKRTSL	PGACGAAC	QPPCRNGG	SCVOP	120
Db	61	ACSTYRTTYR	YRSPGLAPRPRYACCPGWKRTSL	PGACGAAC	QPPCRNGG	SCVOP	120
Qy	121	GRCRPAGWGT	QSDVDECSARRGCPQRCVNTAGSYWCQ	WEGHSL	SADGTL	CVPKG	180
Db	121	GRCRPAGWGT	QSDVDECSARRGCPQRCVNTAGSYWCQ	WEGHSL	SADGTL	CVPKG	180
Qy	181	GPVRVAPNPT	GVDSAMKEEVQRLSRVDLLEEKQLVLA	PLHSLASQ	ALEHGL	PDGSL	240
Db	181	GPVRVAPNPT	GVDSAMKEEVQRLSRVDLLEEKQLVLA	PLHSLASQ	ALEHGL	PDGSL	240
Qy	241	VHSFOQLGRIDS	LSQISFLBEOQLGSCSKKDS	273			
Db	241	VHSFOQLGRIDS	LSQISFLBEOQLGSCSKKDS	273			

RESULT 9

US-09-978-192A-508  
 ; Sequence 508, Application US/09978192A  
 ; Patent No. US2002017753A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ashkenazi, Avi  
 ; APPLICANT: Baker Kevin P.  
 ; APPLICANT: Botstein, David  
 ; APPLICANT: Desnoyers, Luc  
 ; APPLICANT: Eaton, Dan  
 ; APPLICANT: Ferrara, Napoleon  
 ; APPLICANT: Filvaroff, Ellen  
 ; APPLICANT: Fong, Sherman  
 ; APPLICANT: Gao, Wei-Qiang  
 ; APPLICANT: Gerber, Hanspeter  
 ; APPLICANT: Gerritsen, Mary E.  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Godowski, Paul J.  
 ; APPLICANT: Grimaldi, J. Christopher  
 ; APPLICANT: Gurney, Austin L.  
 ; APPLICANT: Hillan, Kenneth J.  
 ; APPLICANT: Kljavin, Ivar J.  
 ; APPLICANT: Kuo, Sophia S.  
 ; APPLICANT: Napier, Mary A.  
 ; APPLICANT: Pan, James  
 ; APPLICANT: Paoni, Nicholas F.  
 ; APPLICANT: Roy, Margaret Ann  
 ; APPLICANT: Shelton, David L.  
 ; APPLICANT: Stewart, Timothy A.  
 ; APPLICANT: Tumas, Daniel  
 ; APPLICANT: Williams, P. Mickey  
 ; APPLICANT: Wood, William I.  
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 ; TITLE OF INVENTION: Acids Encoding the Same  
 ; FILE REFERENCE: P2630PLC9  
 ; CURRENT APPLICATION NUMBER: US/09/978,192A  
 ; CURRENT FILING DATE: 2001-10-15  
 ; PRIOR APPLICATION NUMBER: 09/918585  
 ; PRIOR FILING DATE: 2001-07-30  
 ; PRIOR APPLICATION NUMBER: 60/062250  
 ; PRIOR FILING DATE: 1997-10-17  
 ; PRIOR APPLICATION NUMBER: 60/064249  
 ; PRIOR FILING DATE: 1997-11-03

; PRIOR APPLICATION NUMBER: 60/065311  
 ; PRIOR FILING DATE: 1997-11-13  
 ; PRIOR APPLICATION NUMBER: 60/066364  
 ; PRIOR FILING DATE: 1997-11-21  
 ; PRIOR APPLICATION NUMBER: 60/077450  
 ; PRIOR FILING DATE: 1998-03-10  
 ; PRIOR APPLICATION NUMBER: 60/077632  
 ; PRIOR FILING DATE: 1998-03-11  
 ; PRIOR APPLICATION NUMBER: 60/077641  
 ; PRIOR FILING DATE: 1998-03-11  
 ; PRIOR APPLICATION NUMBER: 60/077649  
 ; PRIOR FILING DATE: 1998-03-11  
 ; PRIOR APPLICATION NUMBER: 60/077791  
 ; PRIOR FILING DATE: 1998-03-12  
 ; PRIOR APPLICATION NUMBER: 60/078004  
 ; PRIOR FILING DATE: 1998-03-13  
 ; PRIOR APPLICATION NUMBER: 60/078886  
 ; PRIOR FILING DATE: 1998-03-20  
 ; PRIOR APPLICATION NUMBER: 60/078936  
 ; PRIOR FILING DATE: 1998-03-20  
 ; PRIOR APPLICATION NUMBER: 60/078910  
 ; PRIOR FILING DATE: 1998-03-20  
 ; PRIOR APPLICATION NUMBER: 60/078939  
 ; PRIOR FILING DATE: 1998-03-20  
 ; PRIOR APPLICATION NUMBER: 60/079294  
 ; PRIOR FILING DATE: 1998-03-25  
 ; PRIOR APPLICATION NUMBER: 60/079656  
 ; PRIOR FILING DATE: 1998-03-26  
 ; PRIOR APPLICATION NUMBER: 60/079664  
 ; PRIOR FILING DATE: 1998-03-27  
 ; PRIOR APPLICATION NUMBER: 60/079689  
 ; PRIOR FILING DATE: 1998-03-27  
 ; PRIOR APPLICATION NUMBER: 60/079663  
 ; PRIOR FILING DATE: 1998-03-27  
 ; PRIOR APPLICATION NUMBER: 60/079728  
 ; PRIOR FILING DATE: 1998-03-27  
 ; PRIOR APPLICATION NUMBER: 60/079786  
 ; PRIOR FILING DATE: 1998-03-27  
 ; PRIOR APPLICATION NUMBER: 60/079920  
 ; PRIOR FILING DATE: 1998-03-30  
 ; PRIOR APPLICATION NUMBER: 60/079923  
 ; PRIOR FILING DATE: 1998-03-30  
 ; PRIOR APPLICATION NUMBER: 60/080105  
 ; PRIOR FILING DATE: 1998-03-31  
 ; PRIOR APPLICATION NUMBER: 60/080107  
 ; PRIOR FILING DATE: 1998-03-31  
 ; PRIOR APPLICATION NUMBER: 60/080165  
 ; PRIOR FILING DATE: 1998-03-31  
 ; PRIOR APPLICATION NUMBER: 60/080194  
 ; PRIOR FILING DATE: 1998-03-31  
 ; PRIOR APPLICATION NUMBER: 60/080327  
 ; PRIOR FILING DATE: 1998-04-01  
 ; PRIOR APPLICATION NUMBER: 60/080328  
 ; PRIOR FILING DATE: 1998-04-01  
 ; PRIOR APPLICATION NUMBER: 60/080333  
 ; PRIOR FILING DATE: 1998-04-01  
 ; PRIOR APPLICATION NUMBER: 60/080334  
 ; PRIOR FILING DATE: 1998-04-01  
 ; PRIOR APPLICATION NUMBER: 60/081070  
 ; PRIOR FILING DATE: 1998-04-08  
 ; PRIOR APPLICATION NUMBER: 60/081049  
 ; PRIOR FILING DATE: 1998-04-08  
 ; PRIOR APPLICATION NUMBER: 60/081071  
 ; PRIOR FILING DATE: 1998-04-08  
 ; PRIOR APPLICATION NUMBER: 60/081195  
 ; PRIOR FILING DATE: 1998-04-08  
 ; PRIOR APPLICATION NUMBER: 60/081203  
 ; PRIOR FILING DATE: 1998-04-09  
 ; PRIOR APPLICATION NUMBER: 60/081229  
 ; PRIOR FILING DATE: 1998-04-09  
 ; PRIOR APPLICATION NUMBER: 60/081955  
 ; PRIOR FILING DATE: 1998-04-15  
 ; PRIOR APPLICATION NUMBER: 60/081817



```

PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081819
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081952
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081838
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/082568
PRIOR FILING DATE: 1998-04-21
PRIOR APPLICATION NUMBER: 60/082569
PRIOR FILING DATE: 1998-04-21
PRIOR APPLICATION NUMBER: 60/082704
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082804
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082700
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082797
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082796
PRIOR FILING DATE: 1998-04-23
PRIOR APPLICATION NUMBER: 60/083336
PRIOR FILING DATE: 1998-04-27
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/083392
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083495
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083496
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083499
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083545
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083554
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083558
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083559
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083500
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083742
PRIOR FILING DATE: 1998-04-30
PRIOR APPLICATION NUMBER: 60/084366
PRIOR FILING DATE: 1998-05-05
PRIOR APPLICATION NUMBER: 60/084414
PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: 60/084441
PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: 60/084637
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084639
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084640
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084598
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084627
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084643
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/085339
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085338
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085323
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085582
PRIOR FILING DATE: 1998-05-15

PRIOR APPLICATION NUMBER: 60/085700
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085689
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085579
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085580
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085573
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085704
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085697

Query Match      99.9%; Score 1504; DB 9; Length 273;
Best Local Similarity 99.6%; Pred. No. 1.5e-100;
Matches 272; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRGSEVLLMMLVLA VGGTEHAYRPPRRVCAVRAGDPVSEFVQRYVQPLTTCDGR 60
Db 1 MRGSEVLLMMLVLA VGGTEHAYRPPRRVCAVRAGDPVSEFVQRYVQPLTTCDGR 60
QY 61 ACSTYRTTYRTAYRSPGLAPAPRYAACCPGWRRTSGLPACGAALCPPCRNNGSCVQP 120
Db 61 ACSTYRTTYRTAYRSPGLAPAPRYAACCPGWRRTSGLPACGAALCPPCRNNGSCVQP 120
QY 121 GRGCPAGMRGDTQSDVDVECSARRGGCPORCVNTAGSYWCOCWEHSHSADGTLCPVPG 180
Db 121 GRGCPAGMRGDTQSDVDVECSARRGGCPORCVNTAGSYWCOCWEHSHSADGTLCPVPG 180
QY 181 GPPRVANPTGVDSAMKEEYORLOSRRVDLLEKLOVLAPLHSLASQALEHGLPDGSL 240
Db 181 GPPRVANPTGVDSAMKEEYORLOSRRVDLLEKLOVLAPLHSLASQALEHGLPDGSL 240
QY 241 VHSFQQLGRIDLSSEQISTLEQLQSCSKXDS 273
Db 241 VHSFQQLGRIDLSSEQISTLEQLQSCSKXDS 273

RESULT 10
US-09-790-264-10
Sequence 10, Application US/09790264
Patent No. US2002028508A1
GENERAL INFORMATION:
Applicant: Holtzman, Douglas A.
Applicant: Goodearl, Andrew D.J.
Applicant: McCarthy, Sean A.
TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
FILE REFERENCE: 07334-322001
CURRENT APPLICATION NUMBER: US/09/790,264
CURRENT FILING DATE: 2001-02-21
PRIOR APPLICATION NUMBER: US 09/065,661
PRIOR FILING DATE: 1998-04-23
PRIOR APPLICATION NUMBER: US 09/298,531
PRIOR FILING DATE: 1999-04-23
PRIOR APPLICATION NUMBER: US 09/065,363
PRIOR FILING DATE: 1998-04-23
PRIOR APPLICATION NUMBER: US 09/337,930
PRIOR FILING DATE: 1999-06-22
PRIOR APPLICATION NUMBER: US 09/102,705
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: US 09/363,630
PRIOR FILING DATE: 1999-07-29
PRIOR APPLICATION NUMBER: US 09/124,538
PRIOR FILING DATE: 1998-07-29
NUMBER OF SEQ ID NOS: 68
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 10
LENGTH: 273
TYPE: PRT
ORGANISM: Homo sapiens
```

Tue Dec 17 14:03:48 2002

```
;
; NAME/KEY: SIGNAL
; LOCATION: (1)...(22)
US-09-790-264-10

Query Match          99.9%; Score 1504; DB 10; Length 273;
Best Local Similarity 99.6%; Pred. No. 1.5e-100;
Matches 272; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRGQEVLLMWLLVLAVGGTTHAVRGRVCAVRAHGDVPSFVQRYVQPFLLTTCDCGHR 60
Db 1 MRGQEVLLMWLLVLAVGGTTHAVRGRVCAVRAHGDVPSFVQRYVQPFLLTTCDCGHR 60

Qy 61 ACSTVRTIYRTAYRRSPGLAPARPRYACCPGKRTSGLPACGAAICQPPCRNGGSCVQP 120
Db 61 ACSTVRTIYRTAYRRSPGLAPARPRYACCPGKRTSGLPACGAAICQPPCRNGGSCVQP 120

Qy 121 GRCPAGWGRDTCOSDVDECSARRGCGPCRCVNTAGSYWCQWEGHSLSDGTLCPVKG 180
Db 121 GRCPAGWGRDTCOSDVDECSARRGCGPCRCVNTAGSYWCQWEGHSLSDGTLCPVKG 180

Qy 161 GPPRVAPNPTGVDSAMKEEVORLSRVLDLEKQLVLAPLHSLASQALEHGLPDPGSL 240
Db 161 GPPRVAPNPTGVDSAMKEEVORLSRVLDLEKQLVLAPLHSLASQALEHGLPDPGSL 240

Qy 241 VHSFOOLGRIDSLSQISFLEEQSCCKKDS 273
Db 241 VHSFOOLGRIDSLSQISFLEEQSCCKKDS 273

RESULT 11
US-09-790-264-12
; Sequence 12, Application US/09790264
; Patent No. US2002028508A1
; GENERAL INFORMATION:
; APPLICANT: Holtzman, Douglas A.
; APPLICANT: Goodearl, Andrew D.J.
; APPLICANT: McCarthy, Sean A.
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
; TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
; TITLE OF INVENTION: USES
; FILE REFERENCE: 07334-322001
; CURRENT APPLICATION NUMBER: US/09/790,264
; CURRENT FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: US 09/065,661
; PRIOR FILING DATE: 1998-04-23
; PRIOR APPLICATION NUMBER: US 09/298,531
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: US 09/065,363
; PRIOR FILING DATE: 1998-04-23
; PRIOR APPLICATION NUMBER: US 09/337,930
; PRIOR FILING DATE: 1999-06-22
; PRIOR APPLICATION NUMBER: US 09/102,705
; PRIOR FILING DATE: 1998-06-22
; PRIOR APPLICATION NUMBER: US 09/363,630
; PRIOR FILING DATE: 1999-07-29
; PRIOR APPLICATION NUMBER: US 09/124,538
; PRIOR FILING DATE: 1998-07-29
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-790-264-12

Query Match          92.5%; Score 1392; DB 10; Length 251;
Best Local Similarity 99.6%; Pred. No. 1.3e-92;
Matches 250; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 23 AYRPGRVCAVRAHGDVPSFVQRYVQPFLLTTCDCGHRACSTVRTIYRTAYRRSPGLA 82
Db 1 AYRPGRVCAVRAHGDVPSFVQRYVQPFLLTTCDCGHRACSTVRTIYRTAYRRSPGLA 60

;
; NAME/KEY: SIGNAL
; LOCATION: (1)...(22)
US-09-978-295A-2
; Sequence 2, Application US/09978295A
; Patent No. US2002015606A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630PIC11
; CURRENT APPLICATION NUMBER: US/09/978,295A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066364
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/077450
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 60/077632
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077641
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077649
; PRIOR FILING DATE: 1998-03-11
```



us-09-852-472-2.rapb

Tue Dec 17 14:03:48 2002

```
; PRIOR APPLICATION NUMBER: 60/085697
Query Match      89.1%; Score 1340.5; DB 9; Length 295;
Best Local Similarity 94.6%; Pred. No. 7e-89;
Matches 246; Conservative 2; Mismatches 9; Indels 3; Gaps 2;

QY 17 VGGTEHAYR-PGRKVCAY--RAHGDPVSESFVQRYVQPLTTCDGHRACSTVRYTAY 73
Db 36 VGSGRHARLPARPLGCVLSRAHGDPVSESFVQRYVQPLTTCDGHRACSTVRYTAY 95
QY 74 RRSGLAPARPRYACCPGKRTSLGACGAAICQPPCRNGGSCVQPGRCRCPCAGWRGDT 133
Db 96 RRSPLAPARPRYACCPGKRTSLGACGAAICQPPCRNGGSCVQPGRCRCPCAGWRGDT 155
QY 134 COSDVECSARRGGCPQRCVNTAGSYWCQWEGHSLASADGTLCPVKGPPRVAPNPTGVD 193
Db 156 COSDVECSARRGGCPQRCVNTAGSYWCQWEGHSLASADGTLCPVKGPPRVAPNPTGVD 215
QY 194 SAMKEEVORLSRVDLLEKQLVLAPLHSLASQALEHGLPDPGSLLVHVSFOQLGRIDSL 253
Db 216 SAMKEEVORLSRVDLLEKQLVLAPLHSLASQALEHGLPDPGSLLVHVSFOQLGRIDSL 275
QY 254 SIOISFLEQLGSCSKKDS 273
Db 276 SIOISFLEQLGSCSKKDS 295

RESULT 13
US-09-978-697-2
; Sequence 2, Application US/09978697
; Patent No. US20020169284A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C27
; CURRENT FILING DATE: 2001-10-16
; CURRENT FILING DATE: 2001-10-16
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066364

; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/077450
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 60/077632
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077641
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077649
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077791
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/078004
; PRIOR FILING DATE: 1998-03-13
; PRIOR APPLICATION NUMBER: 60/078886
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078936
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078939
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079664
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079663
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079786
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079920
; PRIOR FILING DATE: 1998-03-30
; PRIOR APPLICATION NUMBER: 60/079923
; PRIOR FILING DATE: 1998-03-30
; PRIOR APPLICATION NUMBER: 60/080105
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080107
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080165
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080194
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080327
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080328
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080333
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080334
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/081070
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081049
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081071
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081195
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081203
; PRIOR FILING DATE: 1998-04-09
; PRIOR APPLICATION NUMBER: 60/081229
; PRIOR FILING DATE: 1998-04-09
; PRIOR APPLICATION NUMBER: 60/081955
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081817
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081819
; PRIOR FILING DATE: 1998-04-15
```

PRIOR APPLICATION NUMBER: 60/081952  
PRIOR FILING DATE: 1998-04-15  
PRIOR APPLICATION NUMBER: 60/081838  
PRIOR FILING DATE: 1998-04-15  
PRIOR APPLICATION NUMBER: 60/082568  
PRIOR FILING DATE: 1998-04-21  
PRIOR APPLICATION NUMBER: 60/082569  
PRIOR FILING DATE: 1998-04-21  
PRIOR APPLICATION NUMBER: 60/082704  
PRIOR FILING DATE: 1998-04-22  
PRIOR APPLICATION NUMBER: 60/082804  
PRIOR FILING DATE: 1998-04-22  
PRIOR APPLICATION NUMBER: 60/082700  
PRIOR FILING DATE: 1998-04-22  
PRIOR APPLICATION NUMBER: 60/082797  
PRIOR FILING DATE: 1998-04-22  
PRIOR APPLICATION NUMBER: 60/082796  
PRIOR FILING DATE: 1998-04-23  
PRIOR APPLICATION NUMBER: 60/083336  
PRIOR FILING DATE: 1998-04-27  
PRIOR APPLICATION NUMBER: 60/083322  
PRIOR FILING DATE: 1998-04-28  
PRIOR APPLICATION NUMBER: 60/083392  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083495  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083496  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083499  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083545  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083554  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083558  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083559  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083500  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083742  
PRIOR FILING DATE: 1998-04-30  
PRIOR APPLICATION NUMBER: 60/084366  
PRIOR FILING DATE: 1998-05-05  
PRIOR APPLICATION NUMBER: 60/084414  
PRIOR FILING DATE: 1998-05-06  
PRIOR APPLICATION NUMBER: 60/084441  
PRIOR FILING DATE: 1998-05-06  
PRIOR APPLICATION NUMBER: 60/084637  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/084639  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/084640  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/084598  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/084600  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/084627  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/084643  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/085339  
PRIOR FILING DATE: 1998-05-13  
PRIOR APPLICATION NUMBER: 60/085338  
PRIOR FILING DATE: 1998-05-13  
PRIOR APPLICATION NUMBER: 60/085323  
PRIOR FILING DATE: 1998-05-13  
PRIOR APPLICATION NUMBER: 60/085582  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085700  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085689

PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085579  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085580  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085573  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085704  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085697

Query Match 89.1%; Score 1340.5; DB 9; Length 295;  
Best Local Similarity 94.6%; Pred. No. 76-89; Indels 3; Gaps 2;  
Matches 246; Conservative 2; Mismatches 9; Indels 3; Gaps 2;

QY 17 VGGTEHAYR-FGRYCAV--RAHGDVSSFPVORYOPPLTTCDDGHRACSTYRTIYRTAY 73  
DB 36 VSGGRHARL-PARPLGCVLSRAHGDVSSFPVORYOPPLTTCDDGHRACSTYRTIYRTAY 95

QY 74 RSPGGLAPAPRYACCPGMRKTSGLPGAGAAICPPCENGGSCVQPGRCRCPAGMRGPT 133  
DB 96 RSPGGLAPAPRYACCPGMRKTSGLPGAGAAICPPCENGGSCVQPGRCRCPAGMRGPT 155

QY 134 CQSDVDECSARRGCGCPQRCVNTAGSYWCQWEGHSLADGTLCPKGGPVPVAPNPTGVD 193  
DB 156 CQSDVDECSARRGCGCPQRCVNTAGSYWCQWEGHSLADGTLCPKGGPVPVAPNPTGVD 215

QY 194 SAKKEVQRLQSRVLDLEKTLQVLAFLHSLASQALHEGLPDGSLVHSPQGLRIDSL 253  
DB 216 SAKKEVQRLQSRVLDLEKTLQVLAFLHSLASQALHEGLPDGSLVHSPQGLRIDSL 275

QY 254 SEQISFLEQLGSCSCCKDS 273  
DB 276 SEQISFLEQLGSCSCCKDS 295

RESULT 14  
US-09-978-192A-2  
Sequence 2, Application US/09978192A  
Patent No. US2002017553A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tunes, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OR INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630PIC9  
CURRENT APPLICATION NUMBER: US/09/978,192A  
CURRENT FILING DATE: 2001-10-15

**us-09-852-472-2.rapb**

PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/064249  
PRIOR FILING DATE: 1997-11-03  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/066364  
PRIOR FILING DATE: 1997-11-21  
PRIOR APPLICATION NUMBER: 60/077450  
PRIOR FILING DATE: 1998-03-10  
PRIOR APPLICATION NUMBER: 60/077632  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077641  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077649  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077791  
PRIOR FILING DATE: 1998-03-12  
PRIOR APPLICATION NUMBER: 60/078004  
PRIOR FILING DATE: 1998-03-13  
PRIOR APPLICATION NUMBER: 60/078886  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/078936  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/078910  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/078939  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/079294  
PRIOR FILING DATE: 1998-03-25  
PRIOR APPLICATION NUMBER: 60/079656  
PRIOR FILING DATE: 1998-03-26  
PRIOR APPLICATION NUMBER: 60/079664  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/079689  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/079663  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/079728  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/079786  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/079920  
PRIOR FILING DATE: 1998-03-30  
PRIOR APPLICATION NUMBER: 60/079923  
PRIOR FILING DATE: 1998-03-30  
PRIOR APPLICATION NUMBER: 60/080105  
PRIOR FILING DATE: 1998-03-31  
PRIOR APPLICATION NUMBER: 60/080107  
PRIOR FILING DATE: 1998-03-31  
PRIOR APPLICATION NUMBER: 60/080165  
PRIOR FILING DATE: 1998-03-31  
PRIOR APPLICATION NUMBER: 60/080194  
PRIOR FILING DATE: 1998-03-31  
PRIOR APPLICATION NUMBER: 60/080327  
PRIOR FILING DATE: 1998-04-01  
PRIOR APPLICATION NUMBER: 60/080328  
PRIOR FILING DATE: 1998-04-01  
PRIOR APPLICATION NUMBER: 60/080333  
PRIOR FILING DATE: 1998-04-01  
PRIOR APPLICATION NUMBER: 60/080334  
PRIOR FILING DATE: 1998-04-01  
PRIOR APPLICATION NUMBER: 60/081070  
PRIOR FILING DATE: 1998-04-08  
PRIOR APPLICATION NUMBER: 60/081049  
PRIOR FILING DATE: 1998-04-08  
PRIOR APPLICATION NUMBER: 60/081071  
PRIOR FILING DATE: 1998-04-08  
PRIOR APPLICATION NUMBER: 60/081195  
PRIOR FILING DATE: 1998-04-08  
PRIOR APPLICATION NUMBER: 60/081203

PRIOR APPLICATION NUMBER: 60/085338  
PRIOR FILING DATE: 1998-05-13  
PRIOR APPLICATION NUMBER: 60/085323  
PRIOR FILING DATE: 1998-05-13  
PRIOR APPLICATION NUMBER: 60/085582  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085700  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085689  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085579  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085580  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085573  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085704  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085697

Query Match 89.1%; Score 1340.5; DB 9; Length 295;  
Best Local Similarity 94.6%; Pred. No. 7e-89;  
Matches 246; Conservative 2; Mismatches 9; Indels 3; Gaps 2;

QY 17 VGTGTHAAR-GRGVAV--RAHGDVSESVFVRVQPELTTCGHRACSTYRTTAY 73  
DB 36 VGSGRHARLPAARLGCYLSPAHGDPVSESVFVRVQPELTTCGHRACSTYRTTAY 95  
QY 74 RSPGLAPARPRVACCPGKRTSGLPACGAICOPPCRNAGSCVQGRCPAGMGDT 133  
DB 96 RSPGLAPARPRVACCPGKRTSGLPACGAICOPPCRNAGSCVQGRCPAGMGDT 155  
QY 134 QSDVDECSARRGCPQRCVNTAGSYWCQCGEHSLSADGTLCPKGGPRVAPNPTGVD 193  
DB 156 QSDVDECSARRGCPQRCVNTAGSYWCQCGEHSLSADGTLCPKGGPRVAPNPTGVD 215  
QY 194 SAMEEYORLQSRVDLLEKQLVLAPLHSLASQALEHGLPDRSLVHSPQOLGRIDL 253  
DB 216 SAMEEYORLQSRVDLLEKQLVLAPLHSLASQALEHGLPDRSLVHSPQOLGRIDL 275  
QY 254 SEQISFLEBQSGSCCKDS 273  
DB 276 SEQISFLEBQSGSCCKDS 295

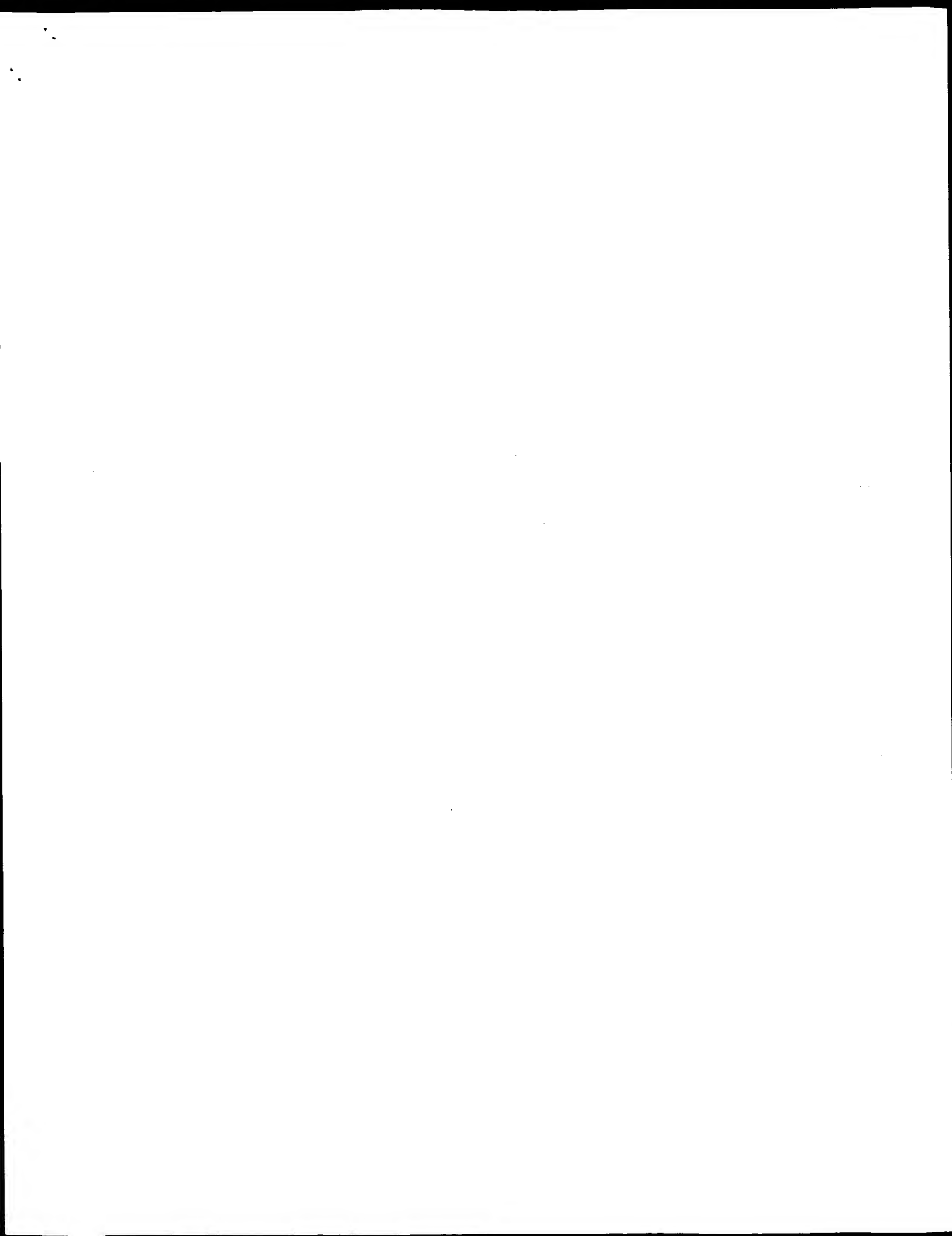
RESULT 15  
US-09-790-264-15  
Sequence 15, Application US/09790264  
Patent No. US2002028508A1  
GENERAL INFORMATION:  
APPLICANT: Holtzman, Douglas A.  
APPLICANT: Goodearl, Andrew D.J.  
TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING  
TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER  
FILE REFERENCE: US83  
CURRENT APPLICATION NUMBER: US/09/790,264  
CURRENT FILING DATE: 2001-02-21  
PRIOR APPLICATION NUMBER: US 09/065,661  
PRIOR FILING DATE: 1998-04-23  
PRIOR APPLICATION NUMBER: US 09/298,531  
PRIOR FILING DATE: 1999-04-23  
PRIOR APPLICATION NUMBER: US 09/065,363  
PRIOR FILING DATE: 1998-04-23  
PRIOR APPLICATION NUMBER: US 09/337,930  
PRIOR FILING DATE: 1999-06-22  
PRIOR APPLICATION NUMBER: US 09/102,705  
PRIOR FILING DATE: 1998-06-22  
PRIOR APPLICATION NUMBER: US 09/363,630  
PRIOR FILING DATE: 1999-07-29  
PRIOR APPLICATION NUMBER: US 09/124,538  
PRIOR FILING DATE: 1998-07-29

NUMBER OF SEQ ID NOS: 68  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 15  
LENGTH: 275  
TYPE: PRT  
ORGANISM: Mus musculus  
US-09-790-264-15

Query Match 78.5%; Score 1181; DB 10; Length 275;  
Best Local Similarity 78.1%; Pred. No. 1.5e-77;  
Matches 214; Conservative 18; Mismatches 40; Indels 2; Gaps 2;

QY 1 MRGSOEVLMTLVLAVG-TEHAARPGRVCAVARHGDVSESVFVRVQPELTTCG 59  
DB 1 MNGSGELVAMFLVLAADGTEHYRPSRYCTVIGSGSISFVQVQPELTTCG 60  
QY 60 RACSTYRTTYRTAYRRSPGLAPARPRVACCPGKRTSGLPACGAICOPPCRNAGSCVQ 119  
DB 61 RACSTYRTTYRTAYRRSPGLAPARPRVACCPGKRTSGLPACGAICOPPCRNAGSCVQ 120  
QY 120 PGRCPAGMRGDTQSDVDECSARRGCPQRCVNTAGSYWCQCGEHSLSADGTLCPK 179  
DB 121 PGRCPAGMRGDTQSDVDECSARRGCPQRCVNTAGSYWCQCGEHSLSADGTLCPK 180  
QY 180 GSPPRVAPNPT-GVDSAMEEYORLQSRVDLLEKQLVLAPLHSLASQALEHGLPDRGS 238  
DB 181 EGSPPRVAPNPT-GVDSAMEEYORLQSRVDLLEKQLVLAPLHSLASQALEHGLPDRGS 240  
QY 239 LVHSPQOLGRIDSLSEQISFLEBQSGSCCKD 272  
DB 241 LVHSPQOLGRIDSLSEQISFLEBQSGSCCKD 274

Search completed: December 17, 2002, 10:09:45  
Job time : 9.80645 secs





GenCore version 5.1.3  
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 17, 2002, 10:00:11 ; Search time 15.0228 Seconds

(Without alignments)  
1746.994 Million cell updates/sec

Title: US-09-852-472-2

Perfect score: 1505

Sequence: 1 MRGQEVLMMLVAVGCT.....SEQISFLEQLGSCCKKDS 273

Scoring table: BLASTN62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: PIR 73:\*

1: PIR1:\*

2: PIR2:\*

3: PIR3:\*

4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	434.5	28.9	293	2 T09065	hypothetical prote
2	257	17.1	1574	2 T13954	MEGF6 protein - ra
3	253.5	16.8	558	2 T17324	hypothetical prote
4	219	14.6	1620	2 T27283	hypothetical prote
5	196	13.0	1964	2 T09059	notch4 - mouse
6	189	12.6	678	2 B48089	growth arrest-spec
7	184	12.2	678	2 B48089	growth arrest-spec
8	182.5	12.1	2907	2 A57278	Nel-homolog protei
9	181	12.0	810	2 T10756	growth potentialin
10	178	11.8	674	2 I55476	fibritillin-1 precu
11	175.5	11.7	3002	2 A47221	notch3 protein - h
12	174.5	11.6	2321	2 S78549	notch protein - fr
13	174	11.5	2703	1 A24420	notch protein - fr
14	173.5	11.5	1247	1 MMHND	notch protein - fr
15	173	11.5	2531	2 A46019	notch protein - fr
16	172	11.4	2531	2 A46019	notch protein - fr
17	171.5	11.4	2871	2 A55624	notch protein - fr
18	170.5	11.3	2871	2 A55624	notch protein - fr
19	170	11.3	675	1 KXMS	notch protein - fr
20	170	11.3	2918	2 A54105	notch protein - fr
21	168.5	11.2	2318	2 S45306	notch protein - fr
22	168	11.2	675	1 KXMS	notch protein - fr
23	168	11.2	833	2 S19087	notch protein - fr
24	165	11.0	882	2 A31246	notch protein - fr
25	165	11.0	882	2 A31246	notch protein - fr
26	165	11.0	2524	2 A35844	notch protein - fr
27	164	10.9	1429	2 S06434	notch protein - fr
28	164	10.9	2555	2 A40043	notch protein - fr
29	163	10.8	3871	2 T22812	notch protein - fr

30	162	10.8	387	2 B49175	notch A protein -
31	162	10.8	646	2 S38819	plasma protein S -
32	162	10.8	646	2 S38819	plasma protein S -
33	160.5	10.7	2531	2 S18188	notch protein homo
34	160	10.6	2437	2 S42612	transmembrane prot
35	159.5	10.6	407	1 KFB07	coagulation factor
36	159	10.6	1820	2 A55494	latent transformin
37	158.5	10.5	456	1 KXBO	protein C (activat
38	157	10.4	676	1 KXMS	plasma protein S p
39	157	10.4	1221	2 A49457	fibulin-2 precursor
40	156	10.4	642	2 S53434	plasma protein S p
41	155.5	10.3	466	1 KFB07	coagulation factor
42	155	10.3	387	2 S38449	extracellular prot
43	155	10.3	1408	2 S16148	gene serrate prote
44	154.5	10.3	3635	2 T10053	laminin alpha 5 ch
45	154	10.2	642	2 S53433	plasma protein S p

## ALIGNMENTS

### RESULT 1

T09065

hypothetical protein - mouse

C/Species: Mus musculus (house mouse)

C/Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 11-Jan-2000

C/Accession: T09065

R/Rowen, L.; Mahatras, G.; Qin, S.; Ahearn, M.E.; Dankers, C.; Lasky, S.; Loretz, C.; Sci

submitted to the EMBL Data Library, October 1997

A/Description: Sequence of the mouse major histocompatibility locus class III region.

A/Reference number: Z16543

A/Accession: T09065

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-293 <ROW>

A/Cross-References: EMBL:AF030001; NID:g2564945; PID:g2564953

C/Genetics:

A/Map position: 17

A/Intons: 34/2; 75/2; 112/1; 144/1; 201/1; 228/3; 280/1

C/Superfamily: unassigned EGF-related proteins; EGF homology

F114-141/Domain: EGF homology <EGF1>

F148-183/Domain: EGF homology <EGF>

Query Match 28.9%; Score 434.5; DB 2; Length 293;

Best Local Similarity 37.3%; Pred. No. 1, 1e-24;

Matches 112; Conservative 36; Mismatches 101; Indels 51; Gaps 14;

QY	1	MRGQEVLMMLVAVG-GTE-HAYRGRVCAVRAHGPV--SESFVQRYQPFITTC	56
DB	11	LRG-----LSFVLVMTGEGTGSGFKESLIGVSKQTLVPLRVNESYSQPVYKPYLTC	65
QY	57	DGHRACSTYRTYRTYRVRSPGLAPRPRVACCPGKRTSLGPACGA-AICQPPCRNG	115
DB	66	ARRRISCTYRTYRVRVRREVP-QTHVCCQGWKPP--PGALTDAICSRKCLNG	122
QY	116	SCVQGRGRCPCAGMRDCCQSDVDECSARRGCPQRCVNTAGSWCQCEGHSADGTL	175
DB	123	VCTGDRCECAFGMGKCHVDVDECRASLTLCSHCINTAGSFLCSPPHVLGLDRT	182
QY	176	CYKKGPPVAVNPRTGV-----DSAMKEEVQLSGRVLLERKQLVLAFL	221
DB	183	CA--GGPPE--SPTSASILVAAREADSEERARLMEVRLERLEKLEQ-----	228
QY	222	HSLASA---LEHGLP-DPGSLVHVSFOQL-----GRDSSEQISFLEQSGSCCKKDS	273
DB	229	--WATQAGWAVRAVLPMPPELRBEQVALMGDRRLISLSDQVLLERLIGACACEDNS	286

### RESULT 2

T13954

MEGF6 protein - rat

C/Species: Rattus norvegicus (Norway rat)

C/Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 21-Jul-2000



Mol. Cell. Biol. 13, 4976-4985, 1993

A:Title: The protein encoded by a growth arrest-specific gene (gas6) is a new member of A:Reference number: A48089; MUID:93330291; PMID:8336730

A:Accession: B48089  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-678 <MAN>

A:Cross-references: GB:L13720; NID:9401766; PIDN:AAA58494.1; PID:9401767  
C:Superfamily: plasma protein S; EGF homology; Glu domain homology; laminin G repeat hom  
F:120-153/Domain: Glu domain homology #status atypical <Glu>  
F:160-195/Domain: EGF homology <EG1>  
F:201-236/Domain: EGF homology <EG2>  
F:242-277/Domain: EGF homology <EG3>  
F:311-671/Domain: sex hormone-binding globulin homology <SB>  
F:321-473/Domain: laminin G repeat homology <LGR>

Query Match  
Best Local Similarity 12.6%; Score 189; DB 2; Length 678;  
Matches 53; Conservative 8; Mismatches 64; Indels 30; Gaps 8;

QY 46 QRYVQPLTTCDEH-----RACSTRTTYTAYRSPGLAPRPRYACC-----PQWK 93  
DB 47 RRAVQVFEBAKQGLHRECEVEELCS--REAEVEFENDPETDYPRYLDCINKYSGPYT 104  
QY 94 RTSG-----LPGAGAAICOPPC-RNGSGCVP--GR--CRCPAGWRSDTCQSDVDEC 141  
DB 105 KNSGFATQVQNPDDC---TPNCDKRGCTACQDLMKNFECCLKAGGRLDKDVNEC 160  
QY 142 SARRGPCPCRCVNTAGSYWCQCBEGHSLADGTLG 176  
DB 161 SQENGCTQICNKGKSFHCSGSELSIDGRYC 195

#### RESULT 7

Growth arrest-specific protein gas6 - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 26-May-1994 #sequence\_revision 26-May-1994 #text\_change 05-Nov-1999

C:Accession: A48089; S37437  
R:Manfioletti, G.; Biancolini, C.; Avanzi, G.; Schneider, C.  
Mol. Cell. Biol. 13, 4976-4985, 1993  
A:Title: The protein encoded by a growth arrest-specific gene (gas6) is a new member of

A:Reference number: A48089; MUID:93330291; PMID:8336730  
A:Accession: A48089  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-673 <MAN>

A:Cross-references: GB:X59846; NID:9407060; PIDN:CAA42507.1; PID:9407061  
A:Note: authors translated the codon CCC for residue 424 as Ile  
C:Genetics:  
A:Gene: gas6  
C:Superfamily: plasma protein S; EGF homology; Glu domain homology; laminin G repeat hom

F:38-89/Domain: Glu domain homology #status atypical <Glu>  
F:117-150/Domain: EGF homology <EG1>  
F:157-199/Domain: EGF homology <EG2>  
F:198-233/Domain: EGF homology <EG3>  
F:239-274/Domain: EGF homology <EG4>  
F:308-666/Domain: sex hormone-binding globulin homology <SB>  
F:318-470/Domain: laminin G repeat homology <LGR>

Query Match  
Best Local Similarity 12.2%; Score 184; DB 2; Length 673;  
Matches 50; Conservative 8; Mismatches 64; Indels 36; Gaps 6;

QY 46 QRYVQPLTTCDEH-----RACSTRTTYTAYRSPGLAPRPRYACC-----PQWK 93  
DB 44 RRAVQVFEBAKQGLHRECEVEELCS--REAEVEFENDPETDYPRYLDCINKYSGPYT 104  
QY 90 --PGW-KRTSGLPAC-----GALICQPCRNKSGCVPGRCRCPAGWRSDTCQSDV 138

DB 102 KNDFPAKCVQNPDDCCTPNPCDKKGTTHIQDLMGN-----PFCVCTDGMGRLCDKDV 154  
QY 139 DECSARRGCGPCRCVNTAGSYWCQCBEGHSLADGTLG 176  
DB 155 NECVQKNGGCGVCHNKRGSPQCHSGSGLASDQTC 192

#### RESULT 8

A57278  
Fibrillin-2 precursor - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 23-Feb-1996 #sequence\_revision 23-Feb-1996 #text\_change 02-Aug-2002

R:Zhang, H.; Hu, W.; Ramirez, F.  
J. Cell Biol. 129, 1165-1176, 1995  
A:Title: Developmental expression of fibrillin genes suggests heterogeneity of extracelli  
A:Reference number: A57278; MUID:95263670; PMID:7744963  
A:Accession: A57278  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-2907 <ZHA>

A:Cross-references: GB:L39790; NID:9762830; PIDN:AAA74908.1; PID:9762831  
C:Superfamily: fibrillin 1; EGF homology  
F:139-1274/Domain: EGF homology <EGF1>  
F:2488-2523/Domain: EGF homology <EGF>

Query Match  
Best Local Similarity 12.1%; Score 182.5; DB 2; Length 2907;  
Matches 59; Conservative 20; Mismatches 85; Indels 87; Gaps 7;

QY 2 RGSQEVLMWLAVAGTEHAY-----RGRRCVAVRAGDPVSESPVQRYVQPLT 54  
DB 77 RQQDELIRG--PNVCGSRFHSYCCPGWKTLPGNQGVIFICANSQDGFCSR--PNMC 130  
QY 55 TCDGRACST--YRTYFAYRSPGLAPRPRYACCPCPKRTSGLPAGCAICQPCPR 112  
DB 131 TSSGQISPTGGRKSIQCSYRCMNGSTCADHDQCCQKGTGTF-----YCGQPVENGCG 185  
QY 113 NCGSCVQGRRCRCPCAGMRDTCQ----- 135  
DB 166 NGRGICGNRCACVGTGPGQCEVDYRTGCFYQVNNQMCQGLGYCTKLCATIGR 245  
QY 136 -----SDVDECSARRGCGP--QRCVNTAGSYWCQCE 165  
DB 246 AMGHPCEWCPAQPCRGRTIPNIRIGACQDVEDCOALPGLCOGNCINTVGSFECRCPA 305  
QY 166 GHSLSADGTLG 176  
DB 306 GHKQSETTQRC 316

#### RESULT 9

T10756  
Ncl-homolog protein - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 16-Jul-1999

R:Kuroda, S.; Yokunaga, C.; Kiyohara, Y.; Konishi, H.; Matsushashi, S.; Kikkawa, U.  
submitted to the EMBL Data Library, November 1998  
A:Description: Protein Kinase C-binding protein.  
A:Reference number: Z17122  
A:Accession: T10756  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-810 <KUR>

A:Cross-references: EMBL:U48246; NID:93851179; PID:93851180  
A:Experimental source: strain Sprague-Dawley, brain

Query Match  
Best Local Similarity 12.0%; Score 181; DB 2; Length 810;  
Matches 36; Conservative 12; Mismatches 38; Indels 10; Gaps 3;

QY 88 CPGWKRTSGLPAGCAICQPCRCNKGSCVQPCRCPCAGWRSDTCQSDVDECSARRG 147

Tue Dec 17 14:03:51 2002

Nature 352, 334-337, 1991

A;Title: Partial sequence of a candidate gene for the Marfan syndrome.  
 A;Reference number: S17064; MUID:91304568; PMID:1852207  
 A;Accession: S17064  
 A;Molecule type: mRNA  
 A;Residues: 1030-3002 <MAS>  
 A;Cross-references: EMBL:X63556  
 R;Dietz, H.C.; Valle, D.; Francomano, C.A.; Kendzior, R.J.  
 Science 259, 680-683, 1993  
 A;Title: The skipping of constitutive exons in vivo induced by nonsense mutations.  
 A;Reference number: 159574; MUID:93157831; PMID:8430317  
 A;Accession: 159574  
 A;Status: preliminary; translated from GB/EMBL/DBJ  
 A;Molecule type: DNA  
 A;Residues: 2217-2288, 'I', 2290-2325 <RES>  
 A;Cross-references: GB:854426; NID:G264860; PIDN:AA825244.1; PID:G264861  
 R;Lee, B.; Godfrey, M.; Vitale, E.; Hori, H.; Mattei, M.G.; Sarfarazi, M.; Tsipouras,  
 Nature 352, 330-334, 1991  
 A;Title: Linkage of Marfan syndrome and a phenotypically related disorder to two differ-  
 A;Reference number: S17062; MUID:91304567; PMID:1852206  
 A;Accession: S17062  
 A;Molecule type: mRNA  
 A;Residues: 'VLTVVVFILSYNKM', 944-1444 <LEB1>  
 A;Cross-references: EMBL:X62008; NID:G31398; PIDN:CAB56534.1; PID:G5924015  
 A;Accession: S62111  
 A;Molecule type: Protein  
 A;Residues: 1166-1176, 'X', 1178-1180, 'D', 1182-1185 <LEB2>  
 R;Maddox, B.K.; Sakai, L.Y.; Keene, D.R.; Glanville, R.W.  
 J. Biol. Chem. 264, 21381-21385, 1989  
 A;Title: Connective tissue microfibrils. Isolation and characterization of three large  
 A;Reference number: A34198; MUID:90078246; PMID:2512293  
 A;Accession: A34198  
 A;Molecule type: protein  
 A;Residues: 585-575, 1890-1892, 'I', 1894-1900 <MAD>  
 C;Comment: Fibrillin is a major component of elastin-associated microfibrils.  
 C;Genetics:  
 C;Gene: GDB:FBN1  
 A;Cross-references: GDB:127115; OMIM:134797; OMIM:154700  
 A;Map position: 15q21.1-15q21.1  
 A;Intons: 2236/1; 2258/1; 2297/1  
 C;Superfamily: fibrillin 1; EGF homology  
 F;Keywords: alternative splicing; calcium binding; extracellular matrix; glycoprotein;  
 F;132-3002/Product: fibrillin (5'-region exon A splice form) #status predicted <MAD>  
 F;132-3002/Product: fibrillin (5'-region exon C splice form) #status predicted <MAD>  
 F;1332-1367/Domain: EGF homology <EGF2>  
 F;1457-1492/Domain: EGF homology <EGF2>  
 F;2262-2295/Domain: EGF homology <EGF1>

Query Match 11.7%; Score 175.5; DB 2; Length 3002;  
 Best Local Similarity 18.9%; Pred. No. 7.2e-05;  
 Matches 52; Conservative 14; Mismatches 48; Indels 161; Gaps 6;

QY 75 RSPGLAPARYACCPGWKRTSLPGA----- 101  
 Db 185 KGNVCGSRYNAYCCPGWKT---LPGNQCIPICRHSCGDGFCSPRNMCTCPSGIAPS 241  
 QY 102 -----CGAATCQPPCRNGSCVQPCRCPA 127  
 Db 242 CGRSIQHCNIRONNGSCSDHCLCQKQYIGTHCQGPVCSGCLNGRCVAPNRCCTY 301  
 QY 128 GWRGDTCC----- 135  
 Db 302 GFTGPQCDYRTGFCFTVTSNQMQQLSGIVCTKQLCCATVGRAGWHPCMCFAQHPH 361  
 QY 136 -----SDVDECSARRGGCP-ORCVNTAGSYWCQWEGHSLSDGTLG----- 176  
 Db 362 CRGFTPIRTGACQDQVDECAIFCLCGGNCINTVSGFECKPAGHKLNEVSQKCEDID 421  
 QY 177 -----VPKGG-----PPRVAFNPPTG 191  
 Db 422 ECSTPIGCEGECTNTVSSYFCKCPGFPYSPDG 456

Db 504 CQPGYVGN-----GTICKAFCECRVGGTCVAPNKCVCPSGFTGSHCEKDIDECAGFVE 559

QY 148 CP--QRCVNTAGSYWCQWEGH-----SLSADGTLGV 177

Db 560 CHNYSRCVNLPGWVHCRCRSGFHDGDTGYSLSGESCI 595

## RESULT 10

155476

growth potentiating factor - rat

C;Species: Rattus sp. (rat)

C;Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 20-Apr-2001

A;Accession: 155476

R;Nakano, T.; Higashino, K.; Kikuchi, N.; Kishino, J.; Nomura, K.; Fujita, H.; Ohara, O.

J. Biol. Chem. 270, 5702-5705, 1995

A;Title: Vascular smooth muscle cell-derived, Gla-containing growth-potentiating factor

A;Reference number: 155476; MUID:95197586; PMID:7890695

A;Accession: 155476

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-674 &lt;RES&gt;

A;Cross-references: GB:D42148; NID:G1526567; PIDN:RAA07719.1; PID:G893402

C;Superfamily: plasma protein S; EGF homology; Gla domain homology; laminin G repeat hom

F;117-150/Domain: EGF homology &lt;EG1&gt;

F;157-192/Domain: EGF homology &lt;EG2&gt;

F;198-233/Domain: EGF homology &lt;EG3&gt;

F;239-274/Domain: EGF homology &lt;EG4&gt;

F;308-667/Domain: sex hormone-binding globulin homology &lt;SHB&gt;

F;318-470/Domain: laminin G repeat homology &lt;LGR&gt;

Query Match 11.8%; Score 178; DB 2; Length 674;  
 Best Local Similarity 30.4%; Pred. No. 1.3e-05;  
 Matches 48; Conservative 8; Mismatches 66; Indels 36; Gaps 6;

QY 46 QRVYQPLTTCTDGH-----RACSTRTTYRTAYRRSPGLAPARYACC----- 89

Db 44 RRAYQVFEBKQHLRECEVEVCSKEA--REVFNDFDYFPRYQCEMKRYGRPD 101

QY 90 --PWKR--TSGLPKAC-----GAATCQPPCRNGSCVQPCRCPAGRGDTQSDV 138

Db 102 KNFNFAFCVKNLPDQCTNPCKKGTLCQDLNGN-----PFLCKDQWGGRLCKDV 154

QY 139 DECSARRGGQPCRVNTAGSYWCQWEGHSLSADGTLG 176

Db 155 NECSQKNGGCSQVCHKNKPGSFQACHSFSLQSDNKC 192

## RESULT 11

A47221

fibrillin 1 precursor - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 02-Jun-1995 #sequence\_revision 25-Apr-1997 #text\_change 02-Aug-2002

A;Accession: A47221; 154355; S17064; 159574; S17062; S62111; A34198

R;Corson, G.M.; Chalberg, S.C.; Dietz, H.C.; Charbonneau, N.L.; Sakai, L.Y.

Genomics 17, 476-484, 1993

A;Title: Fibrillin binds calcium and is coded by cDNAs that reveal a multidomain structu

A;Reference number: A47221; MUID:94010947; PMID:7691719

A;Accession: A47221

A;Molecule type: mRNA

A;Residues: 1-337, 'T', 339-1029 &lt;COR&gt;

A;Cross-references: GB:X63556

R;Perrin, L.V.; D'Alessio, M.; Ramirez, F.; Lynch, J.; Sykes, B.; Pangillan, T.; Bond

Hum. Mol. Genet. 2, 961-968, 1993

A;Title: Genomic organization of the sequence coding for fibrillin, the defective gene F

A;Reference number: 154355; MUID:93372860; PMID:8364578

A;Accession: 154355

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 132-3002 &lt;PER&gt;

A;Cross-references: GB:L13923; NID:G306745; PIDN:AA802036.1; PID:G306746

R;Maslen, C.L.; Corson, G.M.; Maddox, B.K.; Glanville, R.W.; Sakai, L.Y.

## RESULT 12

S78549

notch3 protein - human

C/Species: Homo sapiens (man)

C/Date: 24-Jul-1998 #sequence\_revision 24-Jul-1998 #text\_change 02-Aug-2002

C/Accession: S78549; S78825

R/Author: A.; Tournier-Lasserre, E.

A/Reference number: S78549

A/Accession: S78549

A/Molecule type: mRNA

A/Residues: 1-2321 &lt;OU&gt;

A/Cross-references: EMBL:U97669; NID:92668591; PIDN:AAE93371.1; PID:92668592

R/Author: A.; Coppechot, C.; Ducros, A.; Vahedi, K.; Chabrier, H.; Mouton, F.; Alamowicz

Nature 383, 707-710, 1996

A/Title: Notch3 mutations in CADASIL, a hereditary adult-onset condition causing stroke

A/Reference number: S78825; MUID:97032728; PMID:8878478

A/Accession: S78825

A/Status: nucleic acid sequence not shown

A/Molecule type: DNA

A/Residues: 67-113,138-194,268-333, 'G', 335-346,536-613,716-765,1240-1279,1815-1868 &lt;OU&gt;

A/Cross-references: EMBL:U97669

C/Genetics:

A/Map position: 19p13.1

C/Function:

A/Description: may be involved in pathogenesis of CADASIL, causing a type of stroke and

C/Keywords: tandem repeat; EGF homology; laminin-type EGF-1

F/123-155/Domain: EGF homology &lt;EGF1&gt;

F/162-194/Domain: EGF homology &lt;EGF1&gt;

F/240-271/Domain: EGF homology &lt;EGF1&gt;

F/318-349/Domain: EGF homology &lt;EGF2&gt;

F/473-504/Domain: EGF homology &lt;EGF3&gt;

F/853-884/Domain: EGF homology &lt;EGF3&gt;

F/928-959/Domain: EGF homology &lt;EGF3&gt;

F/1070-1122/Domain: EGF homology &lt;EGF3&gt;

F/1898-1870/Domain: laminin-type EGF-like homology &lt;LEGS&gt;

F/1871-1903/Domain: ankyrin repeat homology &lt;AN1&gt;

F/1805-1937/Domain: ankyrin repeat homology &lt;AN2&gt;

F/1938-1970/Domain: ankyrin repeat homology &lt;AN3&gt;

F/1971-2003/Domain: ankyrin repeat homology &lt;AN5&gt;

Query Match

Best Local Similarity 11.6%; Score 174.5; DB 2; Length 2321;

Matches 50; Conservative 14; Mismatches 44; Indels 37; Gaps 11;

QY 56 CDGHRACSTYRTYRTAVRSPGLAPRPVAC-CPGMRK--TSGLRGACGAATQPPCR 112

DB 87 CAGRGVCS-----SVAGTARFSCRCPRGFRGPDCLPDC-----LSSPCA 129

QY 113 NGSC-VDP-GR--CRCPAGWRGDTCCSDVDEC-----SARRGCGPQRCVNTAGSYWCQW 164

DB 130 HCARSTVGPDRFLCSPGPGYQGRSCSDVDECRVGEPCRHG---TCLNTPGSRFCQCP 166

QY 165 EGHSLASDGLTCVKGKGPVAVNP 189

DB 187 AGYT-----GFLCENPVP--CAPSP 205

RESULT 13

A24420

Notch protein - fruit fly (Drosophila melanogaster)

C/Species: Drosophila melanogaster

C/Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999

C/Accession: A24420; S09358; A05267

R/Author: S.; Kelley, M.R.; Young, M.W.

Mol. Cell. Biol. 6, 3094-3108, 1986

A/Reference number: A24420; MUID:87064624; PMID:3097517

A/Accession: A24420

A/Molecule type: DNA

A/Residues: 1-2703 &lt;KID&gt;

A/Cross-references: GB:K03508; NID:9157991; PIDN:AAA28725.1; PID:9157993

R/Author: K.A.; Johansen, K.M.; Xu, T.; Aravanis-Teakonas, S.

Cell 43, 567-581, 1985

A/Reference number: A24768; MUID:86079539; PMID:3935325

A/Accession: A24768

A/Molecule type: mRNA

A/Residues: 1-48, 'I', 50-118, 'R', 120-230, 'I', 232-256, 'N', 258-266, 'A', 268-872, 'R', 874-958, 'R', 960-1000

A/Note: the authors translated the codon ATC for residue 49 as Thr, ATT for residue 2044

Nucleic Acids Res. 17, 6463-6471, 1989

A/Title: Hypervariability of simple sequences as a general source for polymorphic DNA

A/Reference number: S09358; MUID:89385974; PMID:2780284

A/Accession: S09358

A/Molecule type: DNA

A/Residues: 2505-2551, 'CQQQ', 2552-2576, 'E', 2578-2604, 'TAU'

R/Author: K.A.; Yedvobnick, B.; Finerty, V.G.; Aravanis-Teakonas, S.

Cell 40, 55-62, 1985

A/Title: opa: a novel family of transcribed repeats shared by the Notch locus and other c

A/Reference number: A05267; MUID:85099329; PMID:2981631

A/Accession: A05267

A/Molecule type: DNA

A/Residues: 2504-2576, 'E', 2578-2611 &lt;MHA2&gt;

C/Genetics:

A/Map position: opa

A/Cross-references: FlyBase:FBgn0004647

A/Map position: 8.96-9.36

A/Introns: 53/3; 84/3; 171/3; 240/3; 283/3; 2333/3; 2436/3; 2588/3

C/Keywords: notch protein; ankyrin repeat homology; EGF homology

F/297-328/Domain: transmembrane #status predicted &lt;TM1&gt;

F/530-561/Domain: EGF homology &lt;EGF1&gt;

F/558-599/Domain: EGF homology &lt;EGF1&gt;

F/968-1019/Domain: EGF homology &lt;EGF2&gt;

F/1064-1095/Domain: EGF homology &lt;EGF3&gt;

F/1187-1218/Domain: EGF homology &lt;EGF3&gt;

F/1746-1762/Domain: transmembrane #status predicted &lt;TM2&gt;

F/1950-1982/Domain: ankyrin repeat homology &lt;AN1&gt;

F/1988-2015/Domain: ankyrin repeat homology &lt;AN2&gt;

F/2017-2049/Domain: ankyrin repeat homology &lt;AN3&gt;

F/2050-2082/Domain: ankyrin repeat homology &lt;AN4&gt;

F/2083-2115/Domain: ankyrin repeat homology &lt;AN5&gt;

F/2538-2568/Region: glutamine-rich

Query Match

Best Local Similarity 11.6%; Score 174; DB 1; Length 2703;

Matches 60; Conservative 18; Mismatches 67; Indels 76; Gaps 13;

QY 18 GTEHAYRPRRYCAVRAH--GDPVSEFVQRYQPLTTCGHRACSTYRTYRTAVR 75

DB 70 GGTCTVQNGKTKYACDSHYVD-----YCEHRNPQNSMR--CQNGCTQVTFRNG 118

QY 76 SPGLAPRPVAC-CP-GMKRT--SGLRGACGAATC----- 107

DB 119 HPGI-----SKCPLGFDLSCEIAVPNACHVITCLNGTCTQLTTEYTACANGYT 171

QY 108 -----OPCRNGSCV-----QPRGCRCPAGWRGDTCCSDVDECSEA---RRGC 148

DB 172 GRCETKYLCASSPCKNATYTLALAGSSFTCCGPGFGRDTCSDVDECQSNPKYGG- 230

QY 149 PCRCNTAGSYWCQWBGHSLASDGLTCVKGKGPVAVNP 189

DB 231 --TCVNTHGSYQCCPTGYT-----GKDCDTKYKP--CAPSP 263

RESULT 14

MMH0ND

nidogen precursor - human

N/Alternate names: entactin

C/Species: Homo sapiens (man)

```

192  QY  -----VDSAMKEEVRQLQSRVDLLLEKQLQVLAPLH-SLASQALEHGLPDPGSLVHS 243
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
892  DB  STGYCWCVDGR-EVEGTRTRPGMTPPCLSTVALPFIHQGPAVPTAVIPLP-PGTHILL-- 947
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
244  QY  FQQLGRIDSL 253
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
948  DB  FAQTGKIERL 957
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :

RESULT 15
JP0076
nel protein - chicken
C:Species: gallus gallus (chicken)
C:Date: 24-Feb-1995 #sequence_revision 24-Feb-1995 #text_change 13-Aug-1999
C:Accession: A38963; JP0076
R:Matsumashi, S.; Noji, S.; Koyama, E.; Myokai, F.; Ohuchi, H.; Taniguchi, S.; Hori, K.
R:Matsumashi, S.; Noji, S.; Koyama, E.; Myokai, F.; Ohuchi, H.; Taniguchi, S.; Hori, K.
Dev. Dyn. 203, 212-222, 1995
A:Title: New gene, nel, encoding a Mr 93K protein with EGF-like repeats is strongly ex-
A:Reference number: A38963; MUID:95383734; PMID:7655083
A:Accession: A38963
A:Accession: A38963
A:Molecule type: mRNA
A:Residues: 1-835 <MAT>
A:Cross-references: DDBJ:D45365
A:Experimental source: 9-day embryo
R:Matsumashi, S.; Noji, S.; Koyama, E.; Myokai, F.; Ohuchi, H.; Taniguchi, S.; Hori, K.
submitted to JIPID, January 1995
A:Description: A new gene, nel, encoding a Mr 93K protein with EGF-like repeats is str
A:Reference number: JP0076
A:Accession: JP0076
A:Molecule type: mRNA
A:Residues: 1-835 <MA2>
A:Cross-references: DDBJ:D45365
A:Experimental source: 9-day embryo
C:Superfamily: von Willebrand factor type C repeat homology <EGF homology
F:273-333/Domain: von Willebrand factor type C repeat homology <VWC>
F:273-333/Domain: EGF-like repeats
F:395-592/Region: EGF homology <EGF1>
F:444-480/Domain: EGF homology <EGF>
F:486-521/Domain: EGF homology <EGF2>
F:525-552/Domain: EGF homology <EGF2>

Query Match 11.5%; Score 173; DB 2; Length 835;
Best Local Similarity 41.4%; Pred: No. 3.6e-05;
Matches 29; Conservative 12; Mismatches 27; Indels 2; Gaps 1;

QY 100 GACGAATCQPPCRNGSCVQPGRCRCFAGWRGDTQSDVDECSARRGCGPOR--CVNTAG 157
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
DB 518 GTVCKAFCKGCRNGGACIASNVCACFQGTGPGSCETIDECSDGFOCDSRANCLPG 577
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :

QY 158 SYWCQWEGH 167
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
DB 578 WYHCECRDGY 587
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :

Search completed: December 17, 2002, 10:03:37
Job time : 19.0228 secs

```

C>Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 20-Oct-2000

C:Accession: A33322; A32437; A61367  
C:Cross-references: EMBL:M30269  
R:Nagayoshi, T.; Sanborn, D.; Hickok, N.J.; Olsen, D.R.; Fazio, M.J.; Chu, M.L.; Knowlton, R.N.  
J. Biol. Chem. 268, 581-594, 1993  
A:Title: Human nidogen: complete amino acid sequence and structural domains deduced from cDNA  
A:Reference number: A33322; MUID:90091745; PMID:2574658  
A:Accession: A33322  
A:Molecule type: mRNA  
A:Residues: 1-1247 <NAG>  
A:Cross-references: EMBL:M30269  
R:Olsen, D.R.; Nagayoshi, T.; Fazio, M.; Mattei, M.G.; Passage, E.; Weil, D.; Timpl, R.; Am. J. Hum. Genet. 44, 876-885, 1989  
A:Note: The authors translated the codon AAG for residue 966 as Cys  
F:Fazio, M.J.; O'Leary, J.; Kaeheeril, V.M.; Chen, Y.Q.; Saitta, B.; Uitto, J.  
J. Invest. Dermatol. 97, 281-285, 1991  
A:Title: Human nidogen: cDNA cloning, cellular expression, and mapping of the gene to chromosome 8  
A:Reference number: A32437; MUID:89270475; PMID:2471408  
A:Accession: A32437  
A:Molecule type: mRNA  
A:Residues: 667-1247 <OLS>  
A:Cross-references: EMBL:M27445; NID:G602466; PIDN:AAA57261.1; PID:G602467  
A:Note: The authors translated the codon AAG for residue 966 as Cys  
F:Fazio, M.J.; O'Leary, J.; Kaeheeril, V.M.; Chen, Y.Q.; Saitta, B.; Uitto, J.  
J. Invest. Dermatol. 97, 281-285, 1991  
A:Title: Human nidogen: structural and functional characterization of the 5'-flanking region  
A:Reference number: A61367; MUID:91302882; PMID:1906509  
A:Accession: A61367  
A:Molecule type: DNA  
A:Residues: 1-28 <PAZ>  
C:Comment: This protein is a basement membrane glycoprotein that forms a complex with laminin  
C:Genetics:  
A:Gene: GDB:NID  
A:Cross-references: GDB:120236; OMIM:131390  
A:Map position: 1q43-q43  
C:Superfamily: nidogen; EGF homology; LDL receptor WYTD-containing repeat homology; thyroglobulin  
C:Keywords: basement membrane; beta-hydroxyasparagine; calcium binding; cell binding; collagen binding

protein  
F:1-28/Domain: signal sequence #status predicted <SIG>  
F:29-1247/Product: nidogen #status predicted <MAT>  
F:390-425/Domain: EGF homology <EG1>  
F:672-708/Domain: EGF homology <EG2>  
F:702-704/Region: cell attachment [R-G-D] motif  
F:714-750/Domain: EGF homology <EG3>  
F:762-800/Domain: EGF homology <EG4>  
F:806-839/Domain: EGF homology <EG5>  
F:849-919/Domain: thyroglobulin type I repeat homology <THY1>  
F:990-1032/Domain: LDL receptor WYTD-containing repeat homology <YW1>  
F:1033-1075/Domain: LDL receptor WYTD-containing repeat homology <YW2>  
F:1076-1120/Domain: LDL receptor WYTD-containing repeat homology <YW3>  
F:1121-1160/Domain: LDL receptor WYTD-containing repeat homology <YW4>  
F:1161-1197/Domain: LDL receptor WYTD-containing repeat homology <YW5>  
F:1215-1243/Domain: EGF homology <EG6>  
F:1289, 296/Binding site: sulfate (Tyr) (covalent) #status predicted  
F:129, 819/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted  
F:756/Cross-link: isopeptide (Gln) (interchain to Lys N6-amino of laminin) #status predicted  
F:1137/Binding site: carbohydrate (Asn) (covalent) #status predicted

	Query Match	11.5%	Score 173.5;	DB 1;	Length 1247;
Qy	20	TEHAYRPGRV-----CAVRANG-----DPVSEFQRVYQFLITCDGHRACTYR 66			
Dd	681	TNAACRGPRQTQTCESIGFRGDRTVDICSE-----QP--SVCGSHITCNNH- 730			
Qy	67	TIYTATRRSPLAPARPVACCPGWKTSGLPGAGAAIQQPP-----CRNG----- 114			
Dd	731	-----PGTFRCCEVEGYQSFSD--EGTCVAWVPDRPINYCETGLHCNDIPQR 774			
Qy	115	GSCVQPG-----RCRCPAGWGD--TCOSDVDECSARRGGCPORCVNTAGSVWCOCWEHGS 168			
Dd	775	AQCIVTGSSYTCCLPFGSGDGACO-DVDECQPSRCHPDFAFCYNTPGSTCCCKPGY- 832			
Qy	169	LSADGTLCVP-----KGGPRVAPNPFTG----- 191			
Dd	833	-OGDFRCVPGEVEKTRCOHEREILGAAGATDPQPIPPGLFPVECDAGHYVPTQCHG 891			

GenCore version 5.1.3  
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 17, 2002, 09:45:16 ; Search time 8.80645 Seconds

(without alignments)  
1285.766 Million cell updates/sec

Title: US-09-852-472-2  
Perfect score: 1505  
Sequence: 1 MRSGEVLMLVAVGCT.....SEGISFLEQLGSCSKKDS 273

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	196	13.0	1964	1	NTC4_MOUSE
2	188.5	12.5	2003	1	NTC4_HUMAN
3	184	12.2	816	1	NEL2_MOUSE
4	183	12.2	810	1	NEL1_HUMAN
5	182.5	12.1	2907	1	FBN2_MOUSE
6	181.5	12.1	816	1	NEL2_HUMAN
7	181	12.0	810	1	NEL1_RAT
8	179.5	11.9	816	1	NEL2_RAT
9	176	11.7	652	1	CD93_HUMAN
10	176	11.7	2703	1	NOTC_DROME
11	175.5	11.7	816	1	NEL1_CHICK
12	175.5	11.7	2871	1	FBN1_HUMAN
13	174.5	11.6	2321	1	NTC3_HUMAN
14	173.5	11.5	1247	1	NID0_HUMAN
15	172	11.4	2531	1	NTC1_MOUSE
16	171.5	11.4	2871	1	FBN1_MOUSE
17	170.5	11.3	675	1	PRIS_BOVIN
18	170	11.3	2911	1	FBN2_HUMAN
19	169.5	11.3	2871	1	FBN1_PIG
20	168.5	11.2	2318	1	NTC3_MOUSE
21	168	11.2	675	1	PRIS_RAT
22	166	11.0	833	1	DL_DROME
23	166	11.0	1238	1	JAG2_HUMAN
24	166	11.0	1247	1	JAG2_HUMAN
25	166	11.0	1247	1	JAG2_MOUSE
26	165	11.0	1202	1	JAG2_RAT
27	165	11.0	2524	1	NOTC_XENLA
28	164	10.9	1429	1	LIL2_CAEEL
29	163	10.8	2556	1	NTC1_HUMAN
30	162	10.8	644	1	CD93_MOUSE
31	162	10.8	646	1	PRIS_MOUSE
32	162	10.8	675	1	PRIS_BOVIN
33	161.5	10.7	618	1	DL13_HUMAN

34	161.5	10.7	2319	1	NTC3_RAT	Q91172 ratnus novy
35	161	10.7	459	1	PRIS_PIG	Q91172 sus scrofa
36	160.5	10.7	643	1	CD93_RAT	Q91172 ratnus novy
37	160.5	10.7	2531	1	NTC1_RAT	Q91172 ratnus novy
38	160	10.6	2437	1	NTC1_BRARE	Q91172 ratnus novy
39	159.5	10.6	407	1	FAT7_BOVIN	Q91172 ratnus novy
40	158.5	10.5	456	1	PRIS_BOVIN	Q91172 ratnus novy
41	157.5	10.5	379	1	WIP1_MOUSE	Q91172 ratnus novy
42	157	10.4	676	1	PRIS_HUMAN	Q91172 ratnus novy
43	157	10.4	1221	1	FBL2_MOUSE	Q91172 ratnus novy
44	156	10.4	649	1	PRIS_MACMU	Q91172 ratnus novy
45	156	10.4	1213	1	JAG3_BRARE	Q91172 ratnus novy

## ALIGNMENTS

RESULT 1  
NTC4\_MOUSE  
ID NTC4\_MOUSE STANDARD: PRT: 1964 AA.  
AC P1695; Q62389; Q62390; Q35442; Q9R1M9; Q88314; Q88316; Q9R1X0;  
DT 01-NOV-1993 (Rel. 26, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Neurogenic locus notch homolog protein 4 precursor (Notch 4)  
DE [Contains: Transforming protein Int-3].  
GN NOTCH4 OR INT3 OR INT-3.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
OX NCBI\_TaxID=10090;  
RX MEDLINE=92194507; PubMed=1312643;  
RA Robbins J., Biondel B.U., Callahan D., Callahan R.;  
RT "Mouse mammary tumor gene int-3: a member of the notch gene family  
transforms mammary epithelial cells.";  
RL J. Virol. 66:2594-2599(1992).  
[2]  
RP REVISIONS, SEQUENCE FROM N.A.  
RX MEDLINE=97294599; PubMed=9150355;  
RA Callahan D., Callahan R.;  
RT "The mouse mammary tumor associated gene INT3 is a unique member of  
the NOTCH gene family (NOTCH4).";  
RN Oncogene 14:1883-1890(1997).  
[3]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Lung, and Testis;  
RX MEDLINE=96281668; PubMed=8681805;  
RA Uytendaele H., Marazzi G., Wu G., Yan Q., Saason D., Kitajewski J.;  
RT "Notch4/int-3, a mammary proto-oncogene, is an endothelial  
cell-specific mammalian Notch gene.";  
RN Development 122:2251-2259(1996).  
[4]  
RP SEQUENCE FROM N.A.  
RA Rowen L., Mahalinas G., Qin S., Ahearn M.E., Dankers C., Lasky S.,  
RA Loretz C., Schmidt S., Tipton S., Traicoff R., Zackone K., Hood L.;  
RT "Sequence of the mouse major histocompatibility locus class III  
region.";  
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.  
[5]  
RP SEQUENCE OF 1436-1600 FROM N.A.  
RX MEDLINE=99252212; PubMed=10233982;  
RA Lee J.-S., Hartana T., Ishimoto A., Honjo T., Yanagawa S.-I.;  
RT "Intrastemal type A particle-mediated activation of the Notch4/int3  
gene in a mouse mammary tumor: generation of truncated Notch4/int3  
mRNAs by retroviral splicing events.";  
RL J. Virol. 73:5166-5171(1999).  
[6]  
RP FUNCTION.  
RX MEDLINE=21244657; PubMed=11344305;  
RA Uytendaele H., Ho J., Rossant J., Kitajewski J.;  
RT "Vascular patterning defects associated with expression of activated



RT Notch4 in embryonic endothelium.";  
 RN Proc. Natl. Acad. Sci. U.S.A. 98:5643-5648(2001).  
 RP [7]  
 RP SEQUENCE OF 1463-1964, POST-TRANSLATIONAL PROCESSING, AND MUTAGENESIS  
 OF VAL-1463.  
 RA Saxena M.T., Schroeter E.H., Mumm J.S., Kopan R.;  
 RT "Murine notch homologs (NL-4) undergo presenilin-dependent  
 proteolysis.";  
 RL J. Biol. Chem. 276:40268-40273(2001).  
 RN [8]  
 RN POST-TRANSLATIONAL PROCESSING.  
 RX MEDLINE=21374376; PubMed=11459941;  
 RA Mitutani T., Taniguchi Y., Aoki T., Hashimoto N., Honjo T.;  
 RT "Conservation of the biochemical mechanisms of signal transduction  
 among mammalian Notch family members.";  
 CC Proc. Natl. Acad. Sci. U.S.A. 98:9026-9031(2001).  
 CC -!- FUNCTION: Functions as a receptor for membrane-bound ligands  
 Jagged1, Jagged2 and Delta1 to regulate cell-fate determination.  
 CC Upon ligand activation through the released notch intracellular  
 CC domain (NICD) it forms a transcriptional activator complex with  
 CC RBP-J kappa and activates genes of the enhancer of split locus.  
 CC Affects the implementation of differentiation, proliferation and  
 CC apoptotic programs (By similarity). May regulate branching  
 CC morphogenesis in the developing vascular system.  
 CC -!- SUBUNIT: Heterodimer of a C-terminal fragment N(TM) and a N-  
 CC terminal fragment N(EC) which are probably linked by disulfide  
 CC bonds.  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Following  
 CC proteolytical processing NICD is translocated to the nucleus.  
 CC -!- TISSUE SPECIFICITY: Highly expressed in lung, moderately in heart  
 CC kidney, and at lower levels in the ovary and skeletal muscle. A  
 CC very low expression is seen in the brain, intestine, liver and  
 CC testis.  
 CC -!- DEVELOPMENTAL STAGE: Highly expressed in endothelial cells during  
 CC embryonic development from 9.0 d.p.c.  
 CC -!- PTM: Synthesized in the endoplasmic reticulum as an inactive form  
 CC which is proteolytically cleaved by a furin-like convertase in the  
 CC trans-Golgi network before it reaches the plasma membrane to yield  
 CC an active, ligand-accessible form. Cleavage results in a C-  
 CC terminal fragment N(TM) and a N-terminal fragment N(EC). Following  
 CC ligand binding, it is cleaved by TNF-alpha converting enzyme  
 CC (TACE) to yield a membrane-associated intermediate fragment called  
 CC notch extracellular truncation (NEXT). This fragment is then  
 CC cleaved by presenilin dependent gamma-secretase to release a  
 CC notch-derived peptide containing the intracellular domain (NICD)  
 CC from the membrane.  
 CC -!- PTM: Phosphorylated.  
 CC -!- DISEASE: Loss of the extracellular domain causes constitutive  
 CC activation of the Notch protein, which leads to hyperproliferation  
 CC of glandular epithelial tissues and development of mammary  
 CC carcinomas.  
 CC -!- SIMILARITY: BELONGS TO THE NOTCH FAMILY.  
 CC -!- SIMILARITY: CONTAINS 29 EGF-LIKE DOMAINS.  
 CC -!- SIMILARITY: CONTAINS 3 LIN/NOTCH REPEATS.  
 CC -!- SIMILARITY: CONTAINS 5 ANK REPEATS.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL; M80456; AAB38377.1; -;  
 CC EMBL; U43691; AAC2630.1; -;  
 CC EMBL; AF030001; AAB82004.1; -;  
 CC EMBL; AB016771; BAA32281.1; ALT SEQ.  
 CC EMBL; AB016772; BAA32283.1; ALT INIT.  
 CC EMBL; AB016773; BAA32284.1; ALT\_INIT.  
 CC EMBL; AB016774; BAA32285.1; -;

PIR; A38072; TVMVT3.  
 HSSP; P08709; LBF9.  
 MGI; 107471; Notch4.  
 InterPro; IPR002110; ANK.  
 InterPro; IPR000152; Asx hydroxyl.  
 InterPro; IPR000561; EGF-like.  
 InterPro; IPR000742; EGF\_2.  
 InterPro; IPR001881; EGF-Ca.  
 InterPro; IPR001438; EGF-II.  
 InterPro; IPR000800; Notch.  
 Pfam; PF00008; EGF; 27.  
 Pfam; PF00023; ank; 6.  
 Pfam; PF00066; notch; 2.  
 PRINTS; PR01415; ANKIRIN.  
 PRINTS; PR00010; EGFBLD.  
 PRINTS; PR01452; NOTCH.  
 SMART; SM00248; ANK; 5.  
 SMART; SM00179; EGF\_CA; 11.  
 SMART; SM00001; EGF-like; 15.  
 SMART; SM00004; NL; 2.  
 PROSITE; PS50088; ANK\_REPEAT; 5.  
 PROSITE; PS50297; ANK\_REPEAT\_REGION; 1.  
 PROSITE; PS00010; ASX\_HYDROXYL; 11.  
 PROSITE; PS00022; EGF\_1; 28.  
 PROSITE; PS01186; EGF\_2; 21.  
 PROSITE; PS01187; EGF\_CA; 9.  
 Receptor; Transcription regulation; Activator; Differentiation;  
 Developmental protein; Repeat; ANK repeat; EGF-like domain;  
 Transmembrane; Glycoprotein; Signal; Phosphorylation; Proto-oncogene.  
 SIGNAL 1 20  
 CHAIN 21 1964  
 CHAIN 1411 1964  
 CHAIN 1428 1964  
 CHAIN 1463 1964  
 DOMAIN 21 1443  
 DOMAIN 1444 1464  
 TRANSMEM 1445 1964  
 DOMAIN 21 60  
 DOMAIN 61 112  
 DOMAIN 115 152  
 DOMAIN 153 189  
 DOMAIN 191 229  
 DOMAIN 231 271  
 DOMAIN 273 309  
 DOMAIN 311 350  
 DOMAIN 352 388  
 DOMAIN 389 427  
 DOMAIN 429 470  
 DOMAIN 472 508  
 DOMAIN 510 546  
 DOMAIN 548 584  
 DOMAIN 586 622  
 DOMAIN 623 656  
 DOMAIN 658 686  
 DOMAIN 688 724  
 DOMAIN 726 762  
 DOMAIN 764 800  
 DOMAIN 803 839  
 DOMAIN 841 877  
 DOMAIN 878 924  
 DOMAIN 926 962  
 DOMAIN 964 1000  
 DOMAIN 1002 1040  
 DOMAIN 1042 1081  
 DOMAIN 1083 1122  
 DOMAIN 1126 1167  
 REPEAT 1168 1208  
 REPEAT 1209 1242  
 REPEAT 1243 1282  
 REPEAT 1283 1322  
 REPEAT 1323 1362  
 REPEAT 1363 1402  
 REPEAT 1403 1442  
 REPEAT 1443 1482  
 REPEAT 1483 1522  
 REPEAT 1523 1562  
 REPEAT 1563 1602  
 REPEAT 1603 1642  
 REPEAT 1643 1682  
 REPEAT 1683 1722  
 REPEAT 1723 1762  
 REPEAT 1763 1802  
 REPEAT 1803 1842  
 REPEAT 1843 1882  
 REPEAT 1883 1922  
 REPEAT 1923 1962  
 REPEAT 1963 2002  
 REPEAT 2003 2042  
 REPEAT 2043 2082  
 REPEAT 2083 2122  
 REPEAT 2123 2162  
 REPEAT 2163 2202  
 REPEAT 2203 2242  
 REPEAT 2243 2282  
 REPEAT 2283 2322  
 REPEAT 2323 2362  
 REPEAT 2363 2402  
 REPEAT 2403 2442  
 REPEAT 2443 2482  
 REPEAT 2483 2522  
 REPEAT 2523 2562  
 REPEAT 2563 2602  
 REPEAT 2603 2642  
 REPEAT 2643 2682  
 REPEAT 2683 2722  
 REPEAT 2723 2762  
 REPEAT 2763 2802  
 REPEAT 2803 2842  
 REPEAT 2843 2882  
 REPEAT 2883 2922  
 REPEAT 2923 2962  
 REPEAT 2963 3002  
 REPEAT 3003 3042  
 REPEAT 3043 3082  
 REPEAT 3083 3122  
 REPEAT 3123 3162  
 REPEAT 3163 3202  
 REPEAT 3203 3242  
 REPEAT 3243 3282  
 REPEAT 3283 3322  
 REPEAT 3323 3362  
 REPEAT 3363 3402  
 REPEAT 3403 3442  
 REPEAT 3443 3482  
 REPEAT 3483 3522  
 REPEAT 3523 3562  
 REPEAT 3563 3602  
 REPEAT 3603 3642  
 REPEAT 3643 3682  
 REPEAT 3683 3722  
 REPEAT 3723 3762  
 REPEAT 3763 3802  
 REPEAT 3803 3842  
 REPEAT 3843 3882  
 REPEAT 3883 3922  
 REPEAT 3923 3962  
 REPEAT 3963 4002  
 REPEAT 4003 4042  
 REPEAT 4043 4082  
 REPEAT 4083 4122  
 REPEAT 4123 4162  
 REPEAT 4163 4202  
 REPEAT 4203 4242  
 REPEAT 4243 4282  
 REPEAT 4283 4322  
 REPEAT 4323 4362  
 REPEAT 4363 4402  
 REPEAT 4403 4442  
 REPEAT 4443 4482  
 REPEAT 4483 4522  
 REPEAT 4523 4562  
 REPEAT 4563 4602  
 REPEAT 4603 4642  
 REPEAT 4643 4682  
 REPEAT 4683 4722  
 REPEAT 4723 4762  
 REPEAT 4763 4802  
 REPEAT 4803 4842  
 REPEAT 4843 4882  
 REPEAT 4883 4922  
 REPEAT 4923 4962  
 REPEAT 4963 5002  
 REPEAT 5003 5042  
 REPEAT 5043 5082  
 REPEAT 5083 5122  
 REPEAT 5123 5162  
 REPEAT 5163 5202  
 REPEAT 5203 5242  
 REPEAT 5243 5282  
 REPEAT 5283 5322  
 REPEAT 5323 5362  
 REPEAT 5363 5402  
 REPEAT 5403 5442  
 REPEAT 5443 5482  
 REPEAT 5483 5522  
 REPEAT 5523 5562  
 REPEAT 5563 5602  
 REPEAT 5603 5642  
 REPEAT 5643 5682  
 REPEAT 5683 5722  
 REPEAT 5723 5762  
 REPEAT 5763 5802  
 REPEAT 5803 5842  
 REPEAT 5843 5882  
 REPEAT 5883 5922  
 REPEAT 5923 5962  
 REPEAT 5963 6002  
 REPEAT 6003 6042  
 REPEAT 6043 6082  
 REPEAT 6083 6122  
 REPEAT 6123 6162  
 REPEAT 6163 6202  
 REPEAT 6203 6242  
 REPEAT 6243 6282  
 REPEAT 6283 6322  
 REPEAT 6323 6362  
 REPEAT 6363 6402  
 REPEAT 6403 6442  
 REPEAT 6443 6482  
 REPEAT 6483 6522  
 REPEAT 6523 6562  
 REPEAT 6563 6602  
 REPEAT 6603 6642  
 REPEAT 6643 6682  
 REPEAT 6683 6722  
 REPEAT 6723 6762  
 REPEAT 6763 6802  
 REPEAT 6803 6842  
 REPEAT 6843 6882  
 REPEAT 6883 6922  
 REPEAT 6923 6962  
 REPEAT 6963 7002  
 REPEAT 7003 7042  
 REPEAT 7043 7082  
 REPEAT 7083 7122  
 REPEAT 7123 7162  
 REPEAT 7163 7202  
 REPEAT 7203 7242  
 REPEAT 7243 7282  
 REPEAT 7283 7322  
 REPEAT 7323 7362  
 REPEAT 7363 7402  
 REPEAT 7403 7442  
 REPEAT 7443 7482  
 REPEAT 7483 7522  
 REPEAT 7523 7562  
 REPEAT 7563 7602  
 REPEAT 7603 7642  
 REPEAT 7643 7682  
 REPEAT 7683 7722  
 REPEAT 7723 7762  
 REPEAT 7763 7802  
 REPEAT 7803 7842  
 REPEAT 7843 7882  
 REPEAT 7883 7922  
 REPEAT 7923 7962  
 REPEAT 7963 8002  
 REPEAT 8003 8042  
 REPEAT 8043 8082  
 REPEAT 8083 8122  
 REPEAT 8123 8162  
 REPEAT 8163 8202  
 REPEAT 8203 8242  
 REPEAT 8243 8282  
 REPEAT 8283 8322  
 REPEAT 8323 8362  
 REPEAT 8363 8402  
 REPEAT 8403 8442  
 REPEAT 8443 8482  
 REPEAT 8483 8522  
 REPEAT 8523 8562  
 REPEAT 8563 8602  
 REPEAT 8603 8642  
 REPEAT 8643 8682  
 REPEAT 8683 8722  
 REPEAT 8723 8762  
 REPEAT 8763 8802  
 REPEAT 8803 8842  
 REPEAT 8843 8882  
 REPEAT 8883 8922  
 REPEAT 8923 8962  
 REPEAT 8963 9002  
 REPEAT 9003 9042  
 REPEAT 9043 9082  
 REPEAT 9083 9122  
 REPEAT 9123 9162  
 REPEAT 9163 9202  
 REPEAT 9203 9242  
 REPEAT 9243 9282  
 REPEAT 9283 9322  
 REPEAT 9323 9362  
 REPEAT 9363 9402  
 REPEAT 9403 9442  
 REPEAT 9443 9482  
 REPEAT 9483 9522  
 REPEAT 9523 9562  
 REPEAT 9563 9602  
 REPEAT 9603 9642  
 REPEAT 9643 9682  
 REPEAT 9683 9722  
 REPEAT 9723 9762  
 REPEAT 9763 9802  
 REPEAT 9803 9842  
 REPEAT 9843 9882  
 REPEAT 9883 9922  
 REPEAT 9923 9962  
 REPEAT 9963 10002  
 REPEAT 10003 10042  
 REPEAT 10043 10082  
 REPEAT 10083 10122  
 REPEAT 10123 10162  
 REPEAT 10163 10202  
 REPEAT 10203 10242  
 REPEAT 10243 10282  
 REPEAT 10283 10322  
 REPEAT 10323 10362  
 REPEAT 10363 10402  
 REPEAT 10403 10442  
 REPEAT 10443 10482  
 REPEAT 10483 10522  
 REPEAT 10523 10562  
 REPEAT 10563 10602  
 REPEAT 10603 10642  
 REPEAT 10643 10682  
 REPEAT 10683 10722  
 REPEAT 10723 10762  
 REPEAT 10763 10802  
 REPEAT 10803 10842  
 REPEAT 10843 10882  
 REPEAT 10883 10922  
 REPEAT 10923 10962  
 REPEAT 10963 11002  
 REPEAT 11003 11042  
 REPEAT 11043 11082  
 REPEAT 11083 11122  
 REPEAT 11123 11162  
 REPEAT 11163 11202  
 REPEAT 11203 11242  
 REPEAT 11243 11282  
 REPEAT 11283 11322  
 REPEAT 11323 11362  
 REPEAT 11363 11402  
 REPEAT 11403 11442  
 REPEAT 11443 11482  
 REPEAT 11483 11522  
 REPEAT 11523 11562  
 REPEAT 11563 11602  
 REPEAT 11603 11642  
 REPEAT 11643 11682  
 REPEAT 11683 11722  
 REPEAT 11723 11762  
 REPEAT 11763 11802  
 REPEAT 11803 11842  
 REPEAT 11843 11882  
 REPEAT 11883 11922  
 REPEAT 11923 11962  
 REPEAT 11963 12002  
 REPEAT 12003 12042  
 REPEAT 12043 12082  
 REPEAT 12083 12122  
 REPEAT 12123 12162  
 REPEAT 12163 12202  
 REPEAT 12203 12242  
 REPEAT 12243 12282  
 REPEAT 12283 12322  
 REPEAT 12323 12362  
 REPEAT 12363 12402  
 REPEAT 12403 12442  
 REPEAT 12443 12482  
 REPEAT 12483 12522  
 REPEAT 12523 12562  
 REPEAT 12563 12602  
 REPEAT 12603 12642  
 REPEAT 12643 12682  
 REPEAT 12683 12722  
 REPEAT 12723 12762  
 REPEAT 12763 12802  
 REPEAT 12803 12842  
 REPEAT 12843 12882  
 REPEAT 12883 12922  
 REPEAT 12923 12962  
 REPEAT 12963 13002  
 REPEAT 13003 13042  
 REPEAT 13043 13082  
 REPEAT 13083 13122  
 REPEAT 13123 13162  
 REPEAT 13163 13202  
 REPEAT 13203 13242  
 REPEAT 13243 13282  
 REPEAT 13283 13322  
 REPEAT 13323 13362  
 REPEAT 13363 13402  
 REPEAT 13403 13442  
 REPEAT 13443 13482  
 REPEAT 13483 13522  
 REPEAT 13523 13562  
 REPEAT 13563 13602  
 REPEAT 13603 13642  
 REPEAT 13643 13682  
 REPEAT 13683 13722  
 REPEAT 13723 13762  
 REPEAT 13763 13802  
 REPEAT 13803 13842  
 REPEAT 13843 13882  
 REPEAT 13883 13922  
 REPEAT 13923 13962  
 REPEAT 13963 14002  
 REPEAT 14003 14042  
 REPEAT 14043 14082  
 REPEAT 14083 14122  
 REPEAT 14123 14162  
 REPEAT 14163 14202  
 REPEAT 14203 14242  
 REPEAT 14243 14282  
 REPEAT 14283 14322  
 REPEAT 14323 14362  
 REPEAT 14363 14402  
 REPEAT 14403 14442  
 REPEAT 14443 14482  
 REPEAT 14483 14522  
 REPEAT 14523 14562  
 REPEAT 14563 14602  
 REPEAT 14603 14642  
 REPEAT 14643 14682  
 REPEAT 14683 14722  
 REPEAT 14723 14762  
 REPEAT 14763 14802  
 REPEAT 14803 14842  
 REPEAT 14843 14882  
 REPEAT 14883 14922  
 REPEAT 14923 14962  
 REPEAT 14963 15002  
 REPEAT 15003 15042  
 REPEAT 15043 15082  
 REPEAT 15083 15122  
 REPEAT 15123 15162  
 REPEAT 15163 15202  
 REPEAT 15203 15242  
 REPEAT 15243 15282  
 REPEAT 15283 15322  
 REPEAT 15323 15362  
 REPEAT 15363 15402  
 REPEAT 15403 15442  
 REPEAT 15443 15482  
 REPEAT 15483 15522  
 REPEAT 15523 15562  
 REPEAT 15563 15602  
 REPEAT 15603 15642  
 REPEAT 15643 15682  
 REPEAT 15683 15722  
 REPEAT 15723 15762  
 REPEAT 15763 15802  
 REPEAT 15803 15842  
 REPEAT 15843 15882  
 REPEAT 15883 15922  
 REPEAT 15923 15962  
 REPEAT 15963 16002  
 REPEAT 16003 16042  
 REPEAT 16043 16082  
 REPEAT 16083 16122  
 REPEAT 16123 16162  
 REPEAT 16163 16202  
 REPEAT 16203 16242  
 REPEAT 16243 16282  
 REPEAT 16283 16322  
 REPEAT 16323 16362  
 REPEAT 16363 16402  
 REPEAT 16403 16442  
 REPEAT 16443 16482  
 REPEAT 16483 16522  
 REPEAT 16523 16562  
 REPEAT 16563 16602  
 REPEAT 16603 16642  
 REPEAT 16643 16682  
 REPEAT 16683 16722  
 REPEAT 16723 16762  
 REPEAT 16763 16802  
 REPEAT 16803 16842  
 REPEAT 16843 16882  
 REPEAT 16883 16922  
 REPEAT 16923 16962  
 REPEAT 16963 17002  
 REPEAT 17003 17042  
 REPEAT 17043 17082  
 REPEAT 17083 17122  
 REPEAT 17123 17162  
 REPEAT 17163 17202  
 REPEAT 17203 17242  
 REPEAT 17243 17282  
 REPEAT 17283 17322  
 REPEAT 17323 17362  
 REPEAT 17363 17402  
 REPEAT 17403 17442  
 REPEAT 17443 17482  
 REPEAT 17483 17522  
 REPEAT 17523 17562  
 REPEAT 17563 17602  
 REPEAT 17603 17642  
 REPEAT 17643 17682  
 REPEAT 17683 17722  
 REPEAT 17723 17762  
 REPEAT 17763 17802  
 REPEAT 17803 17842  
 REPEAT 17843 17882  
 REPEAT 17883 17922  
 REPEAT 17923 17962  
 REPEAT 17963 18002  
 REPEAT 18003 18042  
 REPEAT 18043 18082  
 REPEAT 18083 18122  
 REPEAT 18123 18162  
 REPEAT 18163 18202  
 REPEAT 18203 18242  
 REPEAT 18243 18282  
 REPEAT 18283 18322  
 REPEAT 18323 18362  
 REPEAT 18363 18402  
 REPEAT 18403 18442  
 REPEAT 18443 18482  
 REPEAT 18483 18522  
 REPEAT 18523 18562  
 REPEAT 18563 18602  
 REPEAT 18603 18642  
 REPEAT 18643 18682  
 REPEAT 18683 18722  
 REPEAT 18723 18762  
 REPEAT 18763 18802  
 REPEAT 18803 18842  
 REPEAT 18843 18882  
 REPEAT 18883 18922  
 REPEAT 18923 18962  
 REPEAT 18963 19002  
 REPEAT 19003 19042  
 REPEAT 19043 19082  
 REPEAT 19083 19122  
 REPEAT 19123 19162  
 REPEAT 19163 19202  
 REPEAT 19203 19242  
 REPEAT 19243 19282  
 REPEAT 19283 19322  
 REPEAT 19323 19362  
 REPEAT 19363 19402  
 REPEAT 19403 19442  
 REPEAT 19443 19482  
 REPEAT 19483 19522  
 REPEAT 19523 19562  
 REPEAT 19563 19602  
 REPEAT 19603 19642  
 REPEAT 19643 19682  
 REPEAT 19683 19722  
 REPEAT 19723 19762  
 REPEAT 19763 19802  
 REPEAT 19803 19842  
 REPEAT 19843 19882  
 REPEAT 19883 19922  
 REPEAT 19923 19962  
 REPEAT 19963 20002  
 REPEAT 20003 20042  
 REPEAT 20043 20082  
 REPEAT 20083 20122  
 REPEAT 20123 20162  
 REPEAT 20163 20202  
 REPEAT 20203 20242  
 REPEAT 20243 20282  
 REPEAT 20283 20322  
 REPEAT 20323 20362  
 REPEAT 20363 20402  
 REPEAT 20403 20442  
 REPEAT 20443 20482  
 REPEAT 20483 20522  
 REPEAT 20523 20562  
 REPEAT 20563 20602  
 REPEAT 20603 20642  
 REPEAT 20643 20682  
 REPEAT 20683 20722  
 REPEAT 20723 20762  
 REPEAT 20763 20802  
 REPEAT 20803 20842  
 REPEAT 20843 20882  
 REPEAT 20883 20922  
 REPEAT 20923 20962  
 REPEAT 20963 21002  
 REPEAT 21003 21042  
 REPEAT 21043 21082  
 REPEAT 21083 21122  
 REPEAT 21123 21162  
 REPEAT 21163 21202  
 REPEAT 21203 21242  
 REPEAT 21243 21282  
 REPEAT 21283 21322  
 REPEAT 21323 21362  
 REPEAT 21363 21402  
 REPEAT 21403 21442  
 REPEAT 21443 21482  
 REPEAT 21483 21522  
 REPEAT 21523 21562  
 REPEAT 21563 21602  
 REPEAT 21603 21642  
 REPEAT 21643 21682  
 REPEAT 21683 21722  
 REPEAT 21723 21762  
 REPEAT 21763 21802  
 REPEAT 21803 21842  
 REPEAT 21843 21882  
 REPEAT 21883 21922  
 REPEAT 21923 21962  
 REPEAT 21963 22002  
 REPEAT 22003 22042  
 REPEAT 22043 22082  
 REPEAT 22083 22122  
 REPEAT 22123 22162  
 REPEAT 22163 22202  
 REPEAT 22203 22242  
 REPEAT 22243 22282  
 REPEAT 22283 22322  
 REPEAT 22323 22362  
 REPEAT 22363 22402  
 REPEAT 22403 22442  
 REPEAT 22443 22482  
 REPEAT 22483 22522  
 REPEAT 22523 22562  
 REPEAT 22563 22602  
 REPEAT 22603 22642  
 REPEAT 22643 22682  
 REPEAT 22683 22722  
 REPEAT 22723 22762  
 REPEAT 22763 22802  
 REPEAT 22803 22842  
 REPEAT 22843 22882  
 REPEAT 22883 22922  
 REPEAT 22923 22962  
 REPEAT 22963 23002  
 REPEAT 23003 23042  
 REPEAT 23043 23082  
 REPEAT 23083 23122  
 REPEAT 23123 23162  
 REPEAT 23163 23202  
 REPEAT 23203 23242  
 REPEAT 23243 23282  
 REPEAT 23283 23322  
 REPEAT 23323 23362  
 REPEAT 23363 23402  
 REPEAT 23403 23442  
 REPEAT 23443 23482  
 REPEAT 23483 23522  
 REPEAT 23523 23562  
 REPEAT 23563 23602  
 REPEAT 23603 23642



Query Match 13.0%; Score 196; DB 1; Length 1964;  
Best Local Similarity 34.2%; Pred. No. 1.7e-07;  
Matches 50; Conservative 12; Mismatches 54; Indels 30; Gaps 7;

80 APPRISACGK-RFSGPAGCAICOPPCORNGSCVQPG---RCPCPGRDPTQ 135  
DB 134 ASGRPGSCGPGMTGEOCQARFCSA---NPGANGVCLATTPQIQCRCPGEGHTE 189  
136 SDVDECSARRGQPG--RCVNTAGSYWCQ---WEGHLSADTLCP---KGGPRVA 186  
DB 190 RDINEGCLBEPGPGGSGNHTIGSYGCLCPVQGBRQCKLRGACPPGSCUNGTGQLV 249  
187 PNP-----TGVDANKKE 199  
DB 250 PEGHSTFHLCLCPGPGTGLDCEMNP 275

RESULT 2  
NTC4\_HUMAN STANDARD; PRT; 2003 AA.  
AC G99466; O00306; G99940; G99458; G9H358; G9U19; G9U10;  
ID 15-JUN-2002 (Rel. 41, Created)  
DT 15-JUN-2002 (Rel. 41, Last sequence update)  
DE 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Neurogenic locus notch homolog protein 4 precursor (Notch 4)  
DE (Mnecch4).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1] \_SEQUENCE FROM N.A. (ISOFORM 1), AND POLYMORPHISM OF POLY-LEU.  
RP TISSUE=Placenta;  
RC MEDLINE=97311416; PubMed=9168133;  
RA Sugaya K., Sasamura S.-I., Nohara J., Kimura T., Fukagawa T.,  
Nakamura Y., Ando A., Inoko H., Ikemura T., Mita K.;  
"Gene organization of human NOTCH4 and (CTG)n polymorphism in this  
RT human counterpart gene of mouse proto-oncogene Int3.";  
RL Gene 189:235-244(1997).  
RN [2]  
RP SEQUENCE FROM N.A. (ISOFORMS 1, 2 AND 3).  
RC TISSUE=Bone marrow, and Heart;  
RX MEDLINE=9836091; PubMed=9693032;  
RA Li L., Huang G.M., Banta A.B., Deng Y., Smith T., Dong P.,  
Friedman C., Chen L., Trask B.J., Spies T., Rowen L., Hood L.;  
"Cloning, characterization, and the complete 56.8-kilobase DNA  
RT sequence of the human NOTCH4 gene.";  
RL Genomics 51:45-58(1998).  
RN [3]  
RP SEQUENCE OF 1-503 FROM N.A., AND VARIANTS GLN-117 AND GLN-317.  
RA Miyagawa T., Tokunaga K., Hojo H.;  
RT "Human notch4 gene variant.";  
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP IDENTIFICATION OF LIGANDS.  
RX MEDLINE=99180765; PubMed=10079256;  
RA Gray G.E., Mann R.S., Miceliadis E., Henrique D., Carcangiu M.-L.,  
Banks A., Leiman J., Ward D., Ish-Horowitz D., Aravanis-Tsakonas S.;  
"Human ligands of the Notch receptor.";  
RL Am. J. Pathol. 154:785-794(1999).  
CC -1- FUNCTION: Functions as a receptor for membrane-bound ligands  
CC Jagged1, Jagged2 and Delta to regulate cell fate determination.  
CC Upon ligand activation through the released notch intracellular  
CC domain (NICD) it forms a transcriptional activator complex with  
CC RBP-U kappa and activates genes of the enhancer of split locus.  
CC Affects the implementation of differentiation, proliferation and  
CC apoptotic programs. May regulate branching morphogenesis in the  
CC developing vascular system (By similarity).  
CC -1- SUBUNIT: Heterodimer of a C-terminal fragment N(TW) and a N-  
CC terminal fragment N(EC) which are probably linked by disulfide  
CC bonds (By similarity).

CC -1- SUBCELLULAR LOCATION: Type I membrane protein. Following  
CC proteolytic processing, NICD is translocated to the nucleus.  
CC -1- ALTERNATIVE PRODUCTS: 3 isoforms; 1 (shown here), 2 and 3; may be  
CC produced by alternative splicing.  
CC -1- TISSUE SPECIFICITY: Highly expressed in the heart, moderately in  
CC the lung and placenta and at low levels in the liver, skeletal  
CC muscle, kidney, pancreas, spleen, lymph node, thymus, bone marrow  
CC and fetal liver. No expression was seen in adult brain or  
CC peripheral blood leukocytes.  
CC -1- PTM: Synthesized in the endoplasmic reticulum as an inactive form  
CC which is proteolytically cleaved by a furin-like convertase in the  
CC trans-Golgi network before it reaches the plasma membrane to yield  
CC an active, ligand-accessible form. Cleavage results in a C-  
CC terminal fragment N(TW) and a N-terminal fragment N(EC). Following  
CC ligand binding, it is cleaved by TNF-alpha converting enzyme  
CC (TACE) to yield a membrane-associated intermediate fragment called  
CC notch extracellular truncation (NEXT). This fragment is then  
CC cleaved by presenilin dependent gamma-secretase to release a  
CC notch-derived peptide containing the intracellular domain (NICD)  
CC from the membrane (By similarity).  
CC -1- PTM: Phosphorylated (By similarity).  
CC -1- POLYMORPHISM: The poly-Leu region of NOTCH4 (in the signal  
CC peptide) is polymorphic and the number of Leu varies in the  
CC population (from 6 to 12).  
CC -1- SIMILARITY: BELONGS TO THE NOTCH FAMILY.  
CC -1- SIMILARITY: CONTAINS 28 EGF-LIKE DOMAINS.  
CC -1- SIMILARITY: CONTAINS 3 LIN/NOTCH REPEATS.  
CC -1- SIMILARITY: CONTAINS 5 ANK REPEATS.  
CC -1- CAUTION: Ref.1 sequence differs from that shown due to frameshifts  
CC in position 1438 to 1463.  
CC  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC EMBL; D63395; BAA09708.1; ALT\_FRAME.  
CC EMBL; D86566; BAA13116.1; -  
CC EMBL; U95299; AAC32288.1; -  
CC EMBL; U95335; AAC63097.1; -  
CC EMBL; AB023961; BAB20317.1; -  
CC EMBL; AB024520; BAA88951.1; -  
CC EMBL; AB024578; BAA88952.1; -  
CC HSSP; P08709; 1BF9.  
CC GeneW; HGNC:7884; NOTCH4.  
CC MIM; 164951; -  
CC InterPro; IPR002110; ANK.  
CC InterPro; IPR000152; Asx\_hydroxyl.  
CC InterPro; IPR000561; EGF-like.  
CC InterPro; IPR000742; EGF\_2.  
CC InterPro; IPR001881; EGF\_CA.  
CC InterPro; IPR001438; EGF\_11.  
CC InterPro; IPR000800; Notch.  
CC Pfam; PF00008; EGF; 26.  
CC Pfam; PF00023; ank; 6.  
CC Pfam; PF00066; notch; 2.  
CC PRINTS; PR00010; EGFBLDOD.  
CC PRINTS; PR00011; EGFBLMININ.  
CC PRINTS; PR00012; FNTYPEI.  
CC SMART; SM00248; ANK; 5.  
CC SMART; SM00179; EGF\_CA; 11.  
CC SMART; SM00001; EGF\_like; 15.  
CC SMART; SM00004; NL; 2.  
CC PROSITE; PS50088; ANK\_REPEAT; 5.  
CC PROSITE; PS50297; ANK\_REPEAT\_REGION; 1.  
CC PROSITE; PS00010; ASX\_HYDROXYL; 11.  
CC PROSITE; PS00022; EGF\_1; 28.  
CC PROSITE; PS01186; EGF\_2; 21.  
CC PROSITE; PS01187; EGF\_CA; 9.  
CC Receptor; Transcription regulation; Activator; Differentiation;  
KW



```

DR Pfam: PF02210; TSPN; 1.
DR SMART: SM00179; EGF_CA; 3.
DR SMART: SM00001; EGF_Like; 3.
DR SMART: SM00282; LamG; 1.
DR SMART: SM00210; TSPN; 1.
DR SMART: SM00214; WVC; 2.
DR PROSITE: PS00010; ASX_HYDROXYL; 3.
DR PROSITE: PS00022; EGF_1; 1.
DR PROSITE: PS01186; EGF_2; 3.
DR PROSITE: PS01187; EGF_CA; 3.
DR PROSITE: PS01208; WVC; 2.
KW Glycoprotein; EGF-like domain; Repeat; Signal.
FT SIGNAL 1 24
FT CHAIN 1 24
FT DOMAIN 25 816
FT DOMAIN 30 258
FT DOMAIN 272 331
FT DOMAIN 332 396
FT DOMAIN 397 439
FT DOMAIN 440 481
FT DOMAIN 482 522
FT DOMAIN 521 553
FT DOMAIN 555 601
FT DOMAIN 602 637
FT DOMAIN 638 693
FT DOMAIN 698 756
FT DOMAIN 758 813
FT DOMAIN 813 816
FT DISULFID 401 422
FT DISULFID 424 438
FT DISULFID 444 457
FT DISULFID 451 466
FT DISULFID 468 480
FT DISULFID 486 499
FT DISULFID 493 508
FT DISULFID 510 521
FT DISULFID 525 535
FT DISULFID 529 541
FT DISULFID 543 552
FT DISULFID 559 572
FT DISULFID 566 581
FT DISULFID 583 600
FT DISULFID 606 619
FT DISULFID 613 628
FT DISULFID 630 636
FT CARBOHYD 53 53
FT CARBOHYD 225 225
FT CARBOHYD 293 293
FT CARBOHYD 298 298
FT CARBOHYD 517 517
FT CARBOHYD 615 615
FT CARBOHYD 635 635
SQ SEQUENCE 816 AA; 91163 MW; 5BD0A946F87E74D CRC64;

Query Match 12.2%; Score 184; DB 1; Length 816;
Best Local Similarity 28.8%; Pred. No. 6.1e-07;
Matches 46; Conservative 22; Mismatches 64; Indels 28; Gaps 7;

```

```

AC Q92832; Q9Y472;
DT 01-NOV-1997 (Rel. 35, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Protein kinase C-binding protein NEHL1 precursor (NEHL-like protein 1)
DE (NEHL-related protein 1).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OK NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=97131504; PubMed=8975702;
RA Watanabe T.K., Katagiri T., Suzuki M., Shimizu F., Fujiwara T.,
RA Kanemoto N., Nakamura Y., Hirai Y., Maekawa H., Takahashi E.;
RT "Cloning and characterization of two novel human cDNAs (NEHL1 and
RT NEHL2) encoding proteins with six EGF-like repeats.";
RL Genomics 38:273-276 (1996).
RN [2]
RP SEQUENCE OF 363-810 FROM N.A.
RA Ting K., Vascariadis H., Mulliken J.B., Bertolami C., Wen Z.,
RA Young M., Tieu A., Kwong E.;
RT "Nei homolog gene expression in craniofacial anomalies.";
RL Submitted (SEP-1996) to the EMBL/Genbank/DBJ databases.
CC -1- SUBUNIT: HOMOTRIMER. BINDS TO PKC BETA-1 (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).
CC -1- DISEASE: EXPRESSED IN CRANIOFACIAL ANOMALIES.
CC -1- SIMILARITY: CONTAINS 1 TSP N-TERMINAL DOMAIN.
CC -1- SIMILARITY: CONTAINS 5 WVC DOMAINS.
CC -1- SIMILARITY: CONTAINS 6 EGF-LIKE DOMAINS.
CC -1- CAUTION: REF.2 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO FRAMESHIFTS
CC IN POSITIONS 427 AND 771.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC -----
CC EMBL: D83017; BAA11680.1; -
CC EMBL: U57523; AAB06946.1; ALT_FRAME.
CC HSSP: P07204; 1ADX.
CC DR Genew; HGNC:7750; NEHL1.
CC DR MTM; 602319; -
CC DR InterPro: IPR000152; Asx_hydroxyl.
CC DR InterPro: IPR000561; EGF_Like.
CC DR InterPro: IPR001881; EGF_CA.
CC DR InterPro: IPR001791; Laminin_G.
CC DR InterPro: IPR003129; TSPN.
CC DR InterPro: IPR001007; WVC_C.
CC Pfam: PF00008; EGF; 4.
CC Pfam: PF00093; WVC; 3.
CC Pfam: PF02210; TSPN; 1.
CC SMART: SM00179; EGF_CA; 2.
CC SMART: SM00001; EGF_Like; 4.
CC SMART: SM00282; LamG; 1.
CC SMART: SM00214; TSPN; 1.
CC PROSITE: PS00010; ASX_HYDROXYL; 3.
CC PROSITE: PS00022; EGF_1; 1.
CC PROSITE: PS01186; EGF_2; 3.
CC PROSITE: PS01187; EGF_CA; 3.
CC PROSITE: PS01208; WVC; 2.
KW Glycoprotein; EGF-like domain; Repeat; Signal.
FT SIGNAL 1 16
FT CHAIN 1 16
FT DOMAIN 81 810
FT DOMAIN 273 331
FT DOMAIN 335 390
FT WVC 1.
FT WVC 2.

```

FT DOMAIN 391 433 EGF-LIKE 1. CALCIIUM-BINDING (POTENTIAL).  
 FT DOMAIN 434 475 EGF-LIKE 2.  
 FT DOMAIN 476 516 EGF-LIKE 3.  
 FT DOMAIN 515 547 EGF-LIKE 4.  
 FT DOMAIN 549 595 EGF-LIKE 5. CALCIIUM-BINDING (POTENTIAL).  
 FT DOMAIN 596 631 EGF-LIKE 6. CALCIIUM-BINDING (POTENTIAL).  
 FT DOMAIN 632 687 WFC 3.  
 FT DOMAIN 687 750 WFC 4.  
 FT DOMAIN 752 807 WFC 5.  
 FT DISULFID 395 407 BY SIMILARITY.  
 FT DISULFID 401 416 BY SIMILARITY.  
 FT DISULFID 418 432 BY SIMILARITY.  
 FT DISULFID 438 451 BY SIMILARITY.  
 FT DISULFID 445 460 BY SIMILARITY.  
 FT DISULFID 462 474 BY SIMILARITY.  
 FT DISULFID 480 493 BY SIMILARITY.  
 FT DISULFID 487 502 BY SIMILARITY.  
 FT DISULFID 504 515 BY SIMILARITY.  
 FT DISULFID 519 529 BY SIMILARITY.  
 FT DISULFID 523 535 BY SIMILARITY.  
 FT DISULFID 537 546 BY SIMILARITY.  
 FT DISULFID 553 566 BY SIMILARITY.  
 FT DISULFID 560 575 BY SIMILARITY.  
 FT DISULFID 577 594 BY SIMILARITY.  
 FT DISULFID 600 613 BY SIMILARITY.  
 FT DISULFID 607 622 BY SIMILARITY.  
 FT DISULFID 624 630 BY SIMILARITY.  
 FT CARBOHYD 40 40 N-LINKED (GLCNAC. ) (POTENTIAL).  
 FT CARBOHYD 53 53 N-LINKED (GLCNAC. ) (POTENTIAL).  
 FT CARBOHYD 83 83 N-LINKED (GLCNAC. ) (POTENTIAL).  
 FT CARBOHYD 224 224 N-LINKED (GLCNAC. ) (POTENTIAL).  
 FT CARBOHYD 294 294 N-LINKED (GLCNAC. ) (POTENTIAL).  
 FT CARBOHYD 372 372 N-LINKED (GLCNAC. ) (POTENTIAL).  
 FT CARBOHYD 511 511 N-LINKED (GLCNAC. ) (POTENTIAL).  
 FT CARBOHYD 562 562 N-LINKED (GLCNAC. ) (POTENTIAL).  
 FT CARBOHYD 609 609 N-LINKED (GLCNAC. ) (POTENTIAL).  
 FT CARBOHYD 708 708 N-LINKED (GLCNAC. ) (POTENTIAL).  
 FT CARBOHYD 732 732 N-LINKED (GLCNAC. ) (POTENTIAL).  
 FT CARBOHYD 758 758 N-LINKED (GLCNAC. ) (POTENTIAL).  
 FT CONFLICT 383 383 N -> D (IN REF. 2).  
 FT CONFLICT 573 573 Y -> H (IN REF. 2).  
 FT CONFLICT 626 626 S -> C (IN REF. 2).  
 SQ SEQUENCE 810 AA; 89606 MW; 549465EA3F7AEED0 CRC64;  
 Query Match 12.2%; Score 183; DB 1; Length 810;  
 Best Local Similarity 38.5%; Pred. No. 7.3e-07;  
 Matches 37; Conservative 11; Mismatches 36; Indels 10; Gaps 3;  
 QY 88 CCGKRTSGLPACGAATCQPPCRNGSCVOPGRCRCPCAGWRGTCQSDVDECSARRGG 147  
 Db 504 CKPGVGN---GTICRAFCEGCRGTCVAPNKCVCPSGFTSGHCKEIDCECSEGTIE 559  
 QY 148 C--PQRCVNTAGSYWCQWEGH---SLGADGTLGV 177  
 Db 560 CHNHSRCVNLPGWYHCECRSGFGHDDGTYSLSGESCI 595  
 RESULT 5  
 FN2\_MOUSE STANDARD; PRT; 2907 AA.  
 AC Q61555; Q63957;  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Fibrillin 2 precursor.  
 GN FN2 OR FN2-2.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=95263670; PubMed=7744963;

RA Zhang H., Hu W., Ramirez F.;  
 RT "Developmental expression of fibrillin genes suggests heterogeneity  
 of extracellular microfibrils";  
 RL J. Cell Biol. 129:1165-1176(1995).  
 RN [2]  
 RP SEQUENCE OF 210-317 FROM N.A.  
 RX MEDLINE=94140368; PubMed=8307578;  
 RA Li X., Pereira L., Zhang H., Sanguinetti C., Ramirez F., Bonadio J.,  
 RA Francke U.;  
 RT "Fibrillin genes map to regions of conserved mouse/human synteny on  
 mouse chromosomes 2 and 18";  
 RL Genomics 18:667-672(1993).  
 CC -!- FUNCTION: STRUCTURAL COMPONENT OF CONNECTIVE TISSUE MICROFIBRILS  
 THAT BINDS CALCIUM. FIBRILLIN-1-CONTAINING MICROFIBRILS PROVIDE  
 LONG-TERM FORCE BEARING STRUCTURAL SUPPORT.  
 CC -!- SIMILARITY: CONTAINS 47 EGF-LIKE DOMAINS.  
 CC -!- SIMILARITY: CONTAINS 7 TGF-BETA BINDING PROTEIN DOMAINS.  
 CC  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 the European Bioinformatics Institute. There are no restrictions on its  
 use by non-profit institutions as long as its content is in no way  
 modified and this statement is not removed. Usage by and for commercial  
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch))  
 CC  
 DR EMBL; L39790; AAA74908.1; -;  
 DR EMBL; S69359; AAC60685.1; -;  
 DR HSSP; P35855; 1ENW.  
 DR MGD; MGI:95490; Pbn2.  
 DR InterPro; IPR000152; Asx hydroxyl.  
 DR InterPro; IPR000561; EGF-like.  
 DR InterPro; IPR001881; EGF\_Ca.  
 DR InterPro; IPR001438; EGF\_II.  
 DR InterPro; IPR002212; Fibril-assoc.  
 DR Pfam; PF00088; EGF; 46.  
 DR Pfam; PF00683; TB; 9.  
 DR PRINTS; PRO0010; EGFELOOD.  
 DR SMART; SM00179; EGF\_CA; 43.  
 DR SMART; SM00001; EGF\_Like; 3.  
 DR PROSITE; PS00010; ASX HYDROXYL; 43.  
 DR PROSITE; PS00022; EGF\_1; 2.  
 DR PROSITE; PS01186; EGF\_2; 36.  
 DR PROSITE; PS01187; EGF\_Ca; 43.  
 DR Extracellular matrix; Calcium-binding; Glycoprotein; EGF-like domain;  
 KW Repeat; Signal; Multigene family.  
 FT SIGNAL 1 28 POTENTIAL.  
 FT CHAIN 29 2907 FIBRILLIN 2.  
 FT DOMAIN 111 142 EGF-LIKE 1.  
 FT DOMAIN 145 176 EGF-LIKE 2.  
 FT DOMAIN 176 208 EGF-LIKE 3.  
 FT DOMAIN 276 317 EGF-LIKE 4. CALCIIUM-BINDING.  
 FT DOMAIN 318 359 EGF-LIKE 5. CALCIIUM-BINDING.  
 FT REPEAT 360 426 TGFBP 1.  
 FT DOMAIN 487 527 EGF-LIKE 6.  
 FT DOMAIN 528 567 EGF-LIKE 7. CALCIIUM-BINDING.  
 FT DOMAIN 568 609 EGF-LIKE 8. CALCIIUM-BINDING.  
 FT DOMAIN 610 650 EGF-LIKE 9. CALCIIUM-BINDING.  
 FT DOMAIN 651 691 EGF-LIKE 10. CALCIIUM-BINDING.  
 FT REPEAT 692 760 TGFBP 2.  
 FT DOMAIN 761 802 EGF-LIKE 11. CALCIIUM-BINDING.  
 FT DOMAIN 803 844 EGF-LIKE 12. CALCIIUM-BINDING.  
 FT DOMAIN 845 883 EGF-LIKE 13. CALCIIUM-BINDING.  
 FT DOMAIN 948 989 EGF-LIKE 14. CALCIIUM-BINDING.  
 FT REPEAT 990 1065 TGFBP 3.  
 FT DOMAIN 1066 1107 EGF-LIKE 15. CALCIIUM-BINDING.  
 FT DOMAIN 1108 1150 EGF-LIKE 16. CALCIIUM-BINDING.  
 FT DOMAIN 1151 1192 EGF-LIKE 17. CALCIIUM-BINDING.  
 FT DOMAIN 1193 1234 EGF-LIKE 18. CALCIIUM-BINDING.  
 FT DOMAIN 1235 1275 EGF-LIKE 19. CALCIIUM-BINDING.  
 FT DOMAIN 1276 1317 EGF-LIKE 20. CALCIIUM-BINDING.  
 FT DOMAIN 1318 1359 EGF-LIKE 21. CALCIIUM-BINDING.  
 FT DOMAIN 1360 1400 EGF-LIKE 22. CALCIIUM-BINDING.

```

FT DOMAIN 1401 1441 EGF-LIKE 23, CALCIUM-BINDING.
FT DOMAIN 1442 1483 EGF-LIKE 24, CALCIUM-BINDING.
FT DOMAIN 1484 1524 EGF-LIKE 25, CALCIUM-BINDING.
FT DOMAIN 1525 1565 EGF-LIKE 26, CALCIUM-BINDING.
FT REPEAT 1566 1642 TGFBP 4.
FT DOMAIN 1643 1684 EGF-LIKE 27, CALCIUM-BINDING.
FT DOMAIN 1685 1726 EGF-LIKE 28, CALCIUM-BINDING.
FT REPEAT 1727 1800 TGFBP 5.
FT DOMAIN 1801 1842 EGF-LIKE 29, CALCIUM-BINDING.
FT DOMAIN 1843 1884 EGF-LIKE 30, CALCIUM-BINDING.
FT DOMAIN 1885 1926 EGF-LIKE 31, CALCIUM-BINDING.
FT DOMAIN 1927 1965 EGF-LIKE 32, CALCIUM-BINDING.
FT DOMAIN 1966 2008 EGF-LIKE 33, CALCIUM-BINDING.
FT DOMAIN 2009 2048 EGF-LIKE 34, CALCIUM-BINDING.
FT DOMAIN 2049 2090 EGF-LIKE 35, CALCIUM-BINDING.
FT REPEAT 2091 2163 TGFBP 6.
FT DOMAIN 2164 2205 EGF-LIKE 36, CALCIUM-BINDING.
FT DOMAIN 2206 2245 EGF-LIKE 37, CALCIUM-BINDING.
FT DOMAIN 2246 2286 EGF-LIKE 38, CALCIUM-BINDING.
FT DOMAIN 2287 2330 EGF-LIKE 39, CALCIUM-BINDING.
FT DOMAIN 2331 2372 EGF-LIKE 40, CALCIUM-BINDING.
FT REPEAT 2373 2441 TGFBP 7.
FT DOMAIN 2442 2483 EGF-LIKE 41, CALCIUM-BINDING.
FT DOMAIN 2484 2524 EGF-LIKE 42, CALCIUM-BINDING.
FT DOMAIN 2525 2563 EGF-LIKE 43, CALCIUM-BINDING.
FT DOMAIN 2564 2606 EGF-LIKE 44, CALCIUM-BINDING.
FT DOMAIN 2607 2646 EGF-LIKE 45, CALCIUM-BINDING.
FT DOMAIN 2647 2687 EGF-LIKE 46, CALCIUM-BINDING.
FT DOMAIN 2688 2727 EGF-LIKE 47, CALCIUM-BINDING.
FT DISULFID 115 124 BY SIMILARITY.
FT DISULFID 119 130 BY SIMILARITY.
FT DISULFID 132 141 BY SIMILARITY.
FT DISULFID 149 159 BY SIMILARITY.
FT DISULFID 153 164 BY SIMILARITY.
FT DISULFID 166 175 BY SIMILARITY.
FT DISULFID 180 190 BY SIMILARITY.
FT DISULFID 184 196 BY SIMILARITY.
FT DISULFID 198 207 BY SIMILARITY.
FT DISULFID 280 292 BY SIMILARITY.
FT DISULFID 287 301 BY SIMILARITY.
FT DISULFID 303 316 BY SIMILARITY.
FT DISULFID 322 334 BY SIMILARITY.
FT DISULFID 329 343 BY SIMILARITY.
FT DISULFID 345 358 BY SIMILARITY.
FT DISULFID 491 503 BY SIMILARITY.
FT DISULFID 498 512 BY SIMILARITY.
FT DISULFID 514 526 BY SIMILARITY.
FT DISULFID 532 542 BY SIMILARITY.
FT DISULFID 537 551 BY SIMILARITY.
FT DISULFID 553 566 BY SIMILARITY.
FT DISULFID 572 584 BY SIMILARITY.
FT DISULFID 579 593 BY SIMILARITY.
FT DISULFID 595 608 BY SIMILARITY.
FT DISULFID 614 625 BY SIMILARITY.
FT DISULFID 620 634 BY SIMILARITY.
FT DISULFID 636 649 BY SIMILARITY.
FT DISULFID 655 666 BY SIMILARITY.
FT DISULFID 661 675 BY SIMILARITY.
FT DISULFID 677 690 BY SIMILARITY.
FT DISULFID 765 777 BY SIMILARITY.
FT DISULFID 772 786 BY SIMILARITY.
FT DISULFID 788 801 BY SIMILARITY.
FT DISULFID 807 819 BY SIMILARITY.
FT DISULFID 814 828 BY SIMILARITY.
FT DISULFID 830 843 BY SIMILARITY.
FT DISULFID 849 859 BY SIMILARITY.
FT DISULFID 868 883 BY SIMILARITY.
FT DISULFID 870 883 BY SIMILARITY.
FT DISULFID 952 964 BY SIMILARITY.
FT DISULFID 959 973 BY SIMILARITY.
FT DISULFID 975 988 BY SIMILARITY.
FT DISULFID 1070 1082 BY SIMILARITY.
FT DISULFID 1077 1091 BY SIMILARITY.

```

```

FT DISULFID 1093 1106 BY SIMILARITY.
FT DISULFID 1112 1124 BY SIMILARITY.
FT DISULFID 1119 1133 BY SIMILARITY.
FT DISULFID 1135 1149 BY SIMILARITY.
FT DISULFID 1155 1167 BY SIMILARITY.
FT DISULFID 1162 1176 BY SIMILARITY.
FT DISULFID 1178 1191 BY SIMILARITY.
FT DISULFID 1197 1209 BY SIMILARITY.
FT DISULFID 1204 1218 BY SIMILARITY.
FT DISULFID 1220 1233 BY SIMILARITY.
FT DISULFID 1239 1250 BY SIMILARITY.
FT DISULFID 1246 1259 BY SIMILARITY.
FT DISULFID 1261 1274 BY SIMILARITY.
FT DISULFID 1280 1292 BY SIMILARITY.
FT DISULFID 1287 1301 BY SIMILARITY.
FT DISULFID 1303 1316 BY SIMILARITY.
FT DISULFID 1322 1334 BY SIMILARITY.
FT DISULFID 1329 1343 BY SIMILARITY.
FT DISULFID 1345 1358 BY SIMILARITY.
FT DISULFID 1364 1377 BY SIMILARITY.
FT DISULFID 1371 1386 BY SIMILARITY.
FT DISULFID 1388 1399 BY SIMILARITY.
FT DISULFID 1405 1418 BY SIMILARITY.
FT DISULFID 1412 1427 BY SIMILARITY.
FT DISULFID 1429 1440 BY SIMILARITY.
FT DISULFID 1446 1458 BY SIMILARITY.
FT DISULFID 1453 1467 BY SIMILARITY.
FT DISULFID 1469 1482 BY SIMILARITY.
FT DISULFID 1488 1499 BY SIMILARITY.
FT DISULFID 1494 1508 BY SIMILARITY.
FT DISULFID 1510 1523 BY SIMILARITY.
FT DISULFID 1529 1540 BY SIMILARITY.
FT DISULFID 1535 1549 BY SIMILARITY.
FT DISULFID 1551 1564 BY SIMILARITY.
FT DISULFID 1647 1659 BY SIMILARITY.
FT DISULFID 1654 1668 BY SIMILARITY.
FT DISULFID 1670 1683 BY SIMILARITY.
FT DISULFID 1689 1701 BY SIMILARITY.
FT DISULFID 1696 1710 BY SIMILARITY.
FT DISULFID 1712 1725 BY SIMILARITY.

```

Query Match 12.1%, Score 182.5, DB 1, Length 2907;  
Best Local Similarity 23.5%, Pred. No. 2.8e-06;  
Matches 59; Conservative 20; Mismatches 85; Indels 87; Gaps 7;

```

QY 2 RGSQVILMWLVAVGHEHAY-----RGRVCAVRAHGDVSPVQRYVQPLT 54
Db 77 RQQETLRG---PNVCSRFHSYCCPGMKTLPGNGQCIIVPICRNSCGGDFCSR---PNWC 130
QY 55 TCDGHRACST--YRTIYTVAYRSPGLAPARPRVYACCPGMKRTSGLPACGAATCOPECR 112
Db 131 TCSGQISPTGCRKSIQQCSVRCMNGGTCADHCCQCGYIGT-----YCCQPVCENCQ 185
QY 113 NGSCVQPRCRCPAGMRDTCQ-----
Db 186 NGRCICGPRCVCVYGTGPOCERDYRTGCFYVNNOMCGQLTGIVCTKLTCATIGR 245
QY 136 -----SDVDECSARGGCP-QRCNTAGSYWCQWE 165
Db 246 AMGHCEMCPPAPQPCRPGFIPNRTGACQDVDECAIPGLCGGNCINTVSGSEPCRP 305
QY 166 GHSLSADGTLQ 176
Db 306 GHKQSETTQKC 316

```

RESULT 6  
NEL2\_HUMAN  
ID NEL2\_HUMAN STANDARD; PRT; 816 AA.  
AC Q99435;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Protein kinase C-binding protein NELL2 precursor (NEL-like protein 2)  
 DE (Nell-related protein 2).  
 GN NELL2 OR NR2.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=97131504; PubMed=8975702;  
 RA Watanabe T.K., Katagiri T., Suzuki M., Shimizu F., Fujiwara T.,  
 RA Kanemoto N., Nakamura Y., Hirai Y., Maekawa H., Takahashi E.;  
 RT "Cloning and characterization of two novel human cDNAs (NELL1 and  
 RT NELL2) encoding proteins with six EGF-like repeats.";  
 RL Genomics 38:273-276(1996).  
 RN [2]  
 RP TSP N-TERMINAL DOMAIN.  
 RC MEDLINE=98153258; PubMed=9480764;  
 RX Beckmann G., Hanke J., Bork P., Reich J.;  
 RA "Merging extracellular domains: fold prediction for laminin G-like  
 RT and amino-terminal thrombospondin-like modules based on homology to  
 RT pentraxins.";  
 RL J. Mol. Biol. 275:725-730(1998).  
 CC -|- SUBUNIT: HOMOTRIMER. BINDS TO PKC BETA-1 (BY SIMILARITY).  
 CC -|- SUBCELLULAR LOCATION: Secreted (By similarity).  
 CC -|- SIMILARITY: CONTAINS 1 TSP N-TERMINAL DOMAIN.  
 CC -|- SIMILARITY: CONTAINS 5 VWFC DOMAINS.  
 CC -|- SIMILARITY: CONTAINS 6 EGF-LIKE DOMAINS.  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL: D83018; BAA11681.1; --  
 DR HSSP: P00740; 1EDM.  
 DR Genew; HGNC: 7751; NELL2.  
 DR MIM: 6023320; --  
 DR InterPro: IPR000152; Asx\_hydroxyl.  
 DR InterPro: IPR000561; EGF-like.  
 DR InterPro: IPR001881; EGF Ca.  
 DR InterPro: IPR001791; Laminin\_G.  
 DR InterPro: IPR003129; TSPN  
 DR InterPro: IPR001007; VWFC\_C.  
 DR Pfam: PF00008; EGF; 5.  
 DR Pfam: PF00093; vwc; 3.  
 DR Pfam: PF02210; TSPN; 1.  
 DR SMART: SM00179; EGF\_CA; 3.  
 DR SMART: SM00001; EGF\_like; 3.  
 DR SMART: SM00282; LamG; 1.  
 DR SMART: SM00210; TSPN; 1.  
 DR SMART: SM00214; VWC; 3.  
 DR PROSITE: PS00010; ASX\_HYDROXYL; 3.  
 DR PROSITE: PS00022; EGF\_1; 1.  
 DR PROSITE: PS00186; EGF\_2; 4.  
 DR PROSITE: PS01187; EGF\_CA; 3.  
 DR PROSITE: PS01208; VWFC; 2.  
 DR Glycoprotein; EGF-like domain; Repeat; Signal.  
 KW SIGNAL 1 24  
 FT CHAIN 25 816  
 FT DOMAIN 30 258  
 FT DOMAIN 272 331  
 FT DOMAIN 332 396  
 FT DOMAIN 337 439  
 FT DOMAIN 440 481  
 FT DOMAIN 482 522  
 FT DOMAIN 521 553  
 FT DOMAIN 555 601  
 FT DOMAIN 602 637  
 FT

FT DOMAIN 638 693  
 FT DOMAIN 698 756  
 FT DOMAIN 758 813  
 FT DISULFID 401 413  
 FT DISULFID 407 422  
 FT DISULFID 424 438  
 FT DISULFID 444 457  
 FT DISULFID 451 466  
 FT DISULFID 468 480  
 FT DISULFID 486 499  
 FT DISULFID 493 508  
 FT DISULFID 510 521  
 FT DISULFID 525 535  
 FT DISULFID 529 541  
 FT DISULFID 543 552  
 FT DISULFID 559 572  
 FT DISULFID 566 581  
 FT DISULFID 583 600  
 FT DISULFID 606 619  
 FT DISULFID 613 628  
 FT DISULFID 630 636  
 FT CARBOHYD 53 53  
 FT CARBOHYD 225 225  
 FT CARBOHYD 293 293  
 FT CARBOHYD 298 298  
 FT CARBOHYD 517 517  
 FT CARBOHYD 615 615  
 FT CARBOHYD 635 635  
 SQ SEQUENCE 816 AA; 91346 MW; 89370B987DC7A324 CRC64;  
 Query Match 12.1%; Score 181.5; DB 1; Length 816;  
 Best Local Similarity 36.8%; Pred. No. 9.6e-07;  
 Matches 35; Conservative 14; Mismatches 37; Indels 9; Gaps 3;  
 QY 88 CPGKWKRTSGLPACAAICQPPCRNGSCVQPCRCPCAGWRGTCQSDVDECSAREGG 147  
 DB 510 CKEGYTGN---GTTCKAFCKDCRCNGGACIAANVACACPGQGTGSCETDIDCSDFVQ 565  
 QY 148 CPQR--CVNTAGSYWCQWEGHSLADGTLVCPKG 180  
 DB 566 CDSRANCINLPGWYHCECRDGYH---DNGMFSPSG 597  
 RESULT 7  
 NELL1 RAT  
 ID NELL1 RAT STANDARD; PRT; 810 AA.  
 AC Q62919;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 30-NOV-2000 (Rel. 39, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Protein kinase C-binding protein NELL1 precursor (NEL-like protein 1).  
 GN NELL1.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Sprague-Dawley; TISSUE=Brain;  
 RX MEDLINE=20017976; PubMed=10548494;  
 RA Kuroda S., Oyasu M., Kawakami M., Kanayama N., Tanizawa K., Saito N.,  
 RA Abe T., Matsubashi S., Ting K.;  
 RT "Biochemical characterization and expression analysis of neural  
 RT thrombospondin-1-like proteins NELL1 and NELL2.";  
 RL Biochem. Biophys. Res. Commun. 265:79-86(1999).  
 CC -|- SUBUNIT: HOMOTRIMER. BINDS TO PKC BETA-1.  
 CC -|- SUBCELLULAR LOCATION: Secreted.  
 CC -|- SIMILARITY: CONTAINS 1 TSP N-TERMINAL DOMAIN.  
 CC -|- SIMILARITY: CONTAINS 5 VWFC DOMAINS.  
 CC -|- SIMILARITY: CONTAINS 6 EGF-LIKE DOMAINS.  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC EMBL: U48246; AAC72252.1; -

DR HSSP; P35555; IEDM.

DR InterPro; IPR000152; Asx\_hydroxyl.

DR InterPro; IPR000561; EGF-like.

DR InterPro; IPR001881; EGF\_Ca.

DR InterPro; IPR001791; laminin\_G.

DR InterPro; IPR003129; TSPN.

DR InterPro; IPR001007; VWF\_C.

DR Pfam; PF00008; EGF; 4.

DR Pfam; PF00093; WVC; 3.

DR Pfam; PF02210; TSPN; 1.

DR SMART; SM00179; EGF\_CA; 2.

DR SMART; SM00001; EGF\_Like; 4.

DR SMART; SM00282; LamG; 1.

DR SMART; SM00210; TSPN; 1.

DR SMART; SM00214; WVC; 4.

DR PROSITE; PS00010; ASX\_HYDROXYL; 3.

DR PROSITE; PS00022; EGF\_1; 1.

DR PROSITE; PS01186; EGF\_2; 3.

DR PROSITE; PS01187; EGF\_CA; 3.

DR PROSITE; PS01208; WVC; 2.

DR GlycoProtein; EGF-Like domain; Repeat; Signal.

KT SIGNAL 1 16

KT CHAIN 17 810

KT DOMAIN 81 230

KT DOMAIN 273 331

KT DOMAIN 335 390

KT DOMAIN 391 433

KT DOMAIN 434 475

KT DOMAIN 476 516

KT DOMAIN 515 547

KT DOMAIN 549 595

KT DOMAIN 596 631

KT DOMAIN 632 687

KT DOMAIN 692 750

KT DOMAIN 752 807

KT DISULFID 395 407

KT DISULFID 401 416

KT DISULFID 418 432

KT DISULFID 438 451

KT DISULFID 445 460

KT DISULFID 462 474

KT DISULFID 480 493

KT DISULFID 487 502

KT DISULFID 504 515

KT DISULFID 519 529

KT DISULFID 523 535

KT DISULFID 537 546

KT DISULFID 553 566

KT DISULFID 560 575

KT DISULFID 577 594

KT DISULFID 600 613

KT DISULFID 607 622

KT DISULFID 624 630

KT DISULFID 624 630

KT CARBOHYD 53 53

KT CARBOHYD 83 83

KT CARBOHYD 224 224

KT CARBOHYD 294 294

KT CARBOHYD 372 372

KT CARBOHYD 511 511

KT CARBOHYD 562 562

KT CARBOHYD 609 609

KT CARBOHYD 708 708

KT SEQUENCE 810 AA; 89212 MW; 46F09C46FA9AB0B CRC64;

Query Match

12.0%; Score 181; DB 1; Length 810;

Best Local Similarity 37.5%; Pred. No. 1e-06; Matches 36; Conservative 12; Mismatches 38; Indels 10; Gaps 3;

QY 88 CCGKMTSILPALCAALICQPCPCNGSCVDPGRCPAGMRGDTGSDVDECSARRG 147

DB 504 CQGVYGN-----GLTKAFEEBCRGYGTCAVANKVCVCSGFTSGCKEIDBCAGFVE 559

QY 148 CP--ORCVNTAGSYWCOCWEH-----SLSDAGTLGV 177

DB 560 CHNYSKCVMLPGWYHCECRSGFRHDDGTYSLSGSECT 595

RESULT 8

NEL2\_RAT

AC 062918; STANDARD; PRT; 816 AA.

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DE 16-OCT-2001 (Rel. 40, Last annotation update)

DE Protein kinase C-binding protein NEL2 precursor (NEL-like protein 2).

OS NEL2 OR NEL.

GN Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.

OX NCBI\_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Sprague-Dawley; TISSUE=Brain;

RX MEDLINE=20017976; PubMed=10548494;

RA Kuroda S., Oyasu M., Kawakami M., Kanayama N., Tanizawa K., Saito N.,

RA Abe T., Matsubashi S., Ting K.;

RT "Biochemical characterization and expression analysis of neural

RL thrombospondin-1-like proteins NEL1 and NEL2.";

RT Biochem. Biophys. Res. Commun. 265:79-86 (1999).

RN [2]

RP TSP N-TERMINAL DOMAIN.

RX MEDLINE=98153258; PubMed=9480764;

RA Beckmann G., Hanke J., Bork P., Reich J.;

RT "Merging extracellular domains: fold prediction for laminin G-like

RL pentraxins.";

RT J. Mol. Biol. 275:725-730 (1998).

CC -1-SUBUNIT: HOMOTRIMER. BINDS TO PKC BETA-1.

CC -1-SUBCELLULAR LOCATION: Secreted.

CC -1-SIMILARITY: CONTAINS 1 TSP N-TERMINAL DOMAIN.

CC -1-SIMILARITY: CONTAINS 5 WVC DOMAINS.

CC -1-SIMILARITY: CONTAINS 6 EGF-LIKE DOMAINS.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its

CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>

CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC EMBL: U48245; AAC72245.1; -

DR HSSP; P00740; IEDM.

DR InterPro; IPR000152; Asx\_hydroxyl.

DR InterPro; IPR000561; EGF-like.

DR InterPro; IPR001881; EGF\_Ca.

DR InterPro; IPR001791; laminin\_G.

DR InterPro; IPR003129; TSPN.

DR InterPro; IPR001007; WVF\_C.

DR Pfam; PF00008; EGF; 5.

DR Pfam; PF00093; WVC; 3.

DR Pfam; PF02210; TSPN; 1.

DR SMART; SM00179; EGF\_CA; 3.

DR SMART; SM00001; EGF\_Like; 3.

DR SMART; SM00282; LamG; 1.

DR SMART; SM00210; TSPN; 1.

DR SMART; SM00214; WVC; 3.

DR PROSITE; PS00010; ASX\_HYDROXYL; 3.



DR PROSITE; PS00022; EGF\_1; 1.  
 DR PROSITE; PS01186; EGF\_2; 4.  
 DR PROSITE; PS01187; EGF\_CA; 3.  
 DR PROSITE; PS01208; WFC; 2.  
 KW Glycoprotein; EGF-like domain; Repeat; Signal.  
 FT SIGNAL 1 24  
 FT CHAIN 25 816  
 FT DOMAIN 30 258  
 FT DOMAIN 272 331  
 FT DOMAIN 332 396  
 FT DOMAIN 397 439  
 FT DOMAIN 440 481  
 FT DOMAIN 482 522  
 FT DOMAIN 521 553  
 FT DOMAIN 555 601  
 FT DOMAIN 602 637  
 FT DOMAIN 638 693  
 FT DOMAIN 698 756  
 FT DOMAIN 758 813  
 FT DISULFID 401 413  
 FT DISULFID 407 422  
 FT DISULFID 424 438  
 FT DISULFID 444 457  
 FT DISULFID 451 466  
 FT DISULFID 468 480  
 FT DISULFID 486 499  
 FT DISULFID 493 508  
 FT DISULFID 510 521  
 FT DISULFID 525 535  
 FT DISULFID 529 541  
 FT DISULFID 543 552  
 FT DISULFID 559 572  
 FT DISULFID 566 581  
 FT DISULFID 583 600  
 FT DISULFID 606 619  
 FT DISULFID 613 628  
 FT DISULFID 630 636  
 FT CARBOHYD 53 53  
 FT CARBOHYD 225 225  
 FT CARBOHYD 293 293  
 FT CARBOHYD 298 298  
 FT CARBOHYD 517 517  
 FT CARBOHYD 615 615  
 FT CARBOHYD 635 635  
 SQ SEQUENCE 816 AA; 90952 MW; A399F7607806D6B CRC64;  
 Query Match 11.9%; Score 179.5; DB 1; Length 816;  
 Best Local Similarity 35.8%; Pred. No. 1.4e-06;  
 Matches 34; Conservative 15; Mismatches 37; Indels 9; Gaps 3;  
 QY 88 CCGPKWRTSGLPGACGAATCQPCRNNGSCVQPGRCRCPAGWRGDTCSVDVDCSARRGG 147  
 Db 510 CKPGYTGNN---GTTCKAFCKDCKNGGACTAANVCACPGQGTGPGSCETIDECSEGFVQ 565  
 QY 148 CQQR--CVNTAGSYWCQCHGSLSDGTLCPVKG 180  
 Db 566 CDSRANCLNPGYHCECRDGH---DNGWFAPGG 597  
 RESULT 9  
 ID CD93\_HUMAN  
 AC Q9NPY3; O00274; STANDARD; PRT; 652 AA.  
 DT 15-JUN-2002 (Rel. 41, Created)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Complement component C1q receptor precursor (Complement component 1, q  
 DE subcomponent, receptor 1) (C1qR) (C1qR(p)) (C1q/MBL/SPA receptor)  
 DE (CD93 antigen) (CDw93).  
 GN ClQRI OR CD93.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
 RX PubMed=9047234;  
 RA Nepomuceno R.R., Henschen-Edman A.H., Burgess W.H., Tenner A.J.;  
 RT "cDNA cloning and primary structure analysis of C1qR(p), the human  
 C1q/MBL/SPA receptor that mediates enhanced phagocytosis in vitro.";  
 RL Immunity 6:119-129(1997).  
 RN [2]  
 RP SEQUENCE FROM N.A., AND VARIANT ALA-318.  
 RX PubMed=11781389;  
 RA Steinberger P., Szekeres A., Wille S., Stockl J., Selenko N.,  
 Prager E., Staffler G., Madic O., Stockinger H., Knapp W.;  
 RT "Identification of human CD93 as the phagocytic C1q receptor (C1qR(p))  
 by expression cloning.";  
 RL J. leukoc. Biol. 71:133-140(2002).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21638749; PubMed=11780052;  
 RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,  
 Jones M., Stavrides G., Almeida J.P., Babbage A.K., Baguley C.L.,  
 Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M., Brown A.J.,  
 Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,  
 Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,  
 Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,  
 Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,  
 Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,  
 Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,  
 Graham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,  
 Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,  
 Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,  
 Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,  
 Lenvasialho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,  
 Marsh V.L., Martin S.L., McConnachie L.J., McElay K., McMurray A.A.,  
 Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,  
 Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,  
 Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,  
 Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkneen R., Sims S.,  
 Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Suleston J.E.,  
 Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,  
 Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M., Williams S.A.,  
 Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,  
 Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,  
 Rogers J.;  
 RT "The DNA sequence and comparative analysis of human chromosome 20.";  
 RL Nature 414:865-871(2001).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RX TISSUE=Leukocyte;  
 RA Strausberg R.;  
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.  
 RN [5]  
 RP CHARACTERIZATION.  
 RX PubMed=11994479;  
 RA McGreal E.P., Ikewaki N., Akatsu H., Morgan B.P., Gasque P.;  
 RT "Human C1qR is identical with CD93 and the mN1-11 antigen but does  
 not bind C1q.";  
 RL J. Immunol. 168:5222-5232(2002).  
 RN [6]  
 RP O-GLYCOSYLATION.  
 RX PubMed=10092817;  
 RA Nepomuceno R.R., Ruiz S., Park M., Tenner A.J.;  
 RT "C1qR is a heavily O-glycosylated cell surface protein involved in  
 the regulation of phagocytic activity.";  
 RL J. Immunol. 162:3583-3589(1999).  
 CC -1- FUNCTION: Receptor (or element of a larger receptor complex) for  
 C1q, mannose-binding lectin (MBL2) and pulmonary surfactant  
 protein A (SPA). May mediate the enhancement of phagocytosis in  
 monocytes and macrophages upon interaction with soluble defense  
 collagens. May play a role in intercellular adhesion.  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -1- TISSUE SPECIFICITY: Highly expressed in endothelial cells,  
 platelets, cells of myeloid origin, such as monocytes and



[illegible]

FT	CONFLICT	155	155	S -> N (IN REF. 1)
FT	CONFLICT	186	186	G -> A (IN AA SEQUENCE) .
FT	CONFLICT	492	492	S -> A (IN AA SEQUENCE) .
FT	CONFLICT	496	496	R -> Q (IN AA SEQUENCE) .
FT	CONFLICT	504	504	R -> G (IN AA SEQUENCE) .
FT	CONFLICT	541	541	P -> S (IN REF. 1) .
SQ	SEQUENCE	652 AA;	68560 MM;	EBCAIFAEAC55FCA62 CRC64;

Query Match            11.7%; Score 176; DB 1; Length 652;  
Best Local Similarity   33.1%; Pred. No. 2e-06;  
Matches 60; Conservative 10; Mismatches 57; Indels 54; Gaps 13;

QY	25	RPGRRV-----CAVRAGDPVSESFVQRVYPFLTTDDGRACSTYTITRTAVRRSPG	78
		:	
Db	288	RPGRFLDDLVTTCASR--NPCSSS-----PCRGATCV-----	318
QY	79	LAPARPRAYC-CP-GMKRTSGLPACGAALCO-DPCRNGSCVQ-PG-RCRPAGMR--	130
Db	319	LGPBGNKNTCTCGPGYQLDSSQDLDCVDVDEQDBSPCAQ-ECVNTPGGFRCECWGVIEFG	376
		:	
QY	131	--GPTCOSDVDECASARRGGCFQRCVNITAGSYWCQMEGHSLA-DGTL-----CVPKGG	181
		:	
Db	377	GGEGACQDVDECALGRSPCAQGCTNTTGDSPHCSCBEGLVALGEDGTGCQDVDEVGEVGG	436
QY	182	P 182	
Db	437	p 437	

RESULT 10	NOTC DROME	STANDARD	PRT	2703 AA.
AC	NOTC DROME			
AD	P07287, P04154, Q97458, Q9M478;			
AE	01-NOV-1986 (Rel. 03, Created)			
BT	15-JUN-2002 (Rel. 41, last sequence update)			
DT	15-JUN-2002 (Rel. 41, last annotation update)			
DE	Neurogenic locus Notch protein precursor.			
GN	N OR EG:140G11.1 OR EG:16A10.2 OR C03936.			
OC	Drosophila melanogaster (fruit fly)			
OC	Eukaryota, Metazoa, Arthropoda, Mandibulata, Pancrustacea, Hexapoda,			
OC	Insecta, Pterygota, Neoptera, Endopterygota, Diptera, Brachycera,			
OC	Muscomorpha, Ephyridioidea, Drosophilidae, Drosophila.			
OX	NCBI_TaxID=72287;			
RP	[1]			
RP	SEQUENCE FROM N.A.			
RP	STRAIN=Oregon-R; TISSUE=Embryo;			
RC	MEDLINE=86079539, PubMed=393532;			
RC	Wharton K.A., Johansen K.M., Xu T., Artavanis-Tsakonas S.;			
RT	"Nucleotide sequence from the neurogenic locus notch implies a gene			
RT	product that shares homology with proteins containing EGF-like			
RT	repeats.";			
RL	Cell 43:567-581(1985).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RP	STRAIN=Canton-S, and Oregon-R; TISSUE=Embryo;			
RC	MEDLINE=87064624, PubMed=3097517;			
RC	Kidd S., Kelley M.R., Young M.W.;			
RT	"Sequence of the notch locus of Drosophila melanogaster: relationship			
RT	of the encoded protein to mammalian clotting and growth factors.";			
RL	Mol. Cell. Biol. 6:3094-3108(1986).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RP	STRAIN=Berkely;			
RC	MEDLINE=20196006; PubMed=10731132;			
RC	Adams M.D., Celisliker S.E., Holt R.A., Evans C.A., Gocayne J.D.,			
RA	Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,			
RA	George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,			
RA	Sutton G.G., Wortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,			
RA	Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,			
RA	Man K.-Y., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,			
RA	Abriil J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,			
RA	Ballew R.M., Basu A., Baxendale A., Bayraktaroglu L., Beasley E.M.,			
RA	Beeson K.T., Berus P.V., Bertan B.P., Bhandari D., Bolintsov S.,			

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,  
RA Burtie K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
RA Cherry J.M., Cawley S., Dahike C., Davenport L.B., Davies P.,  
RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
RA Dodson K., Doup L.B., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
RA Fessler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
RA Jajali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
RA Kammel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
RA Liao X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
RA Merklov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,  
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
RA Swirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weisenbach J.,  
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao O.A.,  
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
RT "The genome sequence of *Drosophila melanogaster*,"  
RL Science 287:2185-2195(2000).  
[4]  
RN SEQUENCE FROM N.A.  
RP STRAIN=Oregon-R;  
RC MEDLINE=20196011; PubMed=10731137;  
RX Benos P.V., Gatt M.K., Ashburner M., Murphy L., Harris D.,  
RA Barrell B.G., Ferraz C., Vidal S., Brun C., Demailles J., Cadieu E.,  
RA Dreano S., Gloux S., Leleval V., Mottier S., Galibert F., Borkova D.,  
RA Minana B., Kafatos F.C., Louis C., Siden-Kiamos I., Bolshakov S.,  
RA Papagiannakis G., Spanos L., Cox S., Madueno E., de Pablo B.,  
RA Modolell J., Peter A., Schoettler P., Werner M., Mourikoti F.,  
RA Beinert N., Dowe G., Schaefer U., Jaekle H., Bucheton A.,  
RA Callister D.M., Campbell L.A., Darlamsou A., Henderson N.S.,  
RA McWilliam P.J., Salles C., Tait E.A., Valenti P., Saunders R.D.C.,  
RA Glover D.M.;  
RT "From sequence to chromosome: the tip of the X chromosome of *D. melanogaster*,"  
RT Science 287:2220-2222(2000).  
[5]  
RN SEQUENCE OF 2505-2611 FROM N.A.  
RP MEDLINE=85099329; PubMed=2981631;  
RX Wharton K.A., Yedvobnick B., Finnerty V.G., Artavanis-Tsakonas S.;  
RA "opa: a novel family of transcribed repeats shared by the Notch locus and other developmentally regulated loci in *D. melanogaster*,"  
RT Cell 40:55-62(1985).  
[6]  
RN SEQUENCE OF 1-8 FROM N.A.  
RP MEDLINE=87257846; PubMed=3037327;  
RX Kelley M.R., Kidd S., Berg R.L., Young M.W.;  
RA "Restriction of P-element insertions at the Notch locus of *Drosophila melanogaster*,"  
RT Mol. Cell. Biol. 7:1545-1548(1987).  
[7]  
RN REVIEW.  
RP Harris W.A.;  
RT "Many cell types specified by Notch function,";  
RL Curr. Biol. 1:120-122(1991).  
CC -!- FUNCTION: Functions as a receptor for membrane-bound ligands Delta and Serrate to regulate cell-fate determination. Upon ligand activation through the released notch intracellular domain (NICD) it forms a transcriptional activator complex with Su(H) (Suppressor of hairless) and activates genes of the enhancer of split locus. Essential for proper differentiation of ectoderm.  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -!- SIMILARITY: BELONGS TO THE NOTCH FAMILY.

CC -!- SIMILARITY: CONTAINS 36 EGF-LIKE DOMAINS.  
CC -!- SIMILARITY: CONTAINS 3 LIN/NOTCH REPEATS.  
CC -!- SIMILARITY: CONTAINS 6 ANK REPEATS.  
-----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
-----  
CC EMBL; M16152; AAB59220.1; -  
CC EMBL; M16153; AAB59220.1; JOINED.  
CC EMBL; M16149; AAB59220.1; JOINED.  
CC EMBL; M16150; AAB59220.1; JOINED.  
CC EMBL; M16151; AAB59220.1; JOINED.  
CC EMBL; M03508; AAA28725.1; -  
CC EMBL; M13689; AAA28725.1; JOINED.  
CC EMBL; K03507; AAA28725.1; JOINED.  
CC EMBL; AE003426; AAF45848.2; -  
CC EMBL; AL035436; CAB37610.1; -  
CC EMBL; AL035395; CAB37610.1; JOINED.  
CC EMBL; M12175; AAA74496.1; -  
CC EMBL; M16025; AAA28726.1; -  
CC PIR; A24420; A24420.  
CC PIR; A24768; A24768.  
CC PIR; A05267; A05267.  
CC HSSP; P00740; 1EDM.  
CC FlyBase; FBgn0004647; N.  
CC InterPro; IPR002110; ANK.  
CC InterPro; IPR000152; Asx\_hydroxyl.  
CC InterPro; IPR000561; EGF-like.  
CC InterPro; IPR000742; EGF\_2.  
CC InterPro; IPR001881; EGF\_Ca.  
CC InterPro; IPR001438; EGF\_II.  
CC InterPro; IPR002049; Laminin\_EGF.  
CC InterPro; IPR000800; Notch.  
CC Pfam; PF00008; EGF; 36.  
CC Pfam; PF00023; ank; 6.  
CC Pfam; PF00066; notch; 3.  
CC PRINTS; PR00010; EGFBLD.  
CC PRINTS; PR00011; EGFLAMIN.  
CC PRINTS; PR01452; NOTCH.  
CC SMART; SM00248; ANK; 7.  
CC SMART; SM00181; EGF; 36.  
CC SMART; SM00179; EGF\_CA; 35.  
CC SMART; SM00004; NL; 2.  
CC PROSITE; PS50088; ANK\_REPEAT; 5.  
CC PROSITE; PS50297; ANK\_REPEAT\_REGION; 1.  
CC PROSITE; PS00010; ASX\_HYDROXYL; 22.  
CC PROSITE; PS00022; EGF\_1; 34.  
CC PROSITE; PS01186; EGF\_2; 28.  
CC PROSITE; PS01187; EGF\_CA; 21.  
KW Receptor; Transcription regulation; Activator; Differentiation;  
KW Developmental protein; Neurogenesis; Repeat; ANK repeat;  
KW EGF-like domain; Transmembrane; Glycoprotein; Signal.  
FT SIGNAL 1 44  
FT CHAIN 45 2703  
FT DOMAIN 45 1745  
FT TRANSMEM 1746 1766  
FT DOMAIN 1767 2703  
FT DOMAIN 58 95  
FT DOMAIN 96 136  
FT DOMAIN 139 176  
FT DOMAIN 177 215  
FT DOMAIN 217 253  
FT DOMAIN 255 291  
FT DOMAIN 293 329  
FT DOMAIN 331 370  
FT DOMAIN 372 408  
FT DOMAIN 409 447  
FT DOMAIN 449 486

```

FT DOMAIN 488 524 EGF-LIKE 12, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 526 562 EGF-LIKE 13, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 564 600 EGF-LIKE 14, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 602 637 EGF-LIKE 15, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 639 675 EGF-LIKE 16, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 677 713 EGF-LIKE 17, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 715 751 EGF-LIKE 18, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 753 789 EGF-LIKE 19, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 791 827 EGF-LIKE 20, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 829 865 EGF-LIKE 21, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 867 905 EGF-LIKE 22, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 907 944 EGF-LIKE 23, CALCIUM-BINDING (POTENTIAL).

Query Match 11.7%; Score 176; DB 1; Length 2703;
Best Local Similarity 25.8%; Pred. No. 8.3e-06;
Matches 58; Conservative 21; Mismatches 62; Indels 84; Gaps 13;

QY 18 GGEHAYRPGRRVCYAVRAH--GDPVSESPFYQRYVPFLTTCDSHRACSYRT---IYRT 71
DB 70 GGCCTVQLNGKTYCACDSHYVD-----YCEHRNPNCSMRCONGSTCQV 113
QY 72 AYRRSGGLAPRRVAC-CP-GWKRT---SLPLGACGAAIC----- 107
DB 114 TFRN-----GRGICGCKPLGFDESLCEIAYNACDHYTCNGTCQKLEBYCACA 167
QY 108 -----QPPCNGSCV-----QPRCRCPAGRGDTQSDVDECSA--R 144
DB 168 NGYTCRCETKNLCASSPCRNATCTALGASSSFTCSCPFGDTCYSYDIEBCQNPCK 227
QY 145 RGGCPCRCVNTAGSYWQCQWEGHSLADGTLVCPKXGPPRVANP 189
DB 228 YGG--TCVTHSGSYQCMCPGTYT---GKDCDTRKYP--CSPSP 263

RESULT 11
NEL_CHICK STANDARD; PRT; 816 AA.
AC 090827;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE NEL protein precursor (93 kDa protein).
OS NEL.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OC NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA MEDLINE=95383734; PubMed=7655083;
RA Matsubashi S., Noji S., Koyama E., Myokai F., Ohuchi H.,
RA Taniguchi S., Hori K.;
RT "New gene, nel, encoding a M(r) 93 K protein with EGF-like repeats is
RT strongly expressed in neural tissues of early stage chick embryos.";
RL Dev. Dyn. 203:212-222(1995).
RN [2]
RP TSP N-TERMINAL DOMAIN
RA MEDLINE=98153258; PubMed=9480764;
RA Beckmann G., Hanke J., Bork P., Reich J.;
RT "Merging extracellular domains: fold prediction for laminin G-like
RT and amino-terminal thrombospondin-like modules based on homology to
RT pentraxins.";
RL J. Mol. Biol. 275:725-730(1998).
CC -1- TISSUE SPECIFICITY: STRONGLY EXPRESSED IN EARLY EMBRYONIC NEURAL
CC TISSUES (BRAIN, SPINAL CORD, DORSAL ROOT GANGLIA), LESS IN OTHER
CC TISSUES SUCH AS CELLS AROUND CARTILAGE, MYOCARDIUM, LUNG
CC MESENCHYMAL CELLS, AND LIVER. AFTER HATCHING EXPRESSION IS
CC RESTRICTED TO NEURAL TISSUES INCLUDING RETINA.
CC -1- SIMILARITY: CONTAINS 1 TSP N-TERMINAL DOMAIN.
CC -1- SIMILARITY: CONTAINS 5 WMFC DOMAINS.
CC -1- SIMILARITY: CONTAINS 6 EGF-LIKE DOMAINS.

```

```

CC CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; D86747; BAA13167.1; -.
CC HSSP; P00740; 1EDM.
CC InterPro; IPR000152; Asx_hydroxyl.
CC InterPro; IPR000561; EGF-Like.
CC InterPro; IPR001851; EGF_Ca.
CC InterPro; IPR001791; Laminin_G.
CC InterPro; IPR003129; TSPN.
CC InterPro; IPR001007; WMF_C.
CC Pfam; PF00008; EGF; 5.
CC Pfam; PF00093; WWC; 3.
CC Pfam; PF02210; TSPN; 1.
CC SMART; SM00179; EGF_CA; 2.
CC SMART; SM00001; EGF_Like; 4.
CC SMART; SM00282; LamG; 1.
CC SMART; SM00210; TSPN; 1.
CC SMART; SM00214; WWC; 2.
CC PROSITE; PS00010; ASX_HYDROXYL; 3.
CC PROSITE; PS00022; EGF_1; 1.
CC PROSITE; PS01186; EGF_2; 4.
CC PROSITE; PS01187; EGF_CA; 3.
CC PROSITE; PS01208; WWC; 2.
CC GlycoProtein; EGF-like domain; Repeat; Signal.
CC SIGNAL 1 24
CC CHAIN 25 816
CC FT DOMAIN 25 816 NEL PROTEIN.
CC FT DOMAIN 30 258 TSP N-TERMINAL.
CC FT DOMAIN 272 331 WMFC 1.
CC FT DOMAIN 332 396 WMFC 2.
CC FT DOMAIN 397 439 EGF-LIKE 1.
CC FT DOMAIN 440 481 EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).
CC FT DOMAIN 482 521 EGF-LIKE 3.
CC FT DOMAIN 521 553 EGF-LIKE 4.
CC FT DOMAIN 555 601 EGF-LIKE 5, CALCIUM-BINDING (POTENTIAL).
CC FT DOMAIN 602 637 EGF-LIKE 6, CALCIUM-BINDING (POTENTIAL).
CC FT DOMAIN 638 693 WMFC 3.
CC FT DOMAIN 698 756 WMFC 4.
CC FT DOMAIN 758 813 WMFC 5.
CC FT DOMAIN 401 413 BY SIMILARITY.
CC FT DISULFID 407 422 BY SIMILARITY.
CC FT DISULFID 424 438 BY SIMILARITY.
CC FT DISULFID 444 457 BY SIMILARITY.
CC FT DISULFID 451 466 BY SIMILARITY.
CC FT DISULFID 468 480 BY SIMILARITY.
CC FT DISULFID 486 499 BY SIMILARITY.
CC FT DISULFID 493 508 BY SIMILARITY.
CC FT DISULFID 510 521 BY SIMILARITY.
CC FT DISULFID 525 535 BY SIMILARITY.
CC FT DISULFID 529 541 BY SIMILARITY.
CC FT DISULFID 543 552 BY SIMILARITY.
CC FT DISULFID 559 572 BY SIMILARITY.
CC FT DISULFID 566 581 BY SIMILARITY.
CC FT DISULFID 583 600 BY SIMILARITY.
CC FT DISULFID 606 619 BY SIMILARITY.
CC FT DISULFID 613 628 BY SIMILARITY.
CC FT DISULFID 630 636 BY SIMILARITY.
CC FT CARBOHYD 53 53 N-LINKED (GLCNAC. .) (POTENTIAL).
CC FT CARBOHYD 225 225 N-LINKED (GLCNAC. .) (POTENTIAL).
CC FT CARBOHYD 293 293 N-LINKED (GLCNAC. .) (POTENTIAL).
CC FT CARBOHYD 298 298 N-LINKED (GLCNAC. .) (POTENTIAL).
CC FT CARBOHYD 517 517 N-LINKED (GLCNAC. .) (POTENTIAL).
CC FT CARBOHYD 615 615 N-LINKED (GLCNAC. .) (POTENTIAL).
CC FT CARBOHYD 635 635 N-LINKED (GLCNAC. .) (POTENTIAL).
CC SEQUENCE 816 AA; 90968 MW; BPCD8C983C02F831 CRC64;

Query Match 11.7%; Score 175.5; DB 1; Length 816;

```

Best Local Similarity 38.6%; Pred. No. 2.8e-06;  
 Matches 32; Conservative 13; Mismatches 33; Indels 5; Gaps 2;

QY 100 GACGAAICQPPCRNGGSCVQGRRCPCAGWGRDTCQSDVDECSARRGGCPOR--CVNTAG 157  
 DB 518 GTVCKAFKCGKNGGACIASNVACACPOGFTGTPSCETIDECSDGFGVQCDSRANCINLPG 577

QY 158 SYWCOCWEGHLSADGTLCPVKG 180  
 DB 578 WYHCECRDGYH---DNGMFPSPG 597

RESULT 12  
 ID FBN1\_HUMAN STANDARD; PRT; 2871 AA.  
 AC P35555;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Fibrillin 1 precursor.  
 GN FBN1 OR FBN.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Placenta;  
 RX MEDLINE=93372860; PubMed=8364578;  
 RA Pereira L.V., D'Alessio M., Ramirez F., Lynch J.R., Sykes B.,  
 RA Pangilinan T., Bonadio J.;  
 RA "Genomic organization of the sequence coding for fibrillin, the  
 RT defective gene product in Marfan syndrome.";  
 RL Hum. Mol. Genet. 2:961-968 (1993).  
 RN [2]  
 RP SEQUENCE OF 1-932 FROM N.A.  
 RC TISSUE=Placenta, and Fibroblast;  
 RX MEDLINE=94010947; PubMed=7691719;  
 RA Corson G.M., Chaberg S.C., Dietz H.C., Charbonneau N.L., Sakai L.Y.;  
 RT "Fibrillin binds calcium and is coded by cDNAs that reveal a  
 RT multidomain structure and alternatively spliced exons at the 5'  
 end.";  
 RL Genomics 17:476-484 (1993).  
 RN [3]  
 RP SEQUENCE OF 899-2871 FROM N.A.  
 RX MEDLINE=91304568; PubMed=1852207;  
 RA Maslen C.L., Corson G.M., Maddox B.K., Glanville R.W., Sakai L.Y.;  
 RT "Partial sequence of a candidate gene for the Marfan syndrome.";  
 RL Nature 352:334-337 (1991).  
 RN [4]  
 RP SEQUENCE OF 813-1313 FROM N.A.  
 RX MEDLINE=91304567; PubMed=1852206;  
 RA Lee B., Godfrey M., Vitale E., Hori H., Mattei M.-G., Sarfarazi M.,  
 RA Tsipouras P., Ramirez F., Hollister D.W.;  
 RT "Linkage of Marfan syndrome and a phenotypically related disorder to  
 RT two different fibrillin genes.";  
 RL Nature 352:330-334 (1991).  
 RN [5]  
 RP CHARACTERIZATION.  
 RX MEDLINE=91317849; PubMed=1860873;  
 RA Sakai L.Y., Keene D.R., Glanville R.W., Bachinger H.P.;  
 RT "Purification and partial characterization of fibrillin, a cysteine-  
 RT rich structural component of connective tissue microfibrils.";  
 RL J. Biol. Chem. 266:14763-14770 (1991).  
 RN [6]  
 RP STRUCTURE BY NMR OF 2054-2125.  
 RX MEDLINE=98031893; PubMed=9362480;  
 RA Yuan X., Downing A.K., Knott V., Handford P.A.;  
 RT "Solution structure of the transforming growth factor beta-binding  
 RT protein-like module, a domain associated with matrix fibrils.";  
 RL EMBO J. 16:6659-6666 (1997).  
 RN [7]  
 RP STRUCTURE BY NMR OF 2124-2205.

RX MEDLINE=96144829; PubMed=8568869;  
 RA Knott V., Downing A.K., Cardy C.M., Handford P.A.;  
 RT "Calcium binding properties of an epidermal growth factor-like domain  
 RL from human fibrillin-1.";  
 RN J. Mol. Biol. 255:22-27 (1996).  
 RP STRUCTURE BY NMR OF 2124-2205.  
 RX MEDLINE=96222301; PubMed=8653794;  
 RA Downing A.K., Knott V., Werner J.M., Cardy C.M., Campbell I.D.,  
 RA Handford P.A.;  
 RT "Solution structure of a pair of calcium-binding epidermal growth  
 RT factor-like domains: implications for the Marfan syndrome and other  
 RT genetic disorders.";  
 RL Cell 85:597-605 (1996).  
 RN [9]  
 RP REVIEW ON MFS VARIANTS.  
 RX MEDLINE=96174615; PubMed=8594563;  
 RA Colod G., Beroud C., Soussi T., Junien C., Boileau C.;  
 RT "Software and database for the analysis of mutations in the human  
 RT FBN1 gene.";  
 RL Nucleic Acids Res. 24:137-141 (1996).  
 RN [10]  
 RP REVIEW ON MFS VARIANTS.  
 RX MEDLINE=97169383; PubMed=9016526;  
 RA Colod-Beroud G., Beroud C., Ades L., Black C., Boxer M., Brock D.J.,  
 RA Godfrey M., Hayward C., Karttunen L., Milewicz D., Peltonen L.,  
 RA Richards R.I., Wang W., Junien C., Boileau C.;  
 RT "Marfan Database (second edition): software and database for the  
 RT analysis of mutations in the human FBN1 gene.";  
 RL Nucleic Acids Res. 25:147-150 (1997).  
 RN [11]  
 RP REVIEW ON VARIANTS.  
 RX MEDLINE=98062175; PubMed=9401003;  
 RA Hayward C., Brock D.J.H.;  
 RT "Fibrillin-1 mutations in Marfan syndrome and other type-1  
 RT fibrillinopathies.";  
 RL Hum. Mutat. 10:415-423 (1997).  
 RN [12]  
 RP VARIANT MFS PRO-1137.  
 RX MEDLINE=91304569; PubMed=1852208;  
 RA Dietz H.C., Cutting G.R., Pyeritz R.E., Maslen C.L., Sakai L.Y.,  
 RA Corson G.M., Puffenberger E.G., Hamosh A., Nanthakumar E.J.,  
 RA Curristin S.M., Stetten G., Meyers D.A., Francomano C.A.;  
 RT "Marfan syndrome caused by a recurrent de novo missense mutation in  
 RT the fibrillin gene.";  
 RL Nature 352:337-339 (1991).  
 RN [13]  
 RP VARIANTS MFS SER-1249; ARG-1663; SER-2221 AND SER-2307.  
 RX MEDLINE=93250834; PubMed=1301946;  
 RA Dietz H.C., Saraiya J.M., Pyeritz R.E., Cutting G.R., Francomano C.A.;  
 RT "Clustering of fibrillin (FBN1) missense mutations in Marfan syndrome  
 RT patients at cysteine residues in EGF-like domains.";  
 RL Hum. Mutat. 1:366-374 (1992).  
 RN [14]  
 RP VARIANT MFS SER-2307.  
 RX MEDLINE=92235290; PubMed=1569206;  
 RA Dietz H.C., Pyeritz R.E., Puffenberger E.G., Kendzior R.J. Jr.,  
 RA Corson G.M., Maslen C.L., Sakai L.Y., Francomano C.A., Cutting G.R.;  
 RT "Marfan phenotype variability in a family segregating a missense  
 RT mutation in the epidermal growth factor-like motif of the fibrillin  
 RT gene.";  
 RL J. Clin. Invest. 89:1674-1680 (1992).  
 RN [15]  
 RP VARIANTS MFS ILE-548 AND ALA-723.  
 RX MEDLINE=94010946; PubMed=8406497;  
 RA Dietz H.C., McIntosh I., Sakai L.Y., Corson G.M., Chaberg S.C.,  
 RA Pyeritz R.E., Francomano C.A.;  
 RT "Four novel FBN1 mutations: significance for mutant transcript level  
 RT and EGF-like domain calcium binding in the pathogenesis of Marfan  
 RL syndrome.";  
 RN Genomics 17:468-475 (1993).  
 RN [16]  
 RP VARIANTS MFS SER-2144.

RA MEDLINE=93278402; PubMed=8504310;  
 RA Hewett D.R., Lynch J.R., Smith R., Sykes B.C.;  
 RT "A novel fibrillin mutation in the Marfan syndrome which could  
 RT disrupt calcium binding of the epidermal growth factor-like module,"  
 RL Hum. Mol. Genet. 2:475-477(1993).  
 RN [17]  
 RP VARIANTS MFS R-862; Y-1117; P-1137 AND F-1589, AND VARIANT A-1148.  
 RX MEDLINE=9410843; PubMed=8281141;  
 RA Tynan K., Comeau K., Pearson M., Wilgenbus P., Levitt D., Gasner C.,  
 RA Berg M.A., Miller D.C., Francke U.;  
 RT "Mutation screening of complete fibrillin-1 coding sequence: report  
 RT of five new mutations, including two in 8-cysteine domains,"  
 RL Hum. Mol. Genet. 2:1813-1821(1993).  
 RN [18]  
 RP VARIANTS MFS GLY-217 AND ARG-2627.  
 RX MEDLINE=95067970; PubMed=7973366;  
 RA Karttunen L., Raghunath M., Lonnqvist L., Peltonen L.;  
 RT "A compound-heterozygous Marfan patient: two defective fibrillin  
 RT alleles result in a lethal phenotype,"  
 RL Am. J. Hum. Genet. 55:1083-1091(1994).  
 RN [19]  
 RP VARIANT EL LYS-2447.  
 RX MEDLINE=94245249; PubMed=8188302;  
 RA Lonnqvist L., Child A., Kainulainen K., Davidson R., Puhakka L.,  
 RA Peltonen L.;  
 RT "A novel mutation of the fibrillin gene causing ectopia lentis,"  
 RL Genomics 19:573-576(1994).  
 RN [20]  
 RP VARIANT MFS CYS-627.  
 RX MEDLINE=94272487; PubMed=8004112;  
 RA Hayward C., Rae A.L., Porteous M.E.M., Logie L.J., Brock L.J.;  
 RT "Two novel mutations and a neutral polymorphism in EGF-like domains  
 RT of the fibrillin gene (FBN1): SSCP screening of exons 15-21 in Marfan  
 RT syndrome patients,"  
 RL Hum. Mol. Genet. 3:373-375(1994).  
 RN [21]  
 RP VARIANT MFS CYS-122.  
 RX MEDLINE=94314977; PubMed=8040326;  
 RA Stahl-Hallengren C., Ukonen T., Kainulainen K., Kristoferson U.,  
 RA Saxne T., Tornqvist K., Peltonen L.;  
 RT "An extra cysteine in one of the non-calcium-binding epidermal growth  
 RT factor-like motifs of the FBN1 polypeptide is connected to a novel  
 RT variant of Marfan syndrome,"  
 RL J. Clin. Invest. 94:709-713(1994).  
 RN [22]  
 RP VARIANT MFS TYR-1223.  
 RX MEDLINE=94351682; PubMed=8071963;  
 RA Hewett D.R., Lynch J.R., Child A., Sykes B.C.;  
 RT "A new missense mutation of fibrillin in a patient with Marfan  
 RT syndrome,"  
 RL J. Med. Genet. 31:338-339(1994).  
 RN [23]  
 RP VARIANT MFS HIS-1170.  
 RX MEDLINE=95174777; PubMed=7870075;  
 RA Hayward C., Porteous M.E.M., Brock D.J.H.;  
 RT "A novel mutation in the fibrillin gene (FBN1) in familial  
 RT aortic dissection,"  
 RL Mol. Cell. Probes 8:325-327(1994).  
 RN [24]  
 RP VARIANTS MFS G-217, N-1023, R-1074, Y-1242, R-1513, E-2127, W-2151,  
 RP K-2447 AND R-2511.  
 RX MEDLINE=94184368; PubMed=8136837;  
 RA Kainulainen K., Karttunen L., Puhakka L., Sakai L., Peltonen L.;  
 RT "Mutations in the fibrillin gene responsible for dominant ectopia  
 RT lentis and neonatal Marfan syndrome,"  
 RL Nat. Genet. 6:64-69(1994).  
 RN [25]  
 RP VARIANT SER-1127.

Query Match 11.7%; Score 175.5; DB 1; Length 2871;  
 Best Local Similarity 18.9%; Pred. No. 9.6e-06;  
 Matches 52; Conservative 14; Mismatches 48; Indels 161; Gaps 6;

QY 75 KSPGLAPRPVRYACCPKMTKTSGLPQA----- 101  
 DB 54 KGPVNCGRSVYNAVCCPKMTK-----LPFGNQICVPICRHSCGDGFCSPRMNCTCPGSGIAPS 110  
 QY 102 -----CGAICQPPRCNGSSCYQPRGRCPA 127  
 DB 111 CGSRRIQHCHNRKXNGSSCSDDHCLCQKGYIGTHCGQVPCEGGLNGRCVAPNRCACTY 170  
 QY 128 GMRGDTCC----- 135  
 DB 171 GFTGQGRDVRTRTGCFTVINQMGQGLSGIVCTKQLCATVGRAMHPCGMPACRPH 230  
 QY 136 -----SDVDEGARRGCGP-QRCVNTAGSYWCQCEGHSLSADGTLTC----- 176  
 DB 231 CRRGFIPIRITGACQDVDECOAIPGLCGGNCINTVSGFECKCPAGHKLNEVSGKCEDID 290  
 QY 177 -----PPKGS-----PPRYANPFG 191  
 DB 291 ECSTIPGICEGGCTNTVSYFCKCPGPGFTYSPDG 325

## RESULT 13

NTCS HUMAN

ID NTCS HUMAN STANDARD; PRT; 2321 AA.

AC Q9DM47; Q9Y6L8; Q9UPL3; Q9UEB3;  
 DT 15-JUN-2002 (Rel. 41, Created)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Neurogenic locus notch homolog protein 3 precursor (Notch 3).  
 GN NOTCH3.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]

RP SEQUENCE FROM N.A.  
 RX MEDLINE=97032728; PubMed=8878478;  
 RA Joutel A., Corpechot C., Ducros A., Vahedi K., Chabriat H., Mouton P.,  
 RA Alomowitch S., Domenga V., Cecillon M., Marechal E., Maciazek J.,  
 RA Vayssières C., Cruaud C., Cabanis E.-A., Ruchoux M.M., Weissenbach J.,  
 RA Bach J.-F., Bousser M.-G., Tournier-Lasserre E.;  
 RT "Notch3 mutations in CADASIL, a hereditary adult-onset condition  
 RT causing stroke and dementia,"  
 RL Nature 383:707-710(1996).  
 RN [2]

RP SEQUENCE FROM N.A.  
 RA Gunel M., Aravanis-Teakonas S.;  
 RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.  
 RN [3]

RP SEQUENCE FROM N.A.  
 RA Lamerdin J.E., McCreedy P.M., Skowronski E., Adamson A.W.,  
 RA Burkhardt-Schultz K., Gordon L., Kyle A., Ramirez M., Stlawegen S.,  
 RA Phan H., Velasco N., Garness J., Dangnan L., Poundstone P.,  
 RA Christensen M., Georgescu A., Avila J., Liu S., Altix C., Andreise T.,  
 RA Trankheim M., Amico-Keller G., Coetfield J., Duarte S., Lucas S.,  
 RA Bruce R., Thomas P., Quan G., Krommiller B., Arellano A.,  
 RA Montgomerie M., Ow D., Nolan M., Trong S., Kobayashi A., Olsen A.S.,  
 RA Carrano A.V.;  
 RT "Sequence analysis of an 1.5 Mb olfactory receptor (OLFR) cluster in  
 RT 1p13.1,"  
 RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.  
 RN [4]

RP VARIANTS CADASIL Y-49; C-71; C-90; C-110; C-133; C-141; R-146; C-153;  
 RP C-169; C-171; C-182; R-185; S-212; G-222; Y-224; C-258; Y-542; C-558;  
 RP C-578; C-728; C-985; C-1006; C-1031; C-1231 AND R-1261, AND VARIANTS  
 RP R-170; L-496; Q-1153; W-1183 AND A-2223.  
 RX MEDLINE=98049753; PubMed=9388399;  
 RA Joutel A., Vahedi K., Corpechot C., Tiesch A., Chabriat H.,  
 RA Vayssières C., Cruaud C., Maciazek J., Weissenbach J., Bousser M.-G.,  
 RA Bach J.-F., Tournier-Lasserre E.;  
 RT "Strong clustering and stereotyped nature of Notch3 mutations in  
 RT CADASIL patients,"  
 RL Lancet 350:1511-1515(1997).

[5] VARIANT CADASIL 114-GUY--PRO-120 DEL.  
 RP MEDLINE=20264473; PubMed=10802807;  
 RA Joutel A., Chabriat H., Vahedi K., Domenga V., Vayssiere C.,  
 RA Ruchoux M.M., Lucas C., Leys D., Bousser M.-G., Tournier-Lasserre E.;  
 RT "Splice site mutation causing a seven amino acid Notch3 in-frame  
 deletion in CADASIL";  
 RL Neurology 54:1874-1875 (2000).  
 [6]  
 RP IDENTIFICATION OF LIGANDS.  
 RX MEDLINE=99180765; PubMed=10079256;  
 RA Gray G.E., Mann R.S., Misiadis E., Henrique D., Carcangiu M.-L.,  
 RA Banks A., Leiman J., Ward D., Ish-Horowitz D., Artavanis-Tsakonas S.;  
 RT "Human ligands of the Notch receptor";  
 RL Am. J. Pathol. 154:785-794 (1999).  
 CC -I- FUNCTION: Functions as a receptor for membrane-bound ligands  
 Jagged1, Jagged2 and Delta to regulate cell-fate determination.  
 CC Upon ligand activation through the released notch intracellular  
 CC domain (NICD) it forms a transcriptional activator complex with  
 CC RBP-J kappa and activates genes of the enhancer of split locus.  
 CC Affects the implementation of differentiation, proliferation and  
 CC apoptotic programs (By similarity).  
 CC -I- SUBUNIT: Heterodimer of a C-terminal fragment N(TW) and a N-  
 CC terminal fragment N(EC) which are probably linked by disulfide  
 CC bonds (By similarity).  
 CC -I- SUBCELLULAR LOCATION: Type I membrane protein. Following  
 CC proteolytical processing NICD is translocated to the nucleus.  
 CC -I- TISSUE SPECIFICITY: Ubiquitously expressed in fetal and adult  
 CC tissues.  
 CC -I- PFM: Synthesized in the endoplasmic reticulum as an inactive form  
 CC which is proteolytically cleaved by a furin-like convertase in the  
 CC trans-Golgi network before it reaches the plasma membrane to yield  
 CC an active, ligand-accessible form. Cleavage results in a C-  
 CC terminal fragment N(TW) and a N-terminal fragment N(EC). Following  
 CC ligand binding, it is cleaved by TNF-alpha converting enzyme  
 CC (TACE) to yield a membrane-associated intermediate fragment called  
 CC notch extracellular truncation (NEXT). This fragment is then  
 CC cleaved by presenilin dependent gamma-secretase to release a  
 CC notch-derived peptide containing the intracellular domain (NICD)  
 CC from the membrane (By similarity).  
 CC -I- PFM: Phosphorylated (By similarity).  
 CC -I- DISEASE: Defects in NOTCH3 are associated with CADASIL (Cerebral  
 CC autosomal dominant arteriopathy with subcortical infarcts and  
 CC leukoencephalopathy) which causes a type of stroke and dementia of  
 CC which key features include recurrent subcortical ischemic events  
 CC and vascular dementia.  
 CC -I- SIMILARITY: BELONGS TO THE NOTCH FAMILY.  
 CC -I- SIMILARITY: CONTAINS 34 EGF-LIKE DOMAINS.  
 CC -I- SIMILARITY: CONTAINS 5 LIN/NOTCH REPEATS.  
 CC -I- SIMILARITY: CONTAINS 5 ANK REPEATS.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL; U97669; AAB91371.1; --  
 DR EMBL; AF058900; AAC14346.1; --  
 DR EMBL; AF058881; AAC14346.1; JOINED.  
 DR EMBL; AF058882; AAC14346.1; JOINED.  
 DR EMBL; AF058883; AAC14346.1; JOINED.  
 DR EMBL; AF058894; AAC14346.1; JOINED.  
 DR EMBL; AF058895; AAC14346.1; JOINED.  
 DR EMBL; AF058886; AAC14346.1; JOINED.  
 DR EMBL; AF058887; AAC14346.1; JOINED.  
 DR EMBL; AF058888; AAC14346.1; JOINED.  
 DR EMBL; AF058889; AAC14346.1; JOINED.  
 DR EMBL; AF058890; AAC14346.1; JOINED.  
 DR EMBL; AF058891; AAC14346.1; JOINED.  
 DR EMBL; AF058892; AAC14346.1; JOINED.

DR EMBL; AF058893; AAC14346.1; JOINED.  
 DR EMBL; AF058894; AAC14346.1; JOINED.  
 DR EMBL; AF058895; AAC14346.1; JOINED.  
 DR EMBL; AF058896; AAC14346.1; JOINED.  
 DR EMBL; AF058897; AAC14346.1; JOINED.  
 DR EMBL; AF058898; AAC14346.1; JOINED.  
 DR EMBL; AF058899; AAC14346.1; JOINED.  
 DR EMBL; AF058900; AAC14346.1; JOINED.  
 DR EMBL; AC004257; AAC04897.1; --  
 DR EMBL; AC004663; AAC15789.1; --  
 DR HSSP; P00740; IEDM.  
 DR Genew; HGNC:7883; NOTCH3.  
 DR MIM; 600276; --  
 DR MIM; 125310; --  
 DR InterPro; IPR002110; ANK.  
 DR InterPro; IPR000152; Asx\_hydroxyl.  
 DR InterPro; IPR000561; EGF-like.  
 DR InterPro; IPR000742; EGF 2.  
 DR InterPro; IPR001881; EGF\_Ca.  
 DR InterPro; IPR001438; EGF-II.  
 DR InterPro; IPR002049; Laminin\_EGF.  
 DR InterPro; IPR000800; Notch.  
 DR Pfam; PF00008; EGF; 34.  
 DR Pfam; PF00023; ank; 6.  
 DR Pfam; PF00066; notch; 3.  
 DR PRINTS; PR00010; EGFBL00D.  
 DR PRINTS; PR00011; EGF\_LAMININ.  
 DR PRINTS; PR01452; NOTCH.  
 DR SMART; SM00248; ANK; 5.  
 DR SMART; SM00179; EGF\_CA; 19.  
 DR SMART; SM00001; EGF\_like; 14.  
 DR SMART; SM00004; NL\_3.  
 DR PROSITE; PS50088; ANK\_REPEAT; 4.  
 DR PROSITE; PS50297; ANK\_REPEAT\_REGION; 1.  
 DR PROSITE; PS00010; ASX\_HYDROXYL; 18.  
 DR PROSITE; PS00022; EGF 1; 33.  
 DR PROSITE; PS01186; EGF 2; 25.  
 DR PROSITE; PS01187; EGF\_CA; 18.  
 KW Receptor; Transcription regulation; Activator; Differentiation;  
 KW Developmental protein; Repeat; ANK repeat; EGF-like domain;  
 KW Transmembrane; Glycoprotein; Signal; Phosphorylation; Polymorphism;  
 KW Disease mutation.  
 FT SIGNAL 1 39  
 FT CHAIN 40 2321  
 FT CHAIN 1629 2321  
 FT CHAIN 1662 2321  
 FT DOMAIN 40 1643  
 FT TRANSMEM 1644 1664  
 FT DOMAIN 1665 2321  
 FT DOMAIN 40 77  
 FT DOMAIN 78 118  
 FT DOMAIN 119 156  
 FT DOMAIN 158 195  
 FT DOMAIN 197 234  
 FT DOMAIN 236 272  
 FT DOMAIN 274 312  
 FT DOMAIN 314 350  
 FT DOMAIN 351 389  
 FT DOMAIN 391 429  
 FT DOMAIN 431 467  
 FT DOMAIN 469 505  
 FT DOMAIN 507 543  
 FT DOMAIN 545 580  
 FT DOMAIN 582 618  
 FT DOMAIN 620 655  
 FT DOMAIN 657 693  
 FT DOMAIN 695 730  
 FT DOMAIN 734 770  
 FT DOMAIN 771 808  
 FT DOMAIN 810 847  
 FT DOMAIN 849 885  
 FT DOMAIN 887 922  
 FT SIGNAL 1 39  
 FT CHAIN 40 2321  
 FT CHAIN 1629 2321  
 FT CHAIN 1662 2321  
 FT DOMAIN 40 1643  
 FT TRANSMEM 1644 1664  
 FT DOMAIN 1665 2321  
 FT DOMAIN 40 77  
 FT DOMAIN 78 118  
 FT DOMAIN 119 156  
 FT DOMAIN 158 195  
 FT DOMAIN 197 234  
 FT DOMAIN 236 272  
 FT DOMAIN 274 312  
 FT DOMAIN 314 350  
 FT DOMAIN 351 389  
 FT DOMAIN 391 429  
 FT DOMAIN 431 467  
 FT DOMAIN 469 505  
 FT DOMAIN 507 543  
 FT DOMAIN 545 580  
 FT DOMAIN 582 618  
 FT DOMAIN 620 655  
 FT DOMAIN 657 693  
 FT DOMAIN 695 730  
 FT DOMAIN 734 770  
 FT DOMAIN 771 808  
 FT DOMAIN 810 847  
 FT DOMAIN 849 885  
 FT DOMAIN 887 922  
 FT SIGNAL 1 39  
 FT CHAIN 40 2321  
 FT CHAIN 1629 2321  
 FT CHAIN 1662 2321  
 FT DOMAIN 40 1643  
 FT TRANSMEM 1644 1664  
 FT DOMAIN 1665 2321  
 FT DOMAIN 40 77  
 FT DOMAIN 78 118  
 FT DOMAIN 119 156  
 FT DOMAIN 158 195  
 FT DOMAIN 197 234  
 FT DOMAIN 236 272  
 FT DOMAIN 274 312  
 FT DOMAIN 314 350  
 FT DOMAIN 351 389  
 FT DOMAIN 391 429  
 FT DOMAIN 431 467  
 FT DOMAIN 469 505  
 FT DOMAIN 507 543  
 FT DOMAIN 545 580  
 FT DOMAIN 582 618  
 FT DOMAIN 620 655  
 FT DOMAIN 657 693  
 FT DOMAIN 695 730  
 FT DOMAIN 734 770  
 FT DOMAIN 771 808  
 FT DOMAIN 810 847  
 FT DOMAIN 849 885  
 FT DOMAIN 887 922  
 FT SIGNAL 1 39  
 FT CHAIN 40 2321  
 FT CHAIN 1629 2321  
 FT CHAIN 1662 2321  
 FT DOMAIN 40 1643  
 FT TRANSMEM 1644 1664  
 FT DOMAIN 1665 2321  
 FT DOMAIN 40 77  
 FT DOMAIN 78 118  
 FT DOMAIN 119 156  
 FT DOMAIN 158 195  
 FT DOMAIN 197 234  
 FT DOMAIN 236 272  
 FT DOMAIN 274 312  
 FT DOMAIN 314 350  
 FT DOMAIN 351 389  
 FT DOMAIN 391 429  
 FT DOMAIN 431 467  
 FT DOMAIN 469 505  
 FT DOMAIN 507 543  
 FT DOMAIN 545 580  
 FT DOMAIN 582 618  
 FT DOMAIN 620 655  
 FT DOMAIN 657 693  
 FT DOMAIN 695 730  
 FT DOMAIN 734 770  
 FT DOMAIN 771 808  
 FT DOMAIN 810 847  
 FT DOMAIN 849 885  
 FT DOMAIN 887 922  
 FT SIGNAL 1 39  
 FT CHAIN 40 2321  
 FT CHAIN 1629 2321  
 FT CHAIN 1662 2321  
 FT DOMAIN 40 1643  
 FT TRANSMEM 1644 1664  
 FT DOMAIN 1665 2321  
 FT DOMAIN 40 77  
 FT DOMAIN 78 118  
 FT DOMAIN 119 156  
 FT DOMAIN 158 195  
 FT DOMAIN 197 234  
 FT DOMAIN 236 272  
 FT DOMAIN 274 312  
 FT DOMAIN 314 350  
 FT DOMAIN 351 389  
 FT DOMAIN 391 429  
 FT DOMAIN 431 467  
 FT DOMAIN 469 505  
 FT DOMAIN 507 543  
 FT DOMAIN 545 580  
 FT DOMAIN 582 618  
 FT DOMAIN 620 655  
 FT DOMAIN 657 693  
 FT DOMAIN 695 730  
 FT DOMAIN 734 770  
 FT DOMAIN 771 808  
 FT DOMAIN 810 847  
 FT DOMAIN 849 885  
 FT DOMAIN 887 922  
 FT SIGNAL 1 39  
 FT CHAIN 40 2321  
 FT CHAIN 1629 2321  
 FT CHAIN 1662 2321  
 FT DOMAIN 40 1643  
 FT TRANSMEM 1644 1664  
 FT DOMAIN 1665 2321  
 FT DOMAIN 40 77  
 FT DOMAIN 78 118  
 FT DOMAIN 119 156  
 FT DOMAIN 158 195  
 FT DOMAIN 197 234  
 FT DOMAIN 236 272  
 FT DOMAIN 274 312  
 FT DOMAIN 314 350  
 FT DOMAIN 351 389  
 FT DOMAIN 391 429  
 FT DOMAIN 431 467  
 FT DOMAIN 469 505  
 FT DOMAIN 507 543  
 FT DOMAIN 545 580  
 FT DOMAIN 582 618  
 FT DOMAIN 620 655  
 FT DOMAIN 657 693  
 FT DOMAIN 695 730  
 FT DOMAIN 734 770  
 FT DOMAIN 771 808  
 FT DOMAIN 810 847  
 FT DOMAIN 849 885  
 FT DOMAIN 887 922  
 FT SIGNAL 1 39  
 FT CHAIN 40 2321  
 FT CHAIN 1629 2321  
 FT CHAIN 1662 2321  
 FT DOMAIN 40 1643  
 FT TRANSMEM 1644 1664  
 FT DOMAIN 1665 2321  
 FT DOMAIN 40 77  
 FT DOMAIN 78 118  
 FT DOMAIN 119 156  
 FT DOMAIN 158 195  
 FT DOMAIN 197 234  
 FT DOMAIN 236 272  
 FT DOMAIN 274 312  
 FT DOMAIN 314 350  
 FT DOMAIN 351 389  
 FT DOMAIN 391 429  
 FT DOMAIN 431 467  
 FT DOMAIN 469 505  
 FT DOMAIN 507 543  
 FT DOMAIN 545 580  
 FT DOMAIN 582 618  
 FT DOMAIN 620 655  
 FT DOMAIN 657 693  
 FT DOMAIN 695 730  
 FT DOMAIN 734 770  
 FT DOMAIN 771 808  
 FT DOMAIN 810 847  
 FT DOMAIN 849 885  
 FT DOMAIN 887 922  
 FT SIGNAL 1 39  
 FT CHAIN 40 2321  
 FT CHAIN 1629 2321  
 FT CHAIN 1662 2321  
 FT DOMAIN 40 1643  
 FT TRANSMEM 1644 1664  
 FT DOMAIN 1665 2321  
 FT DOMAIN 40 77  
 FT DOMAIN 78 118  
 FT DOMAIN 119 156  
 FT DOMAIN 158 195  
 FT DOMAIN 197 234  
 FT DOMAIN 236 272  
 FT DOMAIN 274 312  
 FT DOMAIN 314 350  
 FT DOMAIN 351 389  
 FT DOMAIN 391 429  
 FT DOMAIN 431 467  
 FT DOMAIN 469 505  
 FT DOMAIN 507 543  
 FT DOMAIN 545 580  
 FT DOMAIN 582 618  
 FT DOMAIN 620 655  
 FT DOMAIN 657 693  
 FT DOMAIN 695 730  
 FT DOMAIN 734 770  
 FT DOMAIN 771 808  
 FT DOMAIN 810 847  
 FT DOMAIN 849 885  
 FT DOMAIN 887 922  
 FT SIGNAL 1 39  
 FT CHAIN 40 2321  
 FT CHAIN 1629 2321  
 FT CHAIN 1662 2321  
 FT DOMAIN 40 1643  
 FT TRANSMEM 1644 1664  
 FT DOMAIN 1665 2321  
 FT DOMAIN 40 77  
 FT DOMAIN 78 118  
 FT DOMAIN 119 156  
 FT DOMAIN 158 195  
 FT DOMAIN 197 234  
 FT DOMAIN 236 272  
 FT DOMAIN 274 312  
 FT DOMAIN 314 350  
 FT DOMAIN 351 389  
 FT DOMAIN 391 429  
 FT DOMAIN 431 467  
 FT DOMAIN 469 505  
 FT DOMAIN 507 543  
 FT DOMAIN 545 580  
 FT DOMAIN 582 618  
 FT DOMAIN 620 655  
 FT DOMAIN 657 693  
 FT DOMAIN 695 730  
 FT DOMAIN 734 770  
 FT DOMAIN 771 808  
 FT DOMAIN 810 847  
 FT DOMAIN 849 885  
 FT DOMAIN 887 922  
 FT SIGNAL 1 39  
 FT CHAIN 40 2321  
 FT CHAIN 1629 2321  
 FT CHAIN 1662 2321  
 FT DOMAIN 40 1643  
 FT TRANSMEM 1644 1664  
 FT DOMAIN 1665 2321  
 FT DOMAIN 40 77  
 FT DOMAIN 78 118  
 FT DOMAIN 119 156  
 FT DOMAIN 158 195  
 FT DOMAIN 197 234  
 FT DOMAIN 236 272  
 FT DOMAIN 274 312  
 FT DOMAIN 314 350  
 FT DOMAIN 351 389  
 FT DOMAIN 391 429  
 FT DOMAIN 431 467  
 FT DOMAIN 469 505  
 FT DOMAIN 507 543  
 FT DOMAIN 545 580  
 FT DOMAIN 582 618  
 FT DOMAIN 620 655  
 FT DOMAIN 657 693  
 FT DOMAIN 695 730  
 FT DOMAIN 734 770  
 FT DOMAIN 771 808  
 FT DOMAIN 810 847  
 FT DOMAIN 849 885  
 FT DOMAIN 887 922  
 FT SIGNAL 1 39  
 FT CHAIN 40 2321  
 FT CHAIN 1629 2321  
 FT CHAIN 1662 2321  
 FT DOMAIN 40 1643  
 FT TRANSMEM 1644 1664  
 FT DOMAIN 1665 2321  
 FT DOMAIN 40 77  
 FT DOMAIN 78 118  
 FT DOMAIN 119 156  
 FT DOMAIN 158 195  
 FT DOMAIN 197 234  
 FT DOMAIN 236 272  
 FT DOMAIN 274 312  
 FT DOMAIN 314 350  
 FT DOMAIN 351 389  
 FT DOMAIN 391 429  
 FT DOMAIN 431 467  
 FT DOMAIN 469 505  
 FT DOMAIN 507 543  
 FT DOMAIN 545 580  
 FT DOMAIN 582 618  
 FT DOMAIN 620 655  
 FT DOMAIN 657 693  
 FT DOMAIN 695 730  
 FT DOMAIN 734 770  
 FT DOMAIN 771 808  
 FT DOMAIN 810 847  
 FT DOMAIN 849 885  
 FT DOMAIN 887 922  
 FT SIGNAL 1 39  
 FT CHAIN 40 2321  
 FT CHAIN 1629 2321  
 FT CHAIN 1662 2321  
 FT DOMAIN 40 1643  
 FT TRANSMEM 1644 1664  
 FT DOMAIN 1665 2321  
 FT DOMAIN 40 77  
 FT DOMAIN 78 118  
 FT DOMAIN 119 156  
 FT DOMAIN 158 195  
 FT DOMAIN 197 234  
 FT DOMAIN 236 272  
 FT DOMAIN 274 312  
 FT DOMAIN 314 350  
 FT DOMAIN 351 389  
 FT DOMAIN 391 429  
 FT DOMAIN 431 467  
 FT DOMAIN 469 505  
 FT DOMAIN 507 543  
 FT DOMAIN 545 580  
 FT DOMAIN 582 618  
 FT DOMAIN 620 655  
 FT DOMAIN 657 693  
 FT DOMAIN 695 730  
 FT DOMAIN 734 770  
 FT DOMAIN 771 808  
 FT DOMAIN 810 847  
 FT DOMAIN 849 885  
 FT DOMAIN 887 922  
 FT SIGNAL 1 39  
 FT CHAIN 40 2321  
 FT CHAIN 1629 2321  
 FT CHAIN 1662 2321  
 FT DOMAIN 40 1643  
 FT TRANSMEM 1644 1664  
 FT DOMAIN 1665 2321  
 FT DOMAIN 40 77  
 FT DOMAIN 78 118  
 FT DOMAIN 119 156  
 FT DOMAIN 158 195  
 FT DOMAIN 197 234  
 FT DOMAIN 236 272  
 FT DOMAIN 274 312  
 FT DOMAIN 314 350  
 FT DOMAIN 351 389  
 FT DOMAIN 391 429  
 FT DOMAIN 431 467  
 FT DOMAIN 469 505  
 FT DOMAIN 507 543  
 FT DOMAIN 545 580  
 FT DOMAIN 582 618  
 FT DOMAIN 620 655  
 FT DOMAIN 657 693  
 FT DOMAIN 695 730  
 FT DOMAIN 734 770  
 FT DOMAIN 771 808  
 FT DOMAIN 810 847  
 FT DOMAIN 849 885  
 FT DOMAIN 887 922  
 FT SIGNAL 1 39  
 FT CHAIN 40 2321  
 FT CHAIN 1629 2321  
 FT CHAIN 1662 2321  
 FT DOMAIN 40 1643  
 FT TRANSMEM 1644 1664  
 FT DOMAIN 1665 2321  
 FT DOMAIN 40 77  
 FT DOMAIN 78 118  
 FT DOMAIN 119 156  
 FT DOMAIN 158 195  
 FT DOMAIN 197 234  
 FT DOMAIN 236 272  
 FT DOMAIN 274 312  
 FT DOMAIN 314 350  
 FT DOMAIN 351 389  
 FT DOMAIN 391 429  
 FT DOMAIN 431 467  
 FT DOMAIN 469 505  
 FT DOMAIN 507 543  
 FT DOMAIN 545 580  
 FT DOMAIN 582 618  
 FT DOMAIN 620 655  
 FT DOMAIN 657 693  
 FT DOMAIN 695 730  
 FT DOMAIN 734 770  
 FT DOMAIN 771 808  
 FT DOMAIN 810 847  
 FT DOMAIN 849 885  
 FT DOMAIN 887 922  
 FT SIGNAL 1 39  
 FT CHAIN 40 2321  
 FT CHAIN 1629 2321  
 FT CHAIN 1662 2321  
 FT DOMAIN 40 1643  
 FT TRANSMEM 1644 1664  
 FT DOMAIN 1665 2321  
 FT DOMAIN 40 77  
 FT DOMAIN 78 118  
 FT DOMAIN 119 156  
 FT DOMAIN 158 195  
 FT DOMAIN 197 234  
 FT DOMAIN 236 272  
 FT DOMAIN 274 312  
 FT DOMAIN 314 350  
 FT DOMAIN 351 389  
 FT DOMAIN 391 429  
 FT DOMAIN 431 467  
 FT DOMAIN 469 505  
 FT DOMAIN 507 543  
 FT DOMAIN 545 580  
 FT DOMAIN 582 618  
 FT DOMAIN 620 655  
 FT DOMAIN 657 693  
 FT DOMAIN 695 730  
 FT DOMAIN 734 770  
 FT DOMAIN 771 808  
 FT DOMAIN 810 847  
 FT DOMAIN 849 885  
 FT DOMAIN 887 922  
 FT SIGNAL 1 39  
 FT CHAIN 40 2321  
 FT CHAIN 1629 2321  
 FT CHAIN 1662 2321  
 FT DOMAIN 40 1643  
 FT TRANSMEM 1644 1664  
 FT DOMAIN 1665 2321  
 FT DOMAIN 40 77  
 FT DOMAIN 78 118  
 FT DOMAIN 119 156  
 FT DOMAIN 158 195  
 FT DOMAIN 197 234  
 FT DOMAIN 236 272  
 FT DOMAIN 274 312  
 FT DOMAIN 314 350  
 FT DOMAIN 351 389  
 FT DOMAIN 391 429  
 FT DOMAIN 431 467  
 FT DOMAIN 469 505  
 FT DOMAIN 507 543  
 FT DOMAIN 545 580  
 FT DOMAIN 582 618  
 FT DOMAIN 620 655  
 FT DOMAIN 657 693  
 FT DOMAIN 695 730  
 FT DOMAIN 734 770  
 FT DOMAIN 771 808  
 FT DOMAIN 810 847  
 FT DOMAIN 849 885  
 FT DOMAIN 887 922  
 FT SIGNAL 1 39  
 FT CHAIN 40 2321  
 FT CHAIN 1629 2321  
 FT CHAIN 1662 2321  
 FT DOMAIN 40 1643  
 FT TRANSMEM 1644 1664  
 FT DOMAIN 1665 2321  
 FT DOMAIN 40 77  
 FT DOMAIN 78 118  
 FT DOMAIN 119 156  
 FT DOMAIN 158 195  
 FT DOMAIN 197 234  
 FT DOMAIN 236 272  
 FT DOMAIN 274 312  
 FT DOMAIN 314 350  
 FT DOMAIN 351 389  
 FT DOMAIN 391 429  
 FT DOMAIN 431 467  
 FT DOMAIN 469 505  
 FT DOMAIN 507 543  
 FT DOMAIN 545 580  
 FT DOMAIN 582 618  
 FT DOMAIN 620 655  
 FT DOMAIN 657 693  
 FT DOMAIN 695 730  
 FT DOMAIN 734 770  
 FT DOMAIN 771 808  
 FT DOMAIN 810 847  
 FT DOMAIN 849 885  
 FT DOMAIN 887 922  
 FT SIGNAL 1 39  
 FT CHAIN 40 2321  
 FT CHAIN 1629 2321  
 FT CHAIN 1662 2321  
 FT DOMAIN 40 1643  
 FT TRANSMEM 1644 1664  
 FT DOMAIN 1665 2321  
 FT DOMAIN 40 77  
 FT DOMAIN 78 118  
 FT DOMAIN 119 156  
 FT DOMAIN 158 195  
 FT DOMAIN 197 234  
 FT DOMAIN 236 272  
 FT DOMAIN 274 312  
 FT DOMAIN 314 350  
 FT DOMAIN 351 389  
 FT DOMAIN 391 429  
 FT DOMAIN 431 467  
 FT DOMAIN 469 505  
 FT DOMAIN 507 543  
 FT DOMAIN 545 580  
 FT DOMAIN 582 618  
 FT DOMAIN 620 655  
 FT DOMAIN 657 693  
 FT DOMAIN 695 730  
 FT DOMAIN 734 770  
 FT DOMAIN 771 808  
 FT DOMAIN 810 847  
 FT DOMAIN 849 885  
 FT DOMAIN 887 922  
 FT SIGNAL 1 39  
 FT CHAIN 40 2321  
 FT CHAIN 1629 2321  
 FT CHAIN 1662 2321  
 FT DOMAIN 40 1643  
 FT TRANSMEM 1644 1664  
 FT DOMAIN 1665 2321  
 FT DOMAIN 40 77  
 FT DOMAIN 78 118  
 FT DOMAIN 119 156  
 FT DOMAIN 158 195  
 FT DOMAIN 197 234  
 FT DOMAIN 236 272  
 FT DOMAIN 274 312  
 FT DOMAIN 314 350  
 FT DOMAIN 351 389  
 FT DOMAIN 391 429  
 FT DOMAIN 431 467  
 FT DOMAIN 469 505  
 FT DOMAIN 507 543  
 FT DOMAIN 545 580  
 FT DOMAIN 582 618  
 FT DOMAIN 620 655  
 FT DOMAIN 657 693  
 FT DOMAIN 695 730  
 FT DOMAIN 734 770  
 FT DOMAIN 771 808  
 FT DOMAIN 810 847  
 FT DOMAIN 849 885  
 FT DOMAIN 887 922  
 FT SIGNAL 1 39  
 FT CHAIN 40 2321  
 FT CHAIN 1629 2321  
 FT CHAIN 1662 2321  
 FT DOMAIN 40 1643  
 FT TRANSMEM 1644 1664  
 FT DOMAIN 1665 2321  
 FT DOMAIN 40 77  
 FT DOMAIN 78 118  
 FT DOMAIN 119 156  
 FT DOMAIN 158 195  
 FT DOMAIN 197 234  
 FT DOMAIN 236 272  
 FT DOMAIN 274 312  
 FT DOMAIN 314 350  
 FT DOMAIN 351 389  
 FT DOMAIN 391 429  
 FT DOMAIN 431 467  
 FT DOMAIN 469 505  
 FT DOMAIN 507 543  
 FT DOMAIN 545 580  
 FT DOMAIN 582 618  
 FT DOMAIN 620 655  
 FT DOMAIN 657 693  
 FT DOMAIN 695 730  
 FT DOMAIN 734 770  
 FT DOMAIN 771 808  
 FT DOMAIN 810 847  
 FT DOMAIN 849 885  
 FT DOMAIN 887 922  
 FT SIGNAL 1 39  
 FT CHAIN 40 2321  
 FT CHAIN 1629 2321  
 FT CHAIN 1662 2321  
 FT DOMAIN 40 1643  
 FT TRANSMEM 1644 1664  
 FT DOMAIN 1665 2321  
 FT DOMAIN 40 77  
 FT DOMAIN 78 118  
 FT DOMAIN 119 156  
 FT DOMAIN 158 195  
 FT DOMAIN 197 234  
 FT DOMAIN 236 272  
 FT DOMAIN 274 312  
 FT DOMAIN 314 350  
 FT DOMAIN 351 389  
 FT DOMAIN 391 429  
 FT DOMAIN 431 467  
 FT DOMAIN 469 505  
 FT DOMAIN 507 543  
 FT DOMAIN 545 580  
 FT DOMAIN 582 618  
 FT DOMAIN 620 655  
 FT DOMAIN 657 693  
 FT DOMAIN 695 730  
 FT DOMAIN 734 770  
 FT DOMAIN 771 808  
 FT DOMAIN 810 847  
 FT DOMAIN 849 885  
 FT DOMAIN 887 922  
 FT SIGNAL 1 39  
 FT CHAIN 40 2321  
 FT CHAIN 1629 2321  
 FT CHAIN 1662 2321  
 FT DOMAIN 40 1643  
 FT TRANSMEM 1644 1664  
 FT DOMAIN 1665 2321  
 FT DOMAIN 40 77  
 FT DOMAIN 78 118  
 FT DOMAIN 119 156  
 FT DOMAIN 158 195  
 FT DOMAIN 197 234  
 FT DOMAIN 236 272  
 FT DOMAIN 274 312  
 FT DOMAIN 314 350  
 FT DOMAIN 351 389  
 FT DOMAIN 391 429  
 FT DOMAIN 431 467  
 FT DOMAIN 469 505  
 FT DOMAIN 507 543  
 FT DOMAIN 545 580  
 FT DOMAIN 582 618  
 FT DOMAIN 620 655  
 FT DOMAIN 657 693  
 FT DOMAIN 695 730  
 FT DOMAIN 734 770  
 FT DOMAIN 771 808  
 FT DOMAIN 810 847  
 FT DOMAIN 849 885  
 FT DOMAIN 887 922  
 FT SIGNAL 1 39  
 FT CHAIN 40 2321  
 FT CHAIN 1629 2321  
 FT CHAIN 1662 2321  
 FT DOMAIN 40 1643  
 FT TRANSMEM 1644 1664  
 FT DOMAIN 1665 2321  
 FT DOMAIN 40 77  
 FT DOMAIN 78 118  
 FT DOMAIN 119 156  
 FT DOMAIN 158 195  
 FT DOMAIN 197 234  
 FT DOMAIN 236 272  
 FT DOMAIN 274 312  
 FT DOMAIN 314 350  
 FT DOMAIN 351 389  
 FT DOMAIN 391 429  
 FT DOMAIN 431 467  
 FT DOMAIN 469 505  
 FT DOMAIN 507 543

FT DOMAIN 924 960 EGF-LIKE 24.  
FT DOMAIN 962 998 EGF-LIKE 25.  
FT DOMAIN 1000 1034 EGF-LIKE 26.  
FT DOMAIN 1047 1082 EGF-LIKE 27.

## Query Match

Best Local Similarity 34.5%; Score 174.5; DB 1; Length 2321;  
Matches 50; Conservative 14; Mismatches 44; Indels 37; Gaps 11;

OY 56 CDGACGCTTATYRTAYRSPGLAPAPRYAC-CRQWER--TSGLPGACGAICQPPCR 112  
DB 87 CAGGVCVCS-----SVVAGTARFSCRCRGRFGPDCCSLDPDC-----LSSPCA 129  
OY 113 NGSSC-VOP-CR-CRCPAGMRDTCQSDVDEC--SARRGCGPQRQVNTAGSYWCQCM 164  
DB 130 HGARCSTVGPGRPLCSCPEGYQGRSCRDVDECRVGEPCRHGS--TLANTPGSFRCQCP 186  
OY 165 EGHSLADGTLGVKPKGPPRVANP 189  
DB 187 AGYT-----GPLCENPAVP--CAPSP 205

## RESULT 14

NIDO HUMAN

STANDARD; PRT; 1247 AA.

AC P14543; Q14942;  
DT 01-JAN-1990 (Rel. 13, Created)  
DT 01-JAN-1990 (Rel. 13, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Nidogen precursor (Enactin).  
GN NID.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]

## SEQUENCE FROM N.A.

RA MEDLINE=90091745; PubMed=2574658;  
RA Nagayoshi T., Sanborn D., Hickok N.J., Olsen D.R., Fazio M.J.,  
RA Chu M.-L., Knowlton R., Mann K., Deutzmann R., Timpl R., Utico J.;  
RT "Human nidogen: complete amino acid sequence and structural domains  
RT deduced from cDNAs, and evidence for polymorphism of the gene.";  
RL DNA 8:581-594 (1989).  
RN [2]

## SEQUENCE FROM N.A.

RA MEDLINE=96044428; PubMed=7557988;  
RA Zimmermann K., Hoischen S., Hattner M., Nischt R.;  
RT "Genomic sequences and structural organization of the human nidogen  
RT gene (NID)." ;  
RL Genomics 27:245-250 (1995).  
RN [3]

## SEQUENCE OF 667-1247 FROM N.A.

RC TISSUE=Placenta;  
RX MEDLINE=89270475; PubMed=2471408;  
RX Olsen D.R., Nagayoshi T., Fazio M., Mattei M.-G., Passage E., Weil D.,  
RA Timpl R., Chu M.L., Utico J.;  
RT "Human nidogen: cDNA cloning, cellular expression, and mapping of the  
RT gene to chromosome 1q43." ;  
RL Am. J. Hum. Genet. 44:876-885 (1989).  
CC -1- FUNCTION: SULFATED GLYCOPROTEIN WHICH IS WIDELY DISTRIBUTED IN  
CC ALSO BINDS TO COLLAGEN IV. IT PROBABLY HAS A ROLE IN CELL-  
CC EXTRACELLULAR MATRIX INTERACTIONS.  
CC -1- SUBCELLULAR LOCATION: BASEMENT MEMBRANES.  
CC -1- PTM: N- AND O-GLYCOSYLATED.  
CC -1- SIMILARITY: CONTAINS 6 EGF-LIKE DOMAINS.  
CC -1- SIMILARITY: CONTAINS 1 THYROGLOBULIN TYPE-I DOMAIN.  
CC -1- SIMILARITY: CONTAINS 5 LDL-RECEPTOR WYTD DOMAINS.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation-  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC EMBL; M30269; AA559932.1; -  
CC EMBL; X82245; CAAS7709.1; -  
CC EMBL; X84819; CAAS7709.1; JOINED.  
CC EMBL; X84820; CAAS7709.1; JOINED.  
CC EMBL; X84821; CAAS7709.1; JOINED.  
CC EMBL; X84822; CAAS7709.1; JOINED.  
CC EMBL; X84823; CAAS7709.1; JOINED.  
CC EMBL; X84824; CAAS7709.1; JOINED.  
CC EMBL; X84825; CAAS7709.1; JOINED.  
CC EMBL; X84826; CAAS7709.1; JOINED.  
CC EMBL; X84827; CAAS7709.1; JOINED.  
CC EMBL; X84828; CAAS7709.1; JOINED.  
CC EMBL; X84829; CAAS7709.1; JOINED.  
CC EMBL; X84830; CAAS7709.1; JOINED.  
CC EMBL; X84831; CAAS7709.1; JOINED.  
CC EMBL; X84832; CAAS7709.1; JOINED.  
CC EMBL; X84833; CAAS7709.1; JOINED.  
CC EMBL; X84834; CAAS7709.1; JOINED.  
CC EMBL; X84835; CAAS7709.1; JOINED.  
CC EMBL; X84836; CAAS7709.1; JOINED.  
CC EMBL; X84837; CAAS7709.1; JOINED.  
CC EMBL; M27445; AA557261.1; -  
CC PIR; A33322; MMHUND.  
CC HSSP; P35555; IEMN.  
CC GENE; HGNC:7821; NID.  
CC MIM; 131390;  
CC InterPro; IPR000152; Asx\_hydroxyl.  
CC InterPro; IPR000561; EGF-like.  
CC InterPro; IPR001881; EGF Ca.  
CC InterPro; IPR000033; Ldl\_receptor\_rep.  
CC InterPro; IPR003866; Nidogen\_ext.  
CC Pfam; PF00008; EGF\_6.  
CC Pfam; PF00058; Ldl\_recept\_b; 3.  
CC Pfam; PF00066; thyroglobulin\_1; 1.  
CC SMART; SM00179; EGF\_Ca; 2.  
CC SMART; SM00001; EGF\_like; 4.  
CC SMART; SM00135; LV; 5.  
CC SMART; SM00539; NIDO; 1.  
CC SMART; SM00211; TY; 1.  
CC PROSITE; PS00010; ASX\_HYDROXYL; 3.  
CC PROSITE; PS00484; THYROGLOBULIN\_1; 1.  
CC PROSITE; PS00022; EGF\_1; 1.  
CC PROSITE; PS01186; EGF\_2; 5.  
CC PROSITE; PS01187; EGF\_Ca; 2.  
CC K1 Basal membrane; Extracellular matrix; Glycoprotein; Sulfation;  
CC K1 Signal; Calcium-binding; Repeat; EGF-like domain; Cell adhesion.  
CC K1 SIGNAL 1 28  
CC CHAIN 29 1247  
CC DOMAIN 29 669  
CC DOMAIN 670 917  
CC DOMAIN 918 1247  
CC DOMAIN 386 426  
CC DOMAIN 668 709  
CC DOMAIN 710 751  
CC DOMAIN 758 801  
CC DOMAIN 802 840  
CC DOMAIN 872 919  
CC DOMAIN 969 1030  
CC DOMAIN 1032 1073  
CC DOMAIN 1075 1118  
CC DOMAIN 1124 1163  
CC DOMAIN 1208 1244  
CC MOD\_RES 289 289  
CC MOD\_RES 296 296  
CC DISULFID 672 685  
CC DISULFID 679 695  
CC DISULFID 697 708  
CC DISULFID 714 727  
CC NIDOGN.  
CC I (LARGER GLOBULAR DOMAIN).  
CC II (CYSTEINE-RICH).  
CC III (SMALLER GLOBULAR DOMAIN).  
CC EGF-LIKE 1.  
CC EGF-LIKE 2.  
CC EGF-LIKE 3.  
CC EGF-LIKE 4.  
CC EGF-LIKE 5.  
CC EGF-LIKE 6.  
CC THYROGLOBULIN TYPE I.  
CC LDL-RECEPTOR WYTD MOTIF 1.  
CC LDL-RECEPTOR WYTD MOTIF 2.  
CC LDL-RECEPTOR WYTD MOTIF 3.  
CC LDL-RECEPTOR WYTD MOTIF 4.  
CC SULFATION (POTENTIAL).  
CC SULFATION (POTENTIAL).  
CC BY SIMILARITY.  
CC BY SIMILARITY.  
CC BY SIMILARITY.  
CC BY SIMILARITY.



Tue Dec 17 14:03:52 2002

FT DISULFID 721 736 BY SIMILARITY.  
 FT DISULFID 738 750 BY SIMILARITY.  
 FT DISULFID 762 777 BY SIMILARITY.  
 FT DISULFID 769 787 BY SIMILARITY.  
 FT DISULFID 789 800 BY SIMILARITY.  
 FT DISULFID 806 817 BY SIMILARITY.  
 FT DISULFID 811 826 BY SIMILARITY.  
 FT DISULFID 828 839 BY SIMILARITY.  
 FT DISULFID 1212 1223 BY SIMILARITY.  
 FT DISULFID 1219 1232 BY SIMILARITY.  
 FT DISULFID 1234 1243 BY SIMILARITY.  
 FT SITE 702 704 CELL ATTACHMENT SITE.  
 FT CARBOHYD 1137 1137 N-LINKED (GLCNAC.) (POTENTIAL).  
 FT CONFLICT 33 34 EL -> SS (IN REF. 2).  
 FT CONFLICT 37 42 FGPGQG -> SAPDR (IN REF. 2).  
 FT CONFLICT 1115 1115 H -> T (IN REF. 3).  
 FT SEQUENCE 1247 AA; 136488 MW; 4681BSB3CEC1575B CRC64;  
 SQ  
 Query Match 11.5%; Score 173.5; DB 1; Length 1247;  
 Best Local Similarity 25.8%; Pred. No. 6e-06;  
 Matches 80; Conservative 23; Mismatches 98; Indels 109; Gaps 18;  
 QY 20 TEHAYRGRV-----CAVRHG-----DPVSESVQVYQVFLTCGHRACSTYR 66  
 Db 681 TNAACRPGPTQTCTCSIGFRGDRCTCYDIDECSE-----QF--SVCSHTICNNH- 730  
 QY 67 TIVTAYRRSPGLAPRVPACPGWKRTSGLPGACGAACQPP-----CRNG----- 114  
 Db 731 -----PGTFRCEVEGQFSD--EGTCVAVVDORPINYCETGLHNCIDIPQR 774  
 QY 115 GSCVQPG-----RCPCAGWGD--TCQSDVDECSARGCPCORCVNTAGSYWCOCWGHGS 168  
 QY 775 AQCIYTGSSYTCSCLFSGFSDGACQ--DVDECQPSRCHDPACFYNTPGSTCQCKPGY- 832  
 Db 169 LSADGTLCPV-----KGGPRVAPNPTG----- 191  
 QY 833 -QGDFRCVPGVEVETKQCHERHILGAAGATDPQPIPPGLFVPCDAGHYAFTQCHG 891  
 QY 192 -----VDSAMKEVQRLQSRVLLBEKQLVLAPH--SLASQALEHGLPDGSLVHS 243  
 Db 892 STGYCWCVDORCL-EVEGTRTPGWTBCLSTVAPPHOGPAVPTAVIPLP-PGTHLL-- 947  
 QY 244 FOQLGRIDSL 253  
 Db 948 FAQTGKIERYL 957  
 RESULT 15  
 NTC1\_MOUSE STANDARD; PRT; 2531 AA.  
 ID NTC1\_MOUSE  
 AC Q01705; Q9QW58; Q99JC2; Q06007; Q61905; Q9R0X7;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Neurogenic locus notch homolog protein 1 precursor (Notch 1) (Notch A) (mt14) (p300).  
 OS NOTCH1 OR NOTCH  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN SEQUENCE FROM N.A. (ISOFORM 1).  
 RC TISSUE=Embryo;  
 RX MEDLINE=93194170; PubMed=8449489;  
 RA Franco del Amo P., Gendron-Maguire M., Swiatek P.J., Jenkins N.A., Copeland N.G., Gridley T.;  
 RA "Cloning, analysis, and chromosomal localization of Notch-1, a mouse homolog of Drosophila Notch.";  
 RT Genomics 15:259-264 (1993).  
 RL [2]  
 RN SEQUENCE OF 731-1899 FROM N.A. (ISOFORM 2), AND DEVELOPMENTAL STAGE.  
 RC STRAIN=CD-1; TISSUE=Embryo;

RX MEDLINE=93050801; PubMed=1426644;  
 RA Reaume A.G., Conlon R.A., Ziringibl R., Yamaguchi T.P., Rossant J.;  
 RA "Expression analysis of a Notch homologue in the mouse embryo.";  
 RL Dev. Biol. 154:377-387 (1992).  
 RN [3]  
 RP SEQUENCE OF 1551-1647 FROM N.A. (ISOFORM 1), AND DEVELOPMENTAL STAGE.  
 RC TISSUE=Embryo;  
 RX MEDLINE=93048835; PubMed=1425352;  
 RA Franco del Amo P., Smith D.E., Swiatek P.J., Gendron-Maguire M., Greenspan R.J., McMahon A.P., Gridley T.;  
 RA "Expression pattern of Notch, a mouse homolog of Drosophila Notch, suggests an important role in early postimplantation mouse development.";  
 RT Development 115:737-744 (1992).  
 RL [4]  
 RN SEQUENCE OF 1161-1547 FROM N.A.  
 RC STRAIN=CS7BL/6 X CBA; TISSUE=Embryo;  
 RX MEDLINE=93170563; PubMed=8440332;  
 RA Lardelli M., Lendahl U.; mouse Notch homologues coexpressed in a "Notch A and Notch B-two wide variety of tissues.";  
 RT Exp. Cell Res. 204:364-372 (1993).  
 RL [5]  
 RN SEQUENCE OF 1659-1673 FROM N.A.  
 RP MEDLINE=99364499; PubMed=10437788;  
 RX Lee J.S., Ishimoto A., Yanagawa S.I.;  
 RA "Murine leukemia provirus-mediated activation of the Notch1 gene leads to induction of HES-1 in a mouse T lymphoma cell line, DL-3.";  
 RT FEBS Lett. 455:276-280 (1999).  
 RL [6]  
 RN SEQUENCE OF 1950-2201 FROM N.A.  
 RP MEDLINE=98029496; PubMed=9384671;  
 RX Messerle M., Folio M., Nehls M., Eggert H., Boehm T.;  
 RA "Dynamic changes in gene expression during in vitro differentiation of mouse embryonic stem cells.";  
 RT Cytokines Cell. Mol. Ther. 1:139-143 (1995).  
 RL [7]  
 RN SEQUENCE OF 1655-1659, CLEAVAGE BY FURIN-LIKE CONVERTASE, AND MUTAGENESIS OF 1651-ARG-GLN-ARG-ARG-1654.  
 RP MEDLINE=98318619; PubMed=9653148;  
 RX Logeat F., Bessia C., Brou C., LeBail O., Jarriault S., Seidah N.G., Israel A.;  
 RA "The Notch1 receptor is cleaved constitutively by a furin-like convertase.";  
 RT Proc. Natl. Acad. Sci. U.S.A. 95:8108-8112 (1998).  
 RN [8]  
 RP PARTIAL SEQUENCE, AND POST-TRANSLATIONAL PROCESSING.  
 RX Saxena M.T., Schroeter E.H., Mumm J.S., Kopan R.;  
 RA "Murine notch homologs (N1-4) undergo presenilin-dependent proteolysis.";  
 RT J. Biol. Chem. 276:40268-40273 (2001).  
 RL [9]  
 RN POST-TRANSLATIONAL PROCESSING.  
 RP MEDLINE=21374376; PubMed=11459941;  
 RX Mizutani T., Taniuchi Y., Aoki T., Hashimoto N., Honjo T.;  
 RA "Conservation of the biochemical mechanisms of signal transduction among mammalian Notch family members.";  
 RT Proc. Natl. Acad. Sci. U.S.A. 98:9026-9031 (2001).  
 CC -1- FUNCTION: Functions as a receptor for membrane-bound ligands Jagged1, Jagged2 and Delta to regulate cell-fate determination. Upon ligand activation through the released notch intracellular domain (NICD) it forms a transcriptional activator of split locus. RBP-J kappa and activation of genes of the enhancer of proliferation and affects the implementation of differentiation, proliferation and apoptotic programs (By similarity). May play an essential role in postimplantation development, probably in some aspect of cell specification and/or differentiation. May be involved in mesoderm maturation of both CD4+ and CD8+ cells in the thymus.  
 CC -1- SUBUNIT: Heterodimer of a C-terminal fragment N(TM) and a N-terminal fragment N(BC) which are probably linked by disulfide bonds.

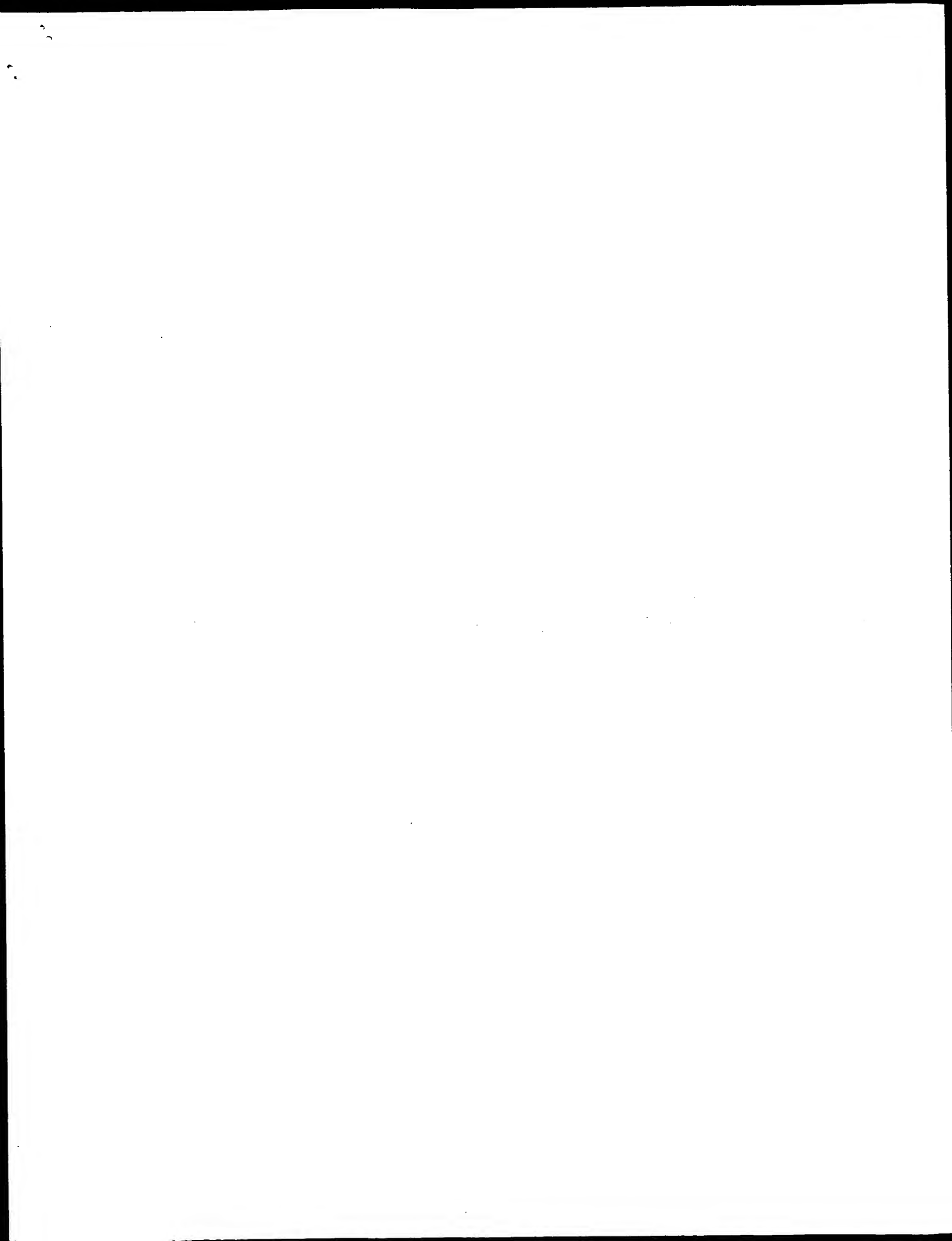


CC -1- SUBCELLULAR LOCATION: Type I membrane protein. Following  
 CC proteolytical processing NICD is translocated to the nucleus.  
 CC -1- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; may be  
 CC produced by alternative splicing.  
 CC -1- TISSUE SPECIFICITY: Highly expressed in the brain, lung and  
 CC thymus. Expressed at lower levels in the spleen, bone-marrow,  
 CC spinal cord, eyes, mammary gland, liver, intestine, skeletal  
 CC muscle, kidney and heart.  
 CC -1- DEVELOPMENTAL STAGE: First detected in the mesoderm at 7.5 d.p.c.  
 CC By 8.5 d.p.c. highly expressed in presomitic mesoderm, mesenchyme  
 CC and endothelial cells, while much lower levels are seen in the  
 CC in the neuroepithelium. Between 9.5-10.5 d.p.c. expressed at high levels  
 CC in the neuroepithelium. At 13.5 d.p.c. expressed in the surface  
 CC ectoderm, eye and developing whisker follicles.  
 CC -1- PTM: Synthesized in the endoplasmic reticulum as an inactive form  
 CC which is proteolytically cleaved by a furin-like convertase in the  
 CC trans-Golgi network before it reaches the plasma membrane to yield  
 CC an active, ligand-accessible form. Cleavage results in a C-  
 CC terminal fragment N(TM) and a N-terminal fragment N(BC). Following  
 CC ligand binding, it is cleaved by TNF-alpha converting enzyme  
 CC (TACE) to yield a membrane-associated intermediate fragment called  
 CC notch extracellular truncation (NEXT). This fragment is then  
 CC cleaved by presenilin dependent gamma-secretase to release a  
 CC notch-derived peptide containing the intracellular domain (NICD)  
 CC from the membrane.  
 CC -1- PTM: Phosphorylated.  
 CC -1- SIMILARITY: BELONGS TO THE NOTCH FAMILY.  
 CC -1- SIMILARITY: CONTAINS 36 EGF-LIKE DOMAINS.  
 CC -1- SIMILARITY: CONTAINS 3 LIN/NOTCH REPEATS.  
 CC -1- SIMILARITY: CONTAINS 5 ANK REPEATS.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use. By non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.ebi.ac.uk/announcements/>  
 CC or send an email to [license@ebi.ac.uk](mailto:license@ebi.ac.uk)).  
 CC -----  
 DR EMBL; Z11886; CAAT7941.1; -;  
 DR EMBL; L02613; AAK14898.1; -;  
 DR EMBL; X68278; CAA48339.1; -;  
 DR EMBL; AJ238029; CAA40733.1; -;  
 DR EMBL; X82562; CAA57909.1; -;  
 DR HSSP; P00740; IEDM.  
 DR MGD; MGI:97363; Notch1.  
 DR InterPro; IPR002110; ANK.  
 DR InterPro; IPR000152; Asx\_hydroxyl.  
 DR InterPro; IPR000561; EGF-like.  
 DR InterPro; IPR000742; EGF\_2.  
 DR InterPro; IPR001881; EGF\_Ca.  
 DR InterPro; IPR001438; EGF\_11.  
 DR InterPro; IPR000800; Notch.  
 DR Pfam; PF00008; EGF; 35.  
 DR Pfam; PF00023; ank; 7.  
 DR Pfam; PF00066; notch; 3.  
 DR PRINTS; PR00010; EGFBLD.  
 DR PRINTS; PR01452; NOTCH.  
 DR SMART; SM00248; ANK; 3.  
 DR SMART; SM00179; EGF\_Ca; 23.  
 DR SMART; SM00001; EGF-like; 11.  
 DR SMART; SM00004; NL; 2.  
 DR PROSITE; PS50088; ANK\_REPEAT; 2.  
 DR PROSITE; PS50297; ANK\_REPEAT\_REGION; 1.  
 DR PROSITE; PS00010; ASX\_HYDROXYL; 22.  
 DR PROSITE; PS00022; EGF\_1; 34.  
 DR PROSITE; PS01186; EGF\_2; 27.  
 DR PROSITE; PS01187; EGF\_Ca; 21.  
 DR Receptor; Transcription regulation; Activator; Differentiation;  
 KM Developmental protein; Repeat; ANK repeat; EGF-like domain;  
 KM Transmembrane; Glycoprotein; Signal; Phosphorylation;  
 KM Alternative splicing.  
 FT SIGNAL 1  
 FT 18 POTENTIAL.

FT	CHAIN	19	2531	NEUROGENIC LOCUS NOTCH HOMOLOG PROTEIN 1.
FT	CHAIN	1711	2531	NORCH EXTRACELLULAR TRUNCATION.
FT	CHAIN	1744	2531	NORCH INTRACELLULAR DOMAIN.
FT	DOMAIN	15	1725	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	1726	1746	POTENTIAL.
FT	DOMAIN	1747	2531	CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	20	58	EGF-LIKE 1.
FT	DOMAIN	59	99	EGF-LIKE 2.
FT	DOMAIN	102	139	EGF-LIKE 3.
FT	DOMAIN	140	176	EGF-LIKE 4.
FT	DOMAIN	178	216	EGF-LIKE 5.
FT	DOMAIN	218	255	EGF-LIKE 6.
FT	DOMAIN	257	293	EGF-LIKE 7.
FT	DOMAIN	295	333	EGF-LIKE 8.
FT	DOMAIN	335	371	EGF-LIKE 9.
FT	DOMAIN	372	410	EGF-LIKE 10.
FT	DOMAIN	412	450	EGF-LIKE 11.
FT	DOMAIN	452	488	EGF-LIKE 12.
FT	DOMAIN	490	526	EGF-LIKE 13.
FT	DOMAIN	528	564	EGF-LIKE 14.
FT	DOMAIN	566	601	EGF-LIKE 15.
FT	DOMAIN	603	639	EGF-LIKE 16.
FT	DOMAIN	641	676	EGF-LIKE 17.
FT	DOMAIN	678	714	EGF-LIKE 18.
FT	DOMAIN	716	751	EGF-LIKE 19.
FT	DOMAIN	753	789	EGF-LIKE 20.
FT	DOMAIN	791	827	EGF-LIKE 21.
FT	DOMAIN	829	867	EGF-LIKE 22.
FT	DOMAIN	869	905	EGF-LIKE 23.
FT	DOMAIN	907	943	EGF-LIKE 24.

Query Match 11.4%; Score 172; DB 1; Length 2531;  
 Best Local Similarity 34.5%; Pred. No. 1.6e-05;  
 Matches 41; Conservative 5; Mismatches 37; Indels 36; Gaps 5;  
 DB 129 CSPGMSGKS-----CQADPCASNPANGGCULFEBSYICRCRPGHGRCPD 178  
 QY 88 CCGWRTSGLPACGAAICP-----PCRNQSGCV---OPGRCPAGRGDPQSD 137  
 QY 138 VDECSARRGCGCP--RCVUTAGSYNQCGEGR-----SIADGTLCPVK 180  
 DB 179 VNECSNPGLCRHGHCHNEISYRCACCATHTGPHCELPVPCSPSPQNGATCRPTG 217

Search completed: December 17, 2002, 10:01:58  
 Job time : 10.8065 secs



GenCore version 5.1.3  
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on:

December 17, 2002, 09:58:37 ; Search time 28.4915 Seconds  
(without alignments)  
1974.306 Million cell updates/sec

Title:  
US-09-852-472-2

Sequence:

1 MRGSEVLMMLLVAVGCT.....SEQISFLERQLGSCSKDKS 273

Scoring table:

Gapop 10.0 , Gapext 0.5

Searched:

671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters:

671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

LifeTag first 45 summaries

SPRMBL 21  
1: sp\_archaea:  
2: sp\_bacteria:  
3: sp\_fungi:  
4: sp\_human:  
5: sp\_invertebrate:  
6: sp\_mammal:  
7: sp\_mhc:  
8: sp\_organelle:  
9: sp\_phage:  
10: sp\_plant:  
11: sp\_protist:  
12: sp\_virus:  
13: sp\_vertebrate:  
14: sp\_unclassified:  
15: sp\_virus:  
16: sp\_bacteriophage:  
17: sp\_archaea:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1505	100.0	273	4 Q9UHF1	Q9UHF1 homo sapien
2	1504	99.9	273	4 Q9E6G0	Q9E6G0 homo sapien
3	1181	78.5	278	11 Q9GXT5	Q9GXT5 mus musculu
4	1104.5	73.4	265	11 Q9DCPS	Q9DCPS mus musculu
5	728.5	48.4	190	11 Q9JXW3	Q9JXW3 mus musculu
6	434.5	28.9	293	11 Q35447	Q35447 mus musculu
7	422.5	28.1	293	4 Q99944	Q99944 mus musculu
8	276.5	18.4	509	5 Q9VZD0	Q9VZD0 mus musculu
9	276.5	18.4	512	5 Q9SR01	Q9SR01 mus musculu
10	257	17.1	1574	11 Q88281	Q88281 mus musculu
11	253.5	16.8	558	4 Q9UHF6	Q9UHF6 mus sapien
12	252.5	16.8	553	4 Q9NZL7	Q9NZL7 mus sapien
13	252.5	16.8	554	4 Q9NY67	Q9NY67 mus sapien
14	246.5	16.4	550	11 Q9JZS5	Q9JZS5 mus musculu
15	223	14.8	561	11 Q9IV88	Q9IV88 mus musculu
16	219	14.6	1664	5 Q9TVQ2	Q9TVQ2 caenorhabdi

17	218.5	14.5	578	11 Q91ZD3	Q91ZD3 mus musculu
18	217.5	14.5	528	11 Q9CXD8	Q9CXD8 mus musculu
19	197.5	13.1	592	11 Q91XLS	Q91XLS mus musculu
20	197	13.1	747	11 Q8VHF4	Q8VHF4 mus musculu
21	197	13.1	1034	11 Q8VHL7	Q8VHL7 mus musculu
22	195	13.0	1034	11 Q8VHL7	Q8VHL7 mus musculu
23	193	12.8	609	11 Q923T5	Q923T5 mus musculu
24	189	12.6	673	4 Q14393	Q14393 mus musculu
25	184	12.2	678	11 Q61592	Q61592 mus musculu
26	184	12.2	674	11 Q99K57	Q99K57 mus musculu
27	183.5	12.2	2906	11 Q9WUH9	Q9WUH9 mus musculu
28	182.5	12.1	648	5 Q9NKD7	Q9NKD7 mus musculu
29	182.5	12.1	701	5 Q9VJT4	Q9VJT4 mus musculu
30	182.5	12.1	816	11 Q8R417	Q8R417 mus musculu
31	182	12.1	1764	11 Q35806	Q35806 mus musculu
32	182	12.1	2809	4 Q960P8	Q960P8 mus musculu
33	181.5	12.1	815	4 Q960S2	Q960S2 mus musculu
34	179	11.9	418	4 Q8TF19	Q8TF19 mus sapien
35	178.5	11.9	4555	11 Q8R508	Q8R508 mus sapien
36	178	11.8	674	11 Q63772	Q63772 mus musculu
37	177.5	11.8	3138	5 Q9VTP0	Q9VTP0 mus musculu
38	177	11.8	4215	5 Q9W332	Q9W332 mus musculu
39	176	11.7	1511	4 Q75412	Q75412 mus sapien
40	175	11.6	1587	4 Q00508	Q00508 mus sapien
41	174.5	11.6	1095	11 Q60784	Q60784 mus musculu
42	174.5	11.6	3857	11 Q88840	Q88840 mus musculu
43	173.5	11.5	1833	11 Q08999	Q08999 mus musculu
44	173.5	11.5	2872	11 Q9WUH8	Q9WUH8 mus musculu
45	172	11.4	1212	13 Q42347	Q42347 gallus gall

## ALIGNMENTS

## RESULT 1

Q9UHF1 PRELIMINARY; PRT; 273 AA.

AC Q9UHF1; 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DE NOTCH4-like protein (Hypothetical 29.6 kDa protein).  
GN ZNEU1 OR DKFZP586I2317.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
OX NCBI\_TaxID=9606;  
RN 1  
RP SEQUENCE FROM N.A.  
RA Sheppard P., Jelinek L., Whitmore T., Blumberg H., Lehnert J.,  
RC Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.  
RN 12  
RP SEQUENCE FROM N.A.  
RA Koehrer K., Beyer A., Mewes H.W., Gassenhuber J., Wiemann S.,  
RC Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF161111; AA01429.1; -  
DR EMBL; AL512735; CAC21666.1; -  
DR HSSP; P08709; IFAK.  
DR InterPro; IPR000152; Asx\_hydroxyl.  
DR InterPro; IPR000561; EGF-like.  
DR Pfam; PF00081; EGF\_Ca.  
DR SMART; SM00179; EGF\_Ca; 1.  
DR SMART; SM00010; ASX\_HYDROXYL; 1.  
DR PROSITE; PS00022; EGF\_1; UNKNOWN\_1.  
DR PROSITE; PS01186; EGF\_2; UNKNOWN\_1.  
DR PROSITE; PS01187; EGF\_Ca; 1.  
KW Calcium-binding; EGF-like domain; Glycoprotein; Hydroxylation; Repeat.  
SQ SEQUENCE 273 AA; 29617 MW; 5740BB845BDA988 CRC64;

Tue Dec 17 14:03:52 2002

Query Match 100.0%; Score 1505; DB 4; Length 273;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-130; Indels 0; Gaps 0;  
 Matches 273; Conservative 0; Mismatches 0;

QY 1 MRGSEVLLMVLAVGGTEHAYRPRGRRVCAVRAHGDVPSSEFVQRYQFLLTTCGHR 60  
 DB 1 MRGSEVLLMVLAVGGTEHAYRPRGRRVCAVRAHGDVPSSEFVQRYQFLLTTCGHR 60

QY 61 ACSTYRTIYRTAYRRSPGLAPAPRYACCPGKRTSGLPGACGAAICOPPCRNNGSCVQ 120  
 DB 61 ACSTYRTIYRTAYRRSPGLAPAPRYACCPGKRTSGLPGACGAAICOPPCRNNGSCVQ 120

QY 121 GRCPAGWGTDCQSDVDECSARRGCPQRCVNTAGSYWCQWEGHSLADGTLCPVK 180  
 DB 121 GRCPAGWGTDCQSDVDECSARRGCPQRCVNTAGSYWCQWEGHSLADGTLCPVK 180

QY 181 GPPRVAPNPTGVDSAMKEEVQRLQSRVLDLLEKQLVLAFLHSLASQALEHGLPDPGSL 240  
 DB 181 GPPRVAPNPTGVDSAMKEEVQRLQSRVLDLLEKQLVLAFLHSLASQALEHGLPDPGSL 240

QY 241 VHSFQOLGRIDSLSQISFLEEQSGSCCKDS 273  
 DB 241 VHSFQOLGRIDSLSQISFLEEQSGSCCKDS 273

RESULT 2  
 Q96EG0 PRELIMINARY; PRT; 273 AA.

AC Q96EG0; (T-EMBLrel. 19, Created)  
 DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)  
 DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)  
 DT 01-MAR-2002 (T-EMBLrel. 20, Last annotation update)  
 DE Similar to NEU1 protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OC NCBI\_TaxID=9606;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RC TISSUE=OVARY;  
 RA Strausberg R.;  
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC012377; AAH12377.1; --  
 DR InterPro; IPR000152; Asx hydroxyl.  
 DR InterPro; IPR000561; EGF-like.  
 DR InterPro; IPR001881; EGF\_Ca.  
 DR Pfam; PF00008; EGF; 2.  
 DR PROSITE; PS00010; ASX HYDROXYL; UNKNOWN\_1.  
 DR PROSITE; PS00022; EGF\_1; UNKNOWN\_1.  
 DR PROSITE; PS01186; EGF\_2; UNKNOWN\_1.  
 DR PROSITE; PS01187; EGF\_Ca; UNKNOWN\_1.  
 DR SEQUENCE 273 AA; 5AD0A4845ED5B688 CRC64;

Query Match 99.9%; Score 1504; DB 4; Length 273;  
 Best Local Similarity 99.6%; Pred. No. 1.4e-130; Indels 0; Gaps 0;  
 Matches 272; Conservative 1; Mismatches 0;

QY 1 MRGSEVLLMVLAVGGTEHAYRPRGRRVCAVRAHGDVPSSEFVQRYQFLLTTCGHR 60  
 DB 1 MRGSEVLLMVLAVGGTEHAYRPRGRRVCAVRAHGDVPSSEFVQRYQFLLTTCGHR 60

QY 61 ACSTYRTIYRTAYRRSPGLAPAPRYACCPGKRTSGLPGACGAAICOPPCRNNGSCVQ 120  
 DB 61 ACSTYRTIYRTAYRRSPGLAPAPRYACCPGKRTSGLPGACGAAICOPPCRNNGSCVQ 120

QY 121 GRCPAGWGTDCQSDVDECSARRGCPQRCVNTAGSYWCQWEGHSLADGTLCPVK 180  
 DB 121 GRCPAGWGTDCQSDVDECSARRGCPQRCVNTAGSYWCQWEGHSLADGTLCPVK 180

QY 181 GPPRVAPNPTGVDSAMKEEVQRLQSRVLDLLEKQLVLAFLHSLASQALEHGLPDPGSL 240  
 DB 181 GPPRVAPNPTGVDSAMKEEVQRLQSRVLDLLEKQLVLAFLHSLASQALEHGLPDPGSL 240

QY 241 VHSFQOLGRIDSLSQISFLEEQSGSCCKDS 273  
 DB 241 VHSFQOLGRIDSLSQISFLEEQSGSCCKDS 273

RESULT 3  
 Q9QXT5 PRELIMINARY; PRT; 278 AA.

ID Q9QXT5  
 AC Q9QXT5; (T-EMBLrel. 13, Created)  
 DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)  
 DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)  
 DT 01-JUN-2002 (T-EMBLrel. 21, Last annotation update)  
 DE NOTCH4-like protein (Vascular endothelial zinc finger 1).  
 GN VEF1 OR ZNEU1.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OC NCBI\_TaxID=10090;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RA Sheppard P.; Jelinek L.; Whitmore T.; Blumberg H.; Lehner J.;  
 RA O'Hara P.;  
 RT "Mus musculus homolog of HLA class III region containing NOTCH4  
 gene.";  
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RN SEQUENCE FROM N.A.  
 RA Presnell S.; Gilbert T.; Whitmore T.; Foster D.; Hart C.; Lehner J.;  
 RA Martinez T.; Hoffman R.; O'Hara P.;  
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RN SEQUENCE FROM N.A.  
 RC TISSUE=LIVER;  
 RA Strausberg R.;  
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF184973; AA01322.1; --  
 DR EMBL; BC024610; AAH24610.1; --  
 DR HGSP; P00740; 1EDW.  
 DR MGD; MGI:1313291; Vezf1.  
 DR InterPro; IPR000561; EGF-like.  
 DR InterPro; IPR001881; EGF\_Ca.  
 DR Pfam; PF00008; EGF; 2.  
 DR SMART; SM00181; EGF; 1.  
 DR SMART; SM00001; EGF-like; 1.  
 DR PROSITE; PS00022; EGF\_1; UNKNOWN\_1.  
 DR PROSITE; PS01186; EGF\_2; UNKNOWN\_1.  
 DR PROSITE; PS01187; EGF\_Ca; 1.  
 DR KW Calcium-binding; EGF-Like domain; Glycoprotein; Repeat.  
 DR SEQUENCE 278 AA; 30125 MW; 863159F567102FA7 CRC64;

Query Match 78.5%; Score 1181; DB 11; Length 278;  
 Best Local Similarity 78.1%; Pred. No. 8.2e-101;  
 Matches 214; Conservative 18; Mismatches 40; Indels 2; Gaps 2;

QY 1 MRGSEVLLMVLAVGG-TEHAYRPRGRRVCAVRAHGDVPSSEFVQRYQFLLTTCGHR 59  
 DB 4 MRGSEVLLMVLAVGG-TEHAYRPRGRRVCAVRAHGDVPSSEFVQRYQFLLTTCGHR 63

QY 60 RACSTYRTIYRTAYRRSPGLAPAPRYACCPGKRTSGLPGACGAAICOPPCRNNGSCVQ 119  
 DB 64 RACSTYRTIYRTAYRRSPGLAPAPRYACCPGKRTSGLPGACGAAICOPPCRNNGSCVQ 123

QY 120 GRCPAGWGTDCQSDVDECSARRGCPQRCVNTAGSYWCQWEGHSLADGTLCPVK 179  
 DB 124 GRCPAGWGTDCQSDVDECSARRGCPQRCVNTAGSYWCQWEGHSLADGTLCPVK 183

QY 180 GPPRVAPNPTGVDSAMKEEVQRLQSRVLDLLEKQLVLAFLHSLASQALEHGLPDPG 238  
 DB 184 GPPRVAPNPTGVDSAMKEEVQRLQSRVLDLLEKQLVLAFLHSLASQALEHGLPDPG 243

QY 239 LLVHSFQOLGRIDSLSQISFLEEQSGSCCKD 272  
 DB 244 LLVHSFQOLGRIDSLSQISFLEEQSGSCCKD 277

RESULT 4  
ID 09DCP5 PRELIMINARY; PRT; 265 AA.  
AC 09DCP5-  
DT 01-JUN-2001 (TEMBLrel. 17, Created)  
DT 01-JUN-2001 (TEMBLrel. 17, Last sequence update)  
DE 01-JUN-2002 (TEMBLrel. 21, Last annotation update)  
GN Vascular endothelial zinc finger 1.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxId=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=KIDNEY;  
RA MEDLINE=21085660; PubMed=11217851;  
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
RA Aizawa K., Izawa M., Nishii K., Kiyosawa H., Adachi J., Fukuda S.,  
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kondo S., Yamana K.,  
RA Fleschmann W., Gaasterland T., Gissi C., King B., Kochwa H.,  
RA Schirml L.M., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,  
RA Sakai K., Oikida T., Furuno M., Kono H., Baldarelli R., Barish G.,  
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
RA Guetters M., Hill D., Hofmann M., Hume D.A., Kimura M., Lee N.H.,  
RA Lyons P., Marchionni L., Mashima M., Mazzarelli J., Mombaerts P.,  
RA Norioka H., Sato K., Schoenbach C., Seta T., Shibata Y., Storch K.-F.,  
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,  
RA Hayashizaki Y., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,  
RT "Functional annotation of a full-length mouse cDNA collection."  
RL Nature 409:685-690 (2001).  
DR EMBL; AK002601; BAB2222.1;  
DR HSSP; P00740; 1EDM.  
DR MGI; MGI:1313291; Vezfl.  
DR InterPro; IPR000561; EGF-like.  
DR PIR; PIR001881; EGF\_Ca.  
DR SMART; SM00181; EGF\_2.  
DR SMART; SM00001; EGF\_1like; 2.  
DR PROSITE; PS00022; EGF\_1; UNKNOWN\_1.  
DR PROSITE; PS01186; EGF\_2; UNKNOWN\_1.  
DR PROSITE; PS01187; EGF\_Ca; 1.  
SQ SEQUENCE 265 AA; 28665 MW; D81EC3DA884F97E CRC64;

Query Match  
Best Local Similarity 73.4%; Score 1104.5; DB 11; Length 265;  
Matches 203; Conservative 17; Mismatches 39; Indels 15; Gaps 3;  
OY 1 MRSOEVLLMVLAVGG-TEHAYRPRGRVCAVRHAGDPVSESTVQRYVOPFLTTCDHG 59  
DB 4 MMSGELVAMFLVADGTEHAYRPRGRVCAVRHAGDPVSESTVQRYVOPFLTTCDHG 59  
OY 60 RACSTYRTITVTRRSBGLAPRPVACCPGKRTSGLPACCAAIICPPCGNGSCVQ 119  
DB 64 RACSTYRTITVTRRSBGLAPRPVACCPGKRTSGLPACCAAIICPPCGNGSCVQ 119  
OY 120 PGRGCRPAKRGDTCSQDVDECSARGGCPORCVNTAGSYWCQMGSHLSADGTLVCPK 179  
DB 124 PGRGCRPAKRGDTCSQDVDECSARGGCPORCVNTAGSYWCQMGSHLSADGTLVCPK 179  
OY 180 GGPFRVAPNPT-GVGSAMKEVYQRIQSRVLDLEKQLVLAFLHSLASQALEHGLPDPGS 238  
DB 184 EGSPVAPNPTGVSAMKEVYQRIQSRVLDLEKQLVLAFLHSLASQALEHGLPDPGS 238  
OY 239 LVHSPQQLGRIDSLSEQISFLEROLGSCCKD 272  
DB 239 LVHSPQQLGRIDSLSEQISFLEROLGSCCKD 272

Db 244 LVHSPQQLGRIDSLSEQISFLEROLGSCCKD 264

RESULT 5  
ID 09JWK3 PRELIMINARY; PRT; 190 AA.  
AC 09JWK3-  
DT 01-OCT-2000 (TEMBLrel. 15, Created)  
DT 01-OCT-2000 (TEMBLrel. 15, Last sequence update)  
DE 01-JUN-2002 (TEMBLrel. 21, Last annotation update)  
GN Rattus norvegicus (Rat).  
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxId=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=SPLN;  
RA Chan M.T.W., Ng C.C.Y., Lim E.K.B., Huynh H.T.,  
RT "Cloning and Characterization of a Novel 20.4kd Estrogen-regulated  
RL protein in the Rat Spleen."  
RN Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.  
RP SEQUENCE FROM N.A.  
RC TISSUE=SPLN;  
RA Marcantonio D., Huynh H.T.,  
RT Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.  
RL EMBL; AF22678; AAF5352.1;  
DR InterPro; IPR000152; Asx\_hydroxyl.  
DR InterPro; IPR000561; Asx\_hydroxyl.  
DR PIR; PIR001881; EGF-like.  
DR PIR; PIR001881; EGF\_Ca.  
DR SMART; SM00179; EGF\_Ca; 1.  
DR SMART; SM00001; EGF\_1like; 1.  
DR PROSITE; PS00022; ASX\_HYDROXYL; 1.  
DR PROSITE; PS01186; EGF\_1; UNKNOWN\_1.  
DR PROSITE; PS01187; EGF\_2; UNKNOWN\_1.  
DR PROSITE; PS01187; EGF\_Ca; 1.  
KV Calcium-binding; EGF-like domain; Glycoprotein; Hydroxylation; Repeat.  
SQ SEQUENCE 190 AA; 20527 MW; C540EF0687F1E998 CRC64;

Query Match  
Best Local Similarity 48.4%; Score 728.5; DB 11; Length 190;  
Matches 131; Conservative 14; Mismatches 23; Indels 1; Gaps 1;  
OY 105 AICPPCRNGSGCVQPPRCRCPCAGMRGDTCSQDVDECSARGGCPORCVNTAGSYWCQW 164  
DB 21 AICPPCRNGSGCTPRRCRCPCAGMRGDTCSQDVDECSARGGCPORCVNTAGSYWCQW 164  
OY 165 EGHSLADGTLVCPKGGPPVAPNPT-GVDSAMKEVYQRIQSRVLDLEKQLVLAFLHSL 223  
DB 81 EGHSLADGTLVCPKGGPPVAPNPT-GVDSAMKEVYQRIQSRVLDLEKQLVLAFLHSL 223  
OY 224 LASQALRHGLPDPGSLHLSFQQLGRIDSLSEQISFLEROLGSCCKD 272  
DB 141 LASQALRHGLPDPGSLHLSFQQLGRIDSLSEQISFLEROLGSCCKD 272  
RESULT 6  
ID 035447 PRELIMINARY; PRT; 293 AA.  
AC 035447-  
DT 01-JAN-1998 (TEMBLrel. 05, Created)  
DT 01-JAN-1998 (TEMBLrel. 05, Last sequence update)  
DE 01-DEC-2001 (TEMBLrel. 19, Last annotation update)  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxId=10090;  
RN [1]

Tue Dec 17 14:03:52 2002

SMART: SM00001; EGF like; 1.  
 DR PROSITE; PS00010; ASX\_HYDROXYL; 1.  
 DR PROSITE; PS00022; EGF 1; UNKNOWN\_1.  
 DR PROSITE; PS01186; EGF 2; 1.  
 DR PROSITE; PS01187; EGF CA; 1.  
 DR PROSITE; PS01187; EGF CA; 1.  
 KW Calcium-binding; EGF-Like domain; Glycoprotein; Hydroxylation; Repeat.  
 KW Calicium-binding; EGF-Like domain; Glycoprotein; Hydroxylation; Repeat.  
 SQ SEQUENCE 293 AA; 32262 MW; 6519CA254FB23PD0 CRC64;

Query Match 28.1%; Score 422.5; DB 4; Length 293;  
 Best Local Similarity 36.5%; Pred. No. 6.3e-31; Indels 35; Gaps 10;  
 Matches 103; Conservative 37; Mismatches 107;

QY 12 LLVLAVGGTGHAYRPRGRVCAVRAHGDV--SESFVQRYQFLLTCDHRACTYRTIY 69  
 19 LLIPIGEGAGKGSRESQVCSKQTLVPLVHVESYQPVYKPYLTLCAGRICSTYRTIY 78  
 DB 70 RTAYRSPGLAPARPRYACCPQWKTSLGCA--CGAAICQPPCRNGSCVQPGRCPCA 127  
 QY 79 RYVM--REVREVQTHAVCCQGWKKRH--PGALT-C-FAICAKPCLNGGVCPDCECAP 134  
 DB 128 GWRGDTCSQVDECSARRGGCPORCVNTAGSYWCQWEGHSLSDAGTLCVPGKGGPRVAP 187  
 QY 135 GMGGKHCHVDDECRITSLTCSHHCFTAGSFTCGPHDLVLGVDGTCTMEGSPPEPTSA 194  
 DB 188 NPTGV-----DSANKKEVQRLQSRVLLBEKQLVLAPLHLSAQA--LEHGLP-D 235  
 QY 195 SILSVAVRAEKDERALKQETHELGRLEQLQ-----WAGQAGWRAVLVFP 243  
 DB 236 PGSLLVHSFOOL-----GRIDLSLSEQISFLSEQLGSCSKKDS 273  
 QY 244 PEELOPQVLAELNGRDRIESLSQVLLLEERLGACSCEDNS 285

RESULT 8  
 QSVZD0  
 ID QSVZD0 PRELIMINARY; PRT; 509 AA.  
 AC QSVZD0 (TRENBLrel. 13, Created)  
 DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)  
 DT 01-MAY-2000 (TRENBLrel. 13, Last annotation update)  
 DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)  
 DE CG7447 protein.  
 OS CG7447 melanogaster (Fruit fly).  
 GN Drosophila melanogaster (Tracheata; Hexapoda; Insecta;  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OC NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BERKELEY; PubMed=10731132;  
 RA MEDLINE=20196006; Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Adams M.D., Celniker S.E., Li P.W., Hoskins M., Henderson S.N.,  
 RA Amanatides P.G., Scher S.E., Richards S., Ashburner M., Chen L.X.,  
 RA George R.A., Lewis S.E., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Sutton G.G., Wortman J.R., Blazie R.G., Chumpe M., Pfeiffer B.D.,  
 RA Brandon R.C., Rogers Y.-H.C., Blazie R.G., Nelson C.R., Miklos G.L.G.,  
 RA Wan K.H., Doyle C., Baxter E.G., Helt J., Andrews-Pfannkuch C., Baldwin D.,  
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkuch C., Beasley E.M.,  
 RA Ballew R.M., Basu P.V., Berman B.P., Brokstein P., Brottier P.,  
 RA Beeson K.Y., Botchan M.R., Bouck J., Brokstein P., Center A., Chandra I.,  
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Center A., Chandra I.,  
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Dew I., Dietz S.M.,  
 RA Cherry J.M., Cawley S., Deng Z., Mays A.D., Mays A.D., Dietz S.M.,  
 RA De Pablos B., Delcher A.A., Deng Z., Mays A.D., Mays A.D., Dietz S.M.,  
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C., Ferraz C., Ferreira S., Fleischmann W.,  
 RA Folsler C., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kemison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

SEQUENCE FROM N.A.  
 Rowen L., Mahairas G., Qin S., Ahearn M.E., Dankers C., Lasky S.,  
 Rowen L., Mahairas G., Qin S., Ahearn M.E., Dankers C., Lasky S.,  
 Loretz C., Schmidt S., Tipson S., Traicoff R., Zackrone K., Hood L.,  
 "Sequence of the mouse major histocompatibility locus class III  
 region." (Oct-1997) to the EMBL/GenBank/DBJ databases.  
 Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.  
 EMBL; AF030001; AAB82010.1; --  
 HSP; P35555; 1EMN  
 InterPro; IPR000152; Asx\_hydroxyl.  
 InterPro; IPR000561; EGF-like.  
 InterPro; IPR001881; EGF\_Ca.  
 Pfam; PF00008; EGF; 2; 1.  
 SMART; SM00017; EGF CA; 1.  
 SMART; SM00001; ASX\_HYDROXYL; 1.  
 PROSITE; PS00010; ASX\_HYDROXYL; 1.  
 PROSITE; PS00022; EGF 1; UNKNOWN\_1.  
 PROSITE; PS01186; EGF 2; 1.  
 PROSITE; PS01187; EGF CA; 1.  
 PROSITE; PS01187; EGF CA; 1.  
 KW Calcium-binding; EGF-Like domain; Glycoprotein; Hydroxylation;  
 KW Calicium-binding; EGF-Like domain; Glycoprotein; Hydroxylation;  
 KW Hypothetical protein; Repeat.  
 KW Hypothetical protein; Repeat.  
 SQ SEQUENCE 293 AA; 32066 MW; 8A99A5EC00A2C62 CRC64;

Query Match 28.9%; Score 434.5; DB 11; Length 293;  
 Best Local Similarity 37.3%; Pred. No. 5e-32; Indels 51; Gaps 14;  
 Matches 112; Conservative 36; Mismatches 101;

QY 1 MRGQEVLMWLLVAVG-GTE-HAYRPRGRVCAVRAHGDV--SESFVQRYQFLLTTC 56  
 11 LRG-----LSFVLVMTGEGTRGGSFKSLGVCSTQTLVPLVHVESYQPVYKPYLTLC 65  
 DB 57 DGHRACTYRTIYRTAYRSPGLAPARPRYACCPQWKTSLGCA--AICQPPCRNGG 115  
 QY 66 AGRICSTYRTIYRTAYRSPGLAPARPRYACCPQWKTSLGCA--AICQPPCRNGG 122  
 DB 116 SCVQPGRCPCAGRGDTCSQVDECSARRGGCPORCVNTAGSYWCQWEGHSLSDAGTLC 175  
 QY 123 VCTGPDRCPCAGRGDTCSQVDECSARRGGCPORCVNTAGSYWCQWEGHSLSDAGTLC 182  
 DB 176 CVPGKGGPRVAPNPTGV-----DSANKKEVQRLQSRVLLBEKQLVLAPL 221  
 QY 183 CA--GGPPE---SPTSAILSVAVRAEKDERALKQETHELGRLEQLQ----- 228  
 DB 222 HSLASA---LEHGLP-DPGSLLVHSFOOL-----GRIDLSLSEQISFLSEQLGSCSKKDS 273  
 QY 229 --WATQAGWRAVLVFPPEELPQVLAELNGRDRIESLSQVLLLEERLGACSCEDNS 286

RESULT 7  
 QSVZD0  
 ID QSVZD0 PRELIMINARY; PRT; 293 AA.  
 AC QSVZD0 (TRENBLrel. 03, Created)  
 DT 01-MAY-1997 (TRENBLrel. 03, Last sequence update)  
 DT 01-MAY-1997 (TRENBLrel. 03, Last annotation update)  
 DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)  
 DE NG3.  
 OS Homo sapiens (Human).  
 GN Homo sapiens (Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OC NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC Rowen L., Dankers C., Baekun D., Faust J., Loretz C., Ahearn M.E.,  
 RA Banta A., Spies T., Hood L.,  
 RA "Sequence determination of 300 kilobases of the human class III MHC  
 locus." (Dec-1999) to the EMBL/GenBank/DBJ databases.  
 RT Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.  
 RL EMBL; U99336; AAB47494.1; --  
 DR HSP; P35555; 1EMN.  
 DR InterPro; IPR000152; Asx\_hydroxyl.  
 DR InterPro; IPR000561; EGF-like.  
 DR InterPro; IPR001881; EGF\_Ca.  
 DR Pfam; PF00008; EGF; 2; 1.  
 DR SMART; SM00017; EGF CA; 1.

RA Liu X., Matvei B., McIntosh T.C., McLeod M.P., McPherson D.,  
RA Merklov G., Mishina N.V., Mobarry C., Morris J., Moshir A.,  
RA Mount S.M., Moy M., Murphy B., Murphy L., Murry D.M., Nelson D.,  
RA Nelson D.R., Nelson K.A., Nixon K., Pollard J.D., Paoletti J.M.,  
RA Palazzolo M., Pittman K., Pan S., Saunders R.D., Scheller F., Smith T.,  
RA Reineck K., Remington K., Simpson M., Skupski M.P., Smith T.,  
RA Shue B.C., Siden-Kiamos I., Stimpson M., Stumpski M.P., Smith T.,  
RA Spter E., Spreding A.C., Stimpson M., Skupski M.P., Smith T.,  
RA Szykasz R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,  
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu H.O.,  
RT "The genome sequence of *Drosophila melanogaster*,"  
RL Science 287.2185-2195(2000).  
DR EMBL: AEO03481; AAF47894.1; -  
DR HSSP: P00740; IEDM.  
DR FlyBase: FBgn0035539; CG7447.  
DR InterPro: IPR000152; Asx\_hydroxyl.  
DR InterPro: IPR000561; EGF-like.  
DR Pfam: PF00008; EGF\_2.  
DR SMART: SM00179; EGF\_CA.1.  
DR SMART: SM00001; EGF\_CA.1.  
DR PROSITE: PS00010; ASX\_HYDROXYL.1.  
DR PROSITE: PS00022; EGF\_1; 1.  
DR PROSITE: PS01186; EGF\_2; 2.  
DR PROSITE: PS01187; EGF\_CA.1.  
DR Calcium-binding; EGF-like domain.  
KW SEQUENCE 509 AA; 57413 MW; F64782E4A6E121F0 CRC64.

Query Match 18.4%; Score 276.5; DB 5; Length 509;  
Best Local Similarity 27.4%; Pred. No. 3.3e-17;  
Matches 72; Conservative 41; Mismatches 113; Indels 37; Gaps 9;  
Qy 28 RRYC-AVRAGSDPV--SESFVORYOPFLITCD---GHRACSTYRTITYTAVRSPGLA 80  
Db RHICMOQRTVTMPVPRTEVYSRPTWGVATPCQPTFGQCTNVQVHQAQAVDIDHK 301  
Qy 81 PAPP-RVACPCGMRKTSGLPGACGAATCQPCRNAGSCVOPGRCPACMRDPTQSDVD 139  
Db TAQOMTYDCTCGMSRBNPDSCKMPICARCONGAGCTAPSTCSTFGTGRCEQDQVD 361  
Qy 140 ECSARRGGCPORCVNTAGSYWCQCGHSHLSADGTLGVKGPAPRYAVN-----P 189  
Db 362 ECQTER-PCDQOCINTHSGYFCRCRQGVLSQDQSC-----KVSTNADDAFEARDE 414  
Qy 190 TGVDSAMKEEYORLOS-----RVDLSEKIOVLAPLHSLASQ--ALBHGLPDGB 237  
Db 415 NDIDPTDAEVATRLQKTEKSLANERVHTLQKSLQATYSVVDTLKSLSTLEKQADVS 474  
Qy 238 SLVHSPFOQLGRISLSEQISFL 260  
Db 475 RLQTNLVKTESRTNKGIMINLL 497

RESULT 9  
ID 095R01 PRELIMINARY; PRT; 512 AA.  
AC 095R01  
DT 01-DEC-2001 (TREMBlrel. 19, Created)  
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
DE LDI6414P. (TREMBlrel. 21, Last annotation update)  
GN CG7447.  
OS *Drosophila melanogaster* (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
OC Ephydroidea; Diptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC NCBI\_Taxid=7227;  
RN [1]  
SEQUENCE FROM N.A.

RC STRAIN-BERKELEY;  
RA Chapeton M., Brokstein P., Hong L., Ashpazzani A., Carlson J.,  
RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,  
RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,  
RA Nuno J., Paoletti J., Paragas V., Park S., Phouanavong S., Wan K.,  
RA Yu C., Lewis S.E., Rubin G.M., Colnik S.,  
RL Submitted (Oct-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AY061220; AAL28768.1; -  
DR FlyBase: FBgn0035539; CG7447.  
DR InterPro: IPR000152; Asx\_hydroxyl.  
DR InterPro: IPR000561; EGF-like.  
DR Pfam: PF00008; EGF\_2.  
DR PROSITE: PS00010; ASX\_HYDROXYL.1.  
DR PROSITE: PS00022; EGF\_1; UNKNOWN.1.  
DR PROSITE: PS01186; EGF\_2; UNKNOWN.2.  
DR PROSITE: PS01187; EGF\_CA; UNKNOWN.1.  
KW SEQUENCE 512 AA; 57770 MW; 4DD372E4A6FE7627 CRC64.

Query Match 18.4%; Score 276.5; DB 5; Length 512;  
Best Local Similarity 27.4%; Pred. No. 3.4e-17;  
Matches 72; Conservative 41; Mismatches 113; Indels 37; Gaps 9;  
Qy 28 RRYC-AVRAGSDPV--SESFVORYOPFLITCD---GHRACSTYRTITYTAVRSPGLA 80  
Db RHICMOQRTVTMPVPRTEVYSRPTWGVATPCQPTFGQCTNVQVHQAQAVDIDHK 301  
Qy 81 PAPP-RVACPCGMRKTSGLPGACGAATCQPCRNAGSCVOPGRCPACMRDPTQSDVD 139  
Db TAQOMTYDCTCGMSRBNPDSCKMPICARCONGAGCTAPSTCSTFGTGRCEQDQVD 361  
Qy 140 ECSARRGGCPORCVNTAGSYWCQCGHSHLSADGTLGVKGPAPRYAVN-----P 189  
Db 362 ECQTER-PCDQOCINTHSGYFCRCRQGVLSQDQSC-----KVSTNADDAFEARDE 414  
Qy 190 TGVDSAMKEEYORLOS-----RVDLSEKIOVLAPLHSLASQ--ALBHGLPDGB 237  
Db 415 NDIDPTDAEVATRLQKTEKSLANERVHTLQKSLQATYSVVDTLKSLSTLEKQADVS 474  
Qy 238 SLVHSPFOQLGRISLSEQISFL 260  
Db 478 RLQTNLVKTESRTNKGIMINLL 500

RESULT 10  
ID 088281 PRELIMINARY; PRT; 1574 AA.  
AC 088281  
DT 01-NOV-1998 (TREMBlrel. 08, Created)  
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)  
DE MEGF6.  
GN MEGF6.  
OS *Rattus norvegicus* (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OC NCBI\_Taxid=10116;  
RN [1]  
SEQUENCE FROM N.A.  
RC STRAIN=SPRAGUE-DWLEY; TISSUE=BRAIN;  
RA MEDLINE=98360089; PubMed=9693030;  
RA Nakayama M., Nakajima D., Nagase T.,  
RT "Identification of high-molecular-weight proteins with multiple EGF-  
RL like motifs by motif-trap screening,"  
DR EMBL: AB011532; BA332462.1; -  
DR HSSP: P00736; IAPQ.  
DR InterPro: IPR000152; Asx\_hydroxyl.  
DR InterPro: IPR000561; EGF-like.  
DR Pfam: PF00008; EGF\_2.  
DR SMART: SM00179; EGF\_CA.1.  
DR SMART: SM00001; EGF\_CA.1.



```

RESULT 11          PRT;   558 AA.
Q9UFK6             PRELIMINARY;
ID Q9UFK6          Created)
DT 01-MAY-2000 (TRENBlurel. 13, Last sequence update)
DT 01-MAY-2000 (TRENBlurel. 13, Last annotation update)
DT 01-JUN-2002 (TRENBlurel. 21, Last annotation update)
DT 01-JUN-2002 (TRENBlurel. 21, Last annotation update)
HYPOtheoretical 61.8 kDa protein (Fragment).
DKFZF564P2063.
CN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxId=9606;
[1]
RN SEQUENCE FROM N.A.
RP TISSUE=BRAIN;
RC Duesterhoef A., Lauber J., Mewes H.W., Gassenhuber J., Wiemann S.;
RA Submitted (SEP-1999) to the EMBL/Genbank/DBJ databases.
RL -1- SIMILARITY: CONTAINS 1 NAM DOMAIN.
CC EMBL; AL117610; CAB56014.1; -.
DR HSSP; P00736; IAFQ; Asx hydroxyl.
DR InterPro; IPRO00152; EGF-like.
DR InterPro; IPRO00561; EGF Ca.
DR InterPro; IPRO01881; EGF Ca.
DR InterPro; IPRO00998; NAM_domain.
DR InterPro; IPRO0008; EGF; 4.
DR Pfam; PF000629; NAM; 1.
DR Pfam; PF00629; EGF CA; 3.
DR SMART; SM00179; EGF like; 2.
DR SMART; SM00001; EGF CA; 3.
DR SMART; SM00137; NAM; 1.
DR PROSITE; PS00010; ASX HYDROXYL; 3.
DR PROSITE; PS00022; EGF 1; UNKNOWN_1.
DR PROSITE; PS01186; EGF 2; 2.
DR PROSITE; PS01187; EGF CA; 2.
DR PROSITE; PS01187; EGF CA; 2.
DR PROSITE; PS00060; NAM 2; 1.
DR Calcium-binding; EGF-like domain; Glycoprotein; Hydroxylation;
KW Calcium-binding; EGF-like domain; Repeat.
KW Hypothetical protein; Repeat.
FT NON TER      1
FT LENGTH       558 AA; 61828 MW; AA38D7DCE402BFA3 CRC64;
SQ              16.8%; Score 253.5; DB 4; Length 558;
Query Match     37.4%; Pred. No. 4.9e-15; Gaps
Best Local Similarity 16; Mismatches 50; Indels 31; Gaps
Matches 58; Conservative
OY 58 GHRACSTYRTIYTRYSGLAPAREPVACCPGWKRTSGLPAGCGAICQPFCRNGGSC 117
Db 26 GNAASARHHGLLASA--ROPGVCHYGTKLACCYGMWRNS--KGVC-EATCFPGCK-FGEC 79
OY 118 VQGRCRCPAGRWGDTCQSDVDECSARGGCPQCYNVTAGSYWCQWEGHSLSADGTLCV 177

```

554 AA.

	PRELIMINARY;	PRT; 554 AA.
RESULT 13		
Q9N67	Q9N67	
ID Q9N67	(Created)	
QC Q9N67	(TREMBlurel. 15, Last sequence update)	
DAT 01-OCT-2000	(TREMBlurel. 15, Last annotation update)	
DT 01-OCT-2000	(TREMBlurel. 21, Last annotation update)	
DT 01-JUN-2002		



DE Hypothetical 61.4 kda protein.  
 GN W80.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=TERATOCARCINOMA/NEURON;  
 RA Franco B.;  
 RL Submitted (AUG-1999) to the EMBL/Genbank/DBJ databases.  
 RP [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=TERATOCARCINOMA/NEURON;  
 RA MEDLINE=20241927; PubMed=10777661;  
 RT Buchner G., Orfanelli U., Quaderni N., Bassi M.T., Andolfi G.;  
 RT "Identification of a new EGF-repeat-containing gene from human Xp22;  
 RL Genomics 65:16-23(2000).  
 CC -1- SIMILARITY: CONTAINS 1 MAM DOMAIN.  
 DR EMBL; AJ245671; CAB92132.1; -.  
 DR HSSP; P00736; IAPQ.  
 DR InterPro; IPR000152; ASX\_hydroxyl.  
 DR InterPro; IPR000561; EGF-like.  
 DR InterPro; IPR001881; EGF\_Ca.  
 DR Pfam; PF00008; EGF\_4.  
 DR Pfam; PF00629; MAM; 1.  
 DR SMART; SM00179; EGF\_CA; 3.  
 DR SMART; SM00001; EGF-like; 2.  
 DR PROSITE; PS00010; ASX\_HYDROXYL; 3.  
 DR PROSITE; PS00022; EGF\_1; UNKNOWN\_1.  
 DR PROSITE; PS01186; EGF\_2; 2.  
 DR PROSITE; PS01187; EGF\_CA; 3.  
 DR Calcium-binding; EGF-like domain; Glycoprotein; Hydroxylation;  
 KW Hypothetical protein; Repeat.  
 SQ SEQUENCE 554 AA; 61388 MW; D519238F2A604101 CRC64;  
 Query Match 16.8%; Score 252.5; DB 4; Length 554;  
 Best Local Similarity 37.4%; Pred. No. 6e-15;  
 Matches 58; Conservative 16; Mismatches 50; Indels 31; Gaps 7;  
 QY 58 GHACSRITRYITAVRSPLAPARPRYACCPGKRTSLPAGCGAATQPPCRNGSGC 117  
 Db 21 GNASAHHGLASA--RQPGVCHYGTLCACCTGRRNS--KGVG-EATCEPGCK-FGEC 74  
 QY 118 VQGRCRCPAGWRGDTCCSDVDECSARAGGCPQRCVNTAGSYWCOCWEGHSLADDTLCV 177  
 Db 75 VGNKCRCPFGYTGKTCSDVDECSARAGGCPQRCVNTAGSYWCOCWEGHSLADDTLCV 177  
 QY 178 -----PRGQPP-----RVAPN 188  
 Db 134 NSRTCAINCOYSCDETEEGPQCLCPSSGLRLAPN 168  
 RESULT 14  
 OS 09J325 PRELIMINARY; PRT; 550 AA.  
 AC 09J325  
 DT 01-OCT-2000 (Tremblrel. 15, Created)  
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)  
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)  
 DE Hypothetical 61.5 kda protein.  
 GN EGF6 OR W80.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Franco B.;

RL Submitted (AUG-1999) to the EMBL/Genbank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC MEDLINE=20241927; PubMed=10777661;  
 RA Buchner G., Orfanelli U., Quaderni N., Bassi M.T., Andolfi G.;  
 RT "Identification of a new EGF-repeat-containing gene from human Xp22;  
 RL Genomics 65:16-23(2000).  
 CC -1- SIMILARITY: CONTAINS 1 MAM DOMAIN.  
 DR EMBL; AJ245672; CAB92138.1; -.  
 DR HSSP; P35555; IEMN.  
 DR MGD; MGJ; 1858599; EGF16.  
 DR InterPro; IPR000152; ASX\_hydroxyl.  
 DR InterPro; IPR000561; EGF-like.  
 DR InterPro; IPR001881; EGF\_Ca.  
 DR Pfam; PF00008; EGF\_4.  
 DR Pfam; PF00629; MAM; 1.  
 DR SMART; SM00179; EGF\_CA; 3.  
 DR SMART; SM00001; EGF-like; 2.  
 DR PROSITE; PS00010; ASX\_HYDROXYL; 3.  
 DR PROSITE; PS00022; EGF\_1; UNKNOWN\_1.  
 DR PROSITE; PS01186; EGF\_2; 2.  
 DR PROSITE; PS01187; EGF\_CA; 3.  
 DR Calcium-binding; EGF-like domain; Glycoprotein; Hydroxylation;  
 KW Hypothetical protein; Repeat.  
 SQ SEQUENCE 550 AA; 61520 MW; DEF936325C9F31B3 CRC64;  
 Query Match 16.4%; Score 246.5; DB 11; Length 550;  
 Best Local Similarity 36.9%; Pred. No. 2.1e-14;  
 Matches 52; Conservative 12; Mismatches 50; Indels 27; Gaps 4;  
 QY 71 TAVRSPLAPARPRYACCPGKRTSLPAGCGAATQPPCRNGSGCVPGRCPAGWR 130  
 Db 30 SALAHQPGVCGYGTMACTGCKKRN--KGVG-EMACEPRCK-FGECVGPNNKCRCPGPT 85  
 QY 131 GDTCCSDVDECSARAGGCPQRCVNTAGSYWCOCWEGHSLADDTLCV----- 175  
 Db 86 GKTCTQDVDECSARAGGCPQRCVNTAGSYWCOCWEGHSLADDTLCV----- 175  
 QY 176 -----CVRGQPPRVAPN 188  
 Db 146 EDTREGPRCPVSSGLRLAPN 166  
 RESULT 15  
 OS 091V88 PRELIMINARY; PRT; 561 AA.  
 AC 091V88  
 DT 01-DEC-2001 (Tremblrel. 19, Created)  
 DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)  
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)  
 DE POEM (NEPHRORECTIN short isoform).  
 GN NPVT OR POEM OR NEPHL.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6;  
 RA MEDLINE=21551216; PubMed=11546798;  
 RA Morimura N., Tezuka Y., Watanabe N., Yasuda M., Miyatani S.,  
 RT "Molecular cloning of POEM, A novel adhesion molecule that interacts  
 RT with alpha8beta1 integrin."  
 RL J. Biol. Chem. 276:42172-42181(2001).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=NIH SWISS; TISSUE=KIDNEY;  
 MEDLINE=21363579; PubMed=11470831;

us-09-852-472-2.rspt

Tue Dec 17 14:03:52 2002

RA Brandenberger R., Schmidt A., Linton J., Wang D., Backus C., Denda S.,  
 RA Muller U., Reichardt L.F.,  
 RT "Identification and characterization of a novel extracellular matrix  
 RT protein nephronectin that is associated with integrin  $\alpha$ 5 $\beta$ 1 in  
 RT the embryonic kidney.",  
 RL J. Cell Biol. 154:447-458 (2001).  
 CC -!- SIMILARITY: CONTAINS 1 MAM DOMAIN.  
 DR EMBL; AB059656; BAB69692.1; -.  
 DR EMBL; AY035898; AAK96010.1; -.  
 DR MGD; MGI:214881; Npnt.  
 DR InterPro; IPR000152; Asx\_hydroxyl.  
 DR InterPro; IPR000561; EGF-like.  
 DR InterPro; IPR001881; EGF\_Ca.  
 DR InterPro; IPR000998; MAM\_domain.  
 DR Pfam; PF00008; EGF; 4.  
 DR Pfam; PF00629; MAM; 1.  
 DR PROSITE; PS00010; ASX\_HYDROXYL; UNKNOWN\_3.  
 DR PROSITE; PS00022; EGF\_1; UNKNOWN\_1.  
 DR PROSITE; PS01186; EGF\_2; UNKNOWN\_3.  
 DR PROSITE; PS01187; EGF\_Ca; UNKNOWN\_3.  
 DR PROSITE; PS00060; MAM\_2; 1.  
 KW Glycoprotein.  
 SQ SEQUENCE 561 AA; 61490 MW; 69E7ACAA0EE3F506 CRC64;  
 Query Match 14.8%; Score 223; DB 11; Length 561;  
 Best Local Similarity 43.4%; Pred. No. 3.2e-12;  
 Matches 43; Conservative 12; Mismatches 40; Indels 4; Gaps 3;  
 QY 76 SPGLAPARPRVACCPGWKRTSGLPACGAAICQPPCNGSGCVQPCRCPCPAGWRGDTCC 135  
 DB 32 SIGLCRYGGRIDCCGWARGSW--GQC-QPVCPQCKH-GEVGNKCKCHGFPAGKTCN 87  
 QY 136 SDVDECSARRGCGPQRCVNTAGSYWCOCWEGHSLSDGT 174  
 DB 88 QDLNECGLKPRPCKHRCMNTFGSYKCYCLNGYMLLPDGS 126

Search completed: December 17, 2002, 10:03:01  
 Job time : 32.4915 secs

LN MO303/503-A2  
XX  
PD 23-DEC-1998.  
XX

PF 18-JUN-1998; 98WO-US12763.  
 XX 18-JUN-1997; 97US-0878322.  
 PR 18-JUN-1997; 97US-0050143.  
 XX (ZYMO ) ZYMOGENETICS INC.  
 XX Blumberg H, Jelinek LJ, Lehner JM, Sheppard PO;  
 PI Whitmore TE;  
 XX WPI; 1999-095324/08.  
 XX New mammalian Zneul polypeptides - used to, e.g. treat Alzheimer's  
 PT disease, cancer and to repopulate blood cells  
 XX Claim 6; Page 48-49; 70pp; English.  
 XX This polypeptide comprises human Zneul mature polypeptide. Zneul  
 CC is a new neuro-growth factor-like protein (see also AAW88381). Its  
 CC closest human homologue is HSMHC3W5A, a gene in the HLA class III  
 CC region, which is contained in a cosmid which contains Notch 4.  
 CC Zneul is also homologous to Notch 4 in its EGF-like domains and may  
 CC be involved in EGF receptor pathways. Zneul is widely expressed in  
 CC adult tissues, with high expression in heart, placenta, spleen,  
 CC testis, thyroid, spinal cord and lymph node. Zneul can be used as  
 CC a growth, maintenance, or differentiation factor in the spinal  
 CC cord, heart, spleen, testis, thyroid and lymph nodes. It may  
 CC play a role in breast cancer, glioblastoma, and pituitary  
 CC adenomas. Zneul may also be used to treat Alzheimer's disease,  
 CC cancer, to repopulate blood cells after chemotherapy, to stimulate  
 CC myofibroblast proliferation, stimulate or inhibit growth factors  
 CC made in the placenta, in fertility and contraception, or to  
 CC regenerate nerves. Claimed Zneul polypeptides (see also AAW88382-97),  
 CC including specific domains of Zneul and epitope-bearing portions of  
 CC Zneul, can be used to raise specific antibodies for use e.g. in  
 CC diagnostic assays.  
 XX Sequence 254 AA;  
 SQ  
 Query Match 100.0%; Score 1411; DB 20; Length 254;  
 Best Local Similarity 100.0%; Pred. No. 3.3e-98;  
 Matches 254; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TEHAVRPGRRVCAVRAHGDPVSESFQVRVYQPLTTCGHRACSTYRTIYRTARRSPGL 60  
 DB 1 TEHAVRPGRRVCAVRAHGDPVSESFQVRVYQPLTTCGHRACSTYRTIYRTARRSPGL 60  
 QY 61 APARPRYACCPGWKRTSGLPAGCGAAICOPPCRNCGSCVQPCRCPCAGWRGDTCCSDVD 120  
 DB 61 APARPRYACCPGWKRTSGLPAGCGAAICOPPCRNCGSCVQPCRCPCAGWRGDTCCSDVD 120  
 QY 121 ECSARRGGCPQRCVNTAGSVWCQWEGHLSADGTLTCLVPKGGPPRVA NPFTGVDSAMKEE 180  
 DB 121 ECSARRGGCPQRCVNTAGSVWCQWEGHLSADGTLTCLVPKGGPPRVA NPFTGVDSAMKEE 180  
 QY 181 VQRLQSRVDLLEKQLVLAPLHSLASQALEHGLPDPGSLVHVSFOQLGRIDLSLEQISF 240  
 DB 181 VQRLQSRVDLLEKQLVLAPLHSLASQALEHGLPDPGSLVHVSFOQLGRIDLSLEQISF 240  
 QY 241 LEEQLGSCCKKDS 254  
 DB 241 LEEQLGSCCKKDS 254  
 RESULT 2  
 ID AAY41771 standard; Protein; 273 AA.  
 XX AAY41771;  
 XX AAY41771;  
 DT 07-DEC-1999 (first entry)  
 XX Human PRO1449 protein sequence.  
 DE

XX Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation;  
 KW probe; blood coagulation disorder; cancer; cellular adhesion disorder;  
 KW secreted protein; transmembrane protein.  
 XX Homo sapiens.  
 OS WO9946281-A2.  
 PN 16-SEP-1999.  
 PD 08-MAR-1999;  
 PF 99WO-US05028.  
 XX 10-MAR-1998; 98US-0077450.  
 PR 11-MAR-1998; 98US-0077632.  
 PR 11-MAR-1998; 98US-0077641.  
 PR 11-MAR-1998; 98US-0077649.  
 PR 12-MAR-1998; 98US-0077791.  
 PR 13-MAR-1998; 98US-0078004.  
 PR 17-MAR-1998; 98US-0040220.  
 PR 20-MAR-1998; 98US-0078886.  
 PR 20-MAR-1998; 98US-0078910.  
 PR 20-MAR-1998; 98US-0078936.  
 PR 20-MAR-1998; 98US-0078939.  
 PR 25-MAR-1998; 98US-0079294.  
 PR 26-MAR-1998; 98US-0079656.  
 PR 27-MAR-1998; 98US-0079663.  
 PR 27-MAR-1998; 98US-0079664.  
 PR 27-MAR-1998; 98US-0079689.  
 PR 27-MAR-1998; 98US-0079728.  
 PR 27-MAR-1998; 98US-0079786.  
 PR 30-MAR-1998; 98US-0079920.  
 PR 30-MAR-1998; 98US-0079923.  
 PR 31-MAR-1998; 98US-0080105.  
 PR 31-MAR-1998; 98US-0080107.  
 PR 31-MAR-1998; 98US-0080165.  
 PR 31-MAR-1998; 98US-0080194.  
 PR 01-APR-1998; 98US-0080327.  
 PR 01-APR-1998; 98US-0080328.  
 PR 01-APR-1998; 98US-0080333.  
 PR 01-APR-1998; 98US-0080334.  
 PR 08-APR-1998; 98US-0081049.  
 PR 08-APR-1998; 98US-0081070.  
 PR 08-APR-1998; 98US-0081071.  
 PR 09-APR-1998; 98US-0081195.  
 PR 09-APR-1998; 98US-0081203.  
 PR 09-APR-1998; 98US-0081229.  
 PR 15-APR-1998; 98US-0081817.  
 PR 15-APR-1998; 98US-0081838.  
 PR 15-APR-1998; 98US-0081952.  
 PR 15-APR-1998; 98US-0081955.  
 PR 21-APR-1998; 98US-0082568.  
 PR 21-APR-1998; 98US-0082569.  
 PR 22-APR-1998; 98US-0082700.  
 PR 22-APR-1998; 98US-0082704.  
 PR 22-APR-1998; 98US-0082804.  
 PR 23-APR-1998; 98US-0082767.  
 PR 23-APR-1998; 98US-0082796.  
 PR 27-APR-1998; 98US-0083336.  
 PR 28-APR-1998; 98US-0083322.  
 PR 29-APR-1998; 98US-0083392.  
 PR 29-APR-1998; 98US-0083495.  
 PR 29-APR-1998; 98US-0083496.  
 PR 29-APR-1998; 98US-0083499.  
 PR 29-APR-1998; 98US-0083500.  
 PR 29-APR-1998; 98US-0083545.  
 PR 29-APR-1998; 98US-0083554.  
 PR 29-APR-1998; 98US-0083558.  
 PR 29-APR-1998; 98US-0083559.  
 PR 30-APR-1998; 98US-0083742.  
 PR 05-MAY-1998; 98US-0084366.  
 PR 06-MAY-1998; 98US-0084414.  
 PR 06-MAY-1998; 98US-0084441.

PR 07-MAY-1998; 98US-0084598.  
 PR 07-MAY-1998; 98US-0084600.  
 PR 07-MAY-1998; 98US-0084627.  
 PR 07-MAY-1998; 98US-0084637.  
 PR 07-MAY-1998; 98US-0084639.  
 PR 07-MAY-1998; 98US-0084640.  
 PR 07-MAY-1998; 98US-0084643.  
 PR 13-MAY-1998; 98US-0085323.  
 PR 13-MAY-1998; 98US-0085338.  
 PR 13-MAY-1998; 98US-0085339.  
 PR 15-MAY-1998; 98US-0085573.  
 PR 15-MAY-1998; 98US-0085579.  
 PR 15-MAY-1998; 98US-0085580.  
 PR 15-MAY-1998; 98US-0085582.  
 PR 15-MAY-1998; 98US-0085589.  
 PR 15-MAY-1998; 98US-0085697.  
 PR 15-MAY-1998; 98US-0085700.  
 PR 15-MAY-1998; 98US-0085704.  
 PR 18-MAY-1998; 98US-0086023.  
 PR 22-MAY-1998; 98US-0086392.  
 PR 22-MAY-1998; 98US-0086414.  
 PR 22-MAY-1998; 98US-0086430.  
 PR 22-MAY-1998; 98US-0086486.  
 PR 28-MAY-1998; 98US-0087098.  
 PR 28-MAY-1998; 98US-0087106.  
 PR 28-MAY-1998; 98US-0087208.  
 PR 30-JUL-1998; 98US-0094651.  
 PR 11-SEP-1998; 98US-0100038.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX

PI Wood WI, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;  
 XX  
 DR WPI; 1999-551358/46.  
 DR N-PSDB; AA234313.

PT New secreted and transmembrane polypeptides and their polynucleotides,  
 PT useful for treating blood coagulation disorders, cancers and cellular  
 PT adhesion disorders -

XX  
 PS Claim 12; Fig 217; 530pp; English.

XX  
 CC The present invention describes secreted and transmembrane polypeptides  
 CC and their polynucleotides. The nucleotide sequences are useful as  
 CC sources of probes, primers, for chromosome mapping, and for generation  
 CC of antisense sequences. They can also be used to create transgenic  
 CC animals. The proteins can be used to treat a variety of diseases and  
 CC disorders, depending on their function. Diseases that may be treated  
 CC include blood coagulation disorders, cancers and cellular adhesion  
 CC disorders. They may also be used to raise antibodies. AA233891 to  
 CC AA234338, and AA41685 to AA41774 represent polynucleotide and  
 CC polypeptide sequence given in the exemplification of the present  
 CC invention.

XX  
 SQ Sequence 273 AA;

Query Match 100.0%; Score 1411; DB 20; Length 273;  
 Best Local Similarity 100.0%; Pred. No. 3.5e-88;  
 Matches 254; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TEHAIRGRRCVCAVRAGDVSSFVORVYQPIITTCGHRACSTRTTYRIYARSPGL 60  
 DB 20 TEHAIRGRRCVCAVRAGDVSSFVORVYQPIITTCGHRACSTRTTYRIYARSPGL 79  
 QY 61 APARPRACCPGMRRTSGLPAGCAATCOPPCNGSCVCPGRCPCAGRGPTCCSDVD 120  
 DB 80 APARPRACCPGMRRTSGLPAGCAATCOPPCNGSCVCPGRCPCAGRGPTCCSDVD 139  
 QY 121 ECSARRGGCPQRCVNTAGSYWCQCEGSHLSADGTLCPKGGPPRYAPNPTGVDSAMKEE 180  
 DB 140 ECSARRGGCPQRCVNTAGSYWCQCEGSHLSADGTLCPKGGPPRYAPNPTGVDSAMKEE 199  
 QY 181 VORLQSRVDLLEBKQLVLAFLPHLSASQALEHGLPDPGSLVHSFOOLGRIDSLSEQISF 240

DB 200 VORLQSRVDLLEBKQLVLAFLPHLSASQALEHGLPDPGSLVHSFOOLGRIDSLSEQISF 259  
 QY 241 LEEQUGSCCKKDS 254  
 DB 260 LEEQUGSCCKKDS 273

# RESULT 3

AAW88381  
 ID AAW88381 standard; Protein; 273 AA.

AC AAW88381;

DT 26-APR-1999 (first entry)

DE Human neuro-growth factor-like protein Zneu1.

XX Zneu-1; neuro-growth factor-like protein; human; breast cancer;  
 KW glioblastoma; pituitary adenoma; Alzheimer's disease; therapy;  
 KW nerve regeneration; haematopoiesis; fertility; contraception;  
 antibody.

OS Homo sapiens.

XX  
 FH Key Location/Qualifiers

FT Peptide 1..19 /note= "putative signal peptide"

FT Protein 20..273 /note= "mature protein"

FT Domain 20..104 /note= "hydrophilic domain (HSM1), homologous to an HSMHC3W5A domain"

FT Domain 105..135 /note= "epidermal growth factor-like domain 1"

FT Domain 136..177 /note= "epidermal growth factor-like domain 2"

FT Domain 178..273 /note= "domain HSM2 homologous to an HSMHC3W5A domain"

XX  
 PM MO9857983-A2.

XX  
 PD 23-DEC-1998.

XX  
 PF 18-JUN-1998; 98MO-US12763.

XX  
 PR 18-JUN-1997; 97US-0878322.

XX  
 PR 18-JUN-1997; 97US-0050143.

XX  
 PA (ZYMO ) ZYMOGENETICS INC.

XX  
 PI Blumberg H, Jelinek LJ, Lehner JM, Sheppard PO;

PI Whitmore TE;

DR WPI; 1999-095324/08.

DR N-PSDB; AAW84341.

XX  
 PT New mammalian Zneu1 polypeptides - used to, e.g. treat Alzheimer's  
 PT disease, cancer and to repopulate blood cells

PS Claim 6; Page 47-48; 70pp; English.

CC This polypeptide comprises human Zneu1, a new neuro-growth factor-  
 CC like protein. Its amino acid sequence was deduced from the  
 CC nucleotide sequence (see AAW84341) of a cDNA clone isolated from a  
 CC brain cDNA library. Zneu1's closest human homologue is HSMHC3W5A,  
 CC a gene in the HLA class III region, which is contained in a cosmid  
 CC which contains Notch 4. Zneu1 is also homologous to Notch 4 in its  
 CC EGF-like domains and may be involved in EGF receptor pathways.  
 CC Zneu1 is widely expressed in adult tissues, with high expression in  
 CC heart, placenta, spleen, testis, thyroid, spinal cord and lymph  
 CC node. Zneu1 polypeptide can be used as a growth, maintenance, or

CC differentiation factor in the spinal cord, heart, spleen, testis,  
 CC thyroid and lymph nodes. It may also play a role in breast cancer,  
 CC glioblastomas, and pituitary adenomas. Zneul may be used to treat  
 CC Alzheimer's disease, cancer, to repopulate blood cells after  
 CC chemotherapy, to stimulate myofibroblast proliferation, stimulate  
 CC or inhibit growth factors made in the placenta, in fertility and  
 CC contraception, or to regenerate nerves. Claimed Zneul  
 CC polypeptides (see also AW88382-97), including specific domains of  
 CC Zneul and epitope-bearing portions of Zneul, can be used to raise  
 CC specific antibodies for use e.g. in diagnostic assays.  
 XX  
 SQ Sequence 273 AA;

Query Match 100.0%; Score 1411; DB 20; Length 273;  
 Best Local Similarity 100.0%; Pred. No. 3.5e-88;  
 Matches 254; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TEHAYRPGRRYCAVRAHGDVPSESFVQRYQPFLLTCDGHRACSTYRTIYRTAYRRSPGL 60  
 DB 20 TEHAYRPGRRYCAVRAHGDVPSESFVQRYQPFLLTCDGHRACSTYRTIYRTAYRRSPGL 79  
 QY 61 APARPRYACCPGKRTSGLPGACGAAICQPPCRNGGSCVQPGRCRCFAGWRGDTCCQSDVD 120  
 DB 80 APARPRYACCPGKRTSGLPGACGAAICQPPCRNGGSCVQPGRCRCFAGWRGDTCCQSDVD 139  
 QY 121 ECSARRGGCPORCVNTAGSYWCQWEGHSLSDGTLCPVKGPPRVPAPNPTGVDSAMKEE 180  
 DB 140 ECSARRGGCPORCVNTAGSYWCQWEGHSLSDGTLCPVKGPPRVPAPNPTGVDSAMKEE 199  
 QY 181 VQRLQSRVDLLEEKQLVLAFLHSLASQALEHGLPDPGSLLVHVSFQQLGRIDSLSQISF 240  
 DB 200 VQRLQSRVDLLEEKQLVLAFLHSLASQALEHGLPDPGSLLVHVSFQQLGRIDSLSQISF 259  
 QY 241 LEEQLGSCCKKDS 254  
 DB 260 LEEQLGSCCKKDS 273

RESULT 4  
 AAB44327  
 ID AAB44327 standard; Protein; 273 AA.  
 XX  
 AC AAB44327;

DT 08-FEB-2001 (first entry)

DE Human PRO1449 protein sequence SEQ ID NO:510.

XX Human; secreted protein; transmembrane protein; PRO; EST; cytostatic;  
 KW expressed sequence tag; detection; cancer.  
 XX

OS Homo sapiens.

PN WO200053756-A2.

XX 14-SEP-2000.

XX 18-FEB-2000; 2000WO-US04341.

XX 08-MAR-1999; 99US-US05028.

PR 12-MAR-1999; 99US-0123957.

PR 29-MAR-1999; 99US-0126773.

PR 21-APR-1999; 99US-0130232.

PR 28-APR-1999; 99US-0131445.

PR 14-MAY-1999; 99US-0134287.

PR 23-JUN-1999; 99US-0141037.

PR 26-JUL-1999; 99US-0145698.

PR 29-OCT-1999; 99US-0162506.

PR 30-NOV-1999; 99WO-US28313.

PR 02-DEC-1999; 99WO-US28551.

PR 02-DEC-1999; 99WO-US28565.

PR 16-DEC-1999; 99WO-US30095.

PR 30-DEC-1999; 99WO-US31243.

PR 30-DEC-1999; 99WO-US31274.  
 PR 05-JAN-2000; 2000WO-US00219.  
 PR 06-JAN-2000; 2000WO-US00277.  
 PR 06-JAN-2000; 2000WO-US00376.

PA (GETH) GENENTECH INC.

XX Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;  
 PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;  
 PI Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;  
 PI KJlavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA;  
 PI Shelton DL, Stewart TA, Tumas D, Williams PM, Wood WI;  
 XX

DR WPI; 2000-611443/58.

DR N-PSDB; AAC78587.

XX Novel PRO polypeptides and polynucleotides used in detection methods,  
 PT to target bioactive molecules to specific cells, and to modulate  
 PT cellular activities -

XX Claim 12; Fig 217; 636pp; English.

XX AAC78458 to AAC78599 represent polynucleotide and EST (expressed  
 CC sequence tag) sequences which encode secreted or transmembrane PRO  
 CC polypeptides. The PRO polynucleotides and polypeptides have cytostatic  
 CC activity. The polynucleotides and polypeptides can be used for detecting  
 CC the presence of PRO polypeptides in samples, for linking bioactive  
 CC molecules to cells and for modulating biological activities of cells,  
 CC using the polypeptides for specific targeting. The polypeptide targeting  
 CC can be used to kill the target cells, e.g. for the treatment of cancers.  
 CC The polypeptide pairs provide specific targeting of bioactive molecules  
 CC to cells. AAC78600 to AAC78987 represent PCR primers and probes used in  
 CC the isolation of the PRO polynucleotide sequences.  
 XX

SQ Sequence 273 AA;

Query Match 100.0%; Score 1411; DB 21; Length 273;  
 Best Local Similarity 100.0%; Pred. No. 3.5e-88;  
 Matches 254; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TEHAYRPGRRYCAVRAHGDVPSESFVQRYQPFLLTCDGHRACSTYRTIYRTAYRRSPGL 60  
 DB 20 TEHAYRPGRRYCAVRAHGDVPSESFVQRYQPFLLTCDGHRACSTYRTIYRTAYRRSPGL 79

QY 61 APARPRYACCPGKRTSGLPGACGAAICQPPCRNGGSCVQPGRCRCFAGWRGDTCCQSDVD 120

DB 80 APARPRYACCPGKRTSGLPGACGAAICQPPCRNGGSCVQPGRCRCFAGWRGDTCCQSDVD 139

QY 121 ECSARRGGCPORCVNTAGSYWCQWEGHSLSDGTLCPVKGPPRVPAPNPTGVDSAMKEE 180

DB 140 ECSARRGGCPORCVNTAGSYWCQWEGHSLSDGTLCPVKGPPRVPAPNPTGVDSAMKEE 199

QY 181 VQRLQSRVDLLEEKQLVLAFLHSLASQALEHGLPDPGSLLVHVSFQQLGRIDSLSQISF 240

DB 200 VQRLQSRVDLLEEKQLVLAFLHSLASQALEHGLPDPGSLLVHVSFQQLGRIDSLSQISF 259

QY 241 LEEQLGSCCKKDS 254

DB 260 LEEQLGSCCKKDS 273

RESULT 5

AAB18675

ID AAB18675 standard; Protein; 273 AA.

XX AAB18675;

AC AAB18675;

XX DT 22-JAN-2001 (first entry)

XX Amino acid sequence of a human a PRO1449 polypeptide.

DE Notch 4 homologue; PRO320; PRO938; PRO1031; PRO296; PRO1449;

XX angiogenesis; cardiovascularisation; PRO1330; cardiovascular disorder;

XX endothelial disorder; angiogenic disorder; cancer; trauma; wound;  
 KW atherosclerosis; cardiac hypertrophy.  
 XX Homo sapiens.  
 XX Key Location/Qualifiers  
 FH Peptide 1..19  
 FT /note= "signal sequence"  
 FT Modified-site 19..25  
 FT /note= "N-myristoylation site"  
 FT Modified-site 26..30  
 FT /note= "amidation site"  
 FT Modified-site 78..84  
 FT /note= "N-myristoylation site"  
 FT Modified-site 93..97  
 FT /note= "CAMP- and GMP-dependent protein kinase phosphorylation site"  
 FT Modified-site 97..103  
 FT /note= "N-myristoylation site"  
 FT Modified-site 100..106  
 FT /note= "N-myristoylation site"  
 FT Modified-site 103..109  
 FT /note= "N-myristoylation site"  
 FT Region 123..135  
 FT /note= "EGF-like domain cysteine pattern signature"  
 FT Region 130..133  
 FT /note= "cell attachment sequence"  
 FT Modified-site 152..164  
 FT /note= "aspartic acid and asparagine hydroxylation site"  
 FT Modified-site 157..163  
 FT /note= "N-myristoylation site"  
 FT Modified-site 191..197  
 FT /note= "N-myristoylation site"  
 FT Modified-site 265..271  
 FT /note= "N-myristoylation site"  
 XX WO200053752-A2.  
 XX PD 14-SEP-2000.  
 XX PF 30-DEC-1999; 99WO-US31274.  
 XX PR 08-MAR-1999; 99WO-US05028.  
 XX PR 21-APR-1999; 99US-0130232.  
 XX PR 26-APR-1999; 99US-0131022.  
 XX PR 28-APR-1999; 99US-0131445.  
 XX PR 14-MAY-1999; 99US-0134287.  
 XX PR 02-DEC-1999; 99WO-US28565.  
 XX (GETH ) GENENTECH INC.  
 XX PA Baker KP, Ferrara N, Goddard A, Gurney AL, Hillan KJ, Williams PM,  
 PI Wood WI;  
 XX WPI; 2000-638138/61.  
 XX N-PSDB; AAA5704.  
 XX A composition useful for treatment and diagnosis of a cardiovascular,  
 PT endothelial or angiogenic disorder, especially cancer, comprises (an  
 PT agonist or antagonist of) a PRO320, PRO938, PRO1031, PRO296, PRO213,  
 PT PRO130 or PRO1449 polypeptide -  
 XX Claim 67; Fig 14; 152pp; English.  
 XX The present sequence represents PRO1449, a human notch 4 homologue.  
 CC The specification describes PRO320, PRO938, PRO1031, PRO296, PRO213,  
 CC PRO130 and PRO1449 polypeptides. The polypeptides promoter or  
 CC inhibit angiogenesis and cardiovascularisation in mammals. The  
 CC polypeptides are used for the treatment and diagnosis of a  
 CC cardiovascular, endothelial or angiogenic disorder, especially  
 CC cancer. Disorders that can be diagnosed, treated or prevented by  
 CC the polypeptides of the invention include trauma such as wounds,  
 CC atherosclerosis, and cardiac hypertrophy.

XX SQ Sequence 273 AA;  
 Query Match 100.0%; Score 1411; DB 21; Length 273;  
 Best Local Similarity 100.0%; Pred. No. 3.5e-88;  
 Matches 254; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TEHAYRPGRRVCAVAHAGDPVSESFVORVYOPFLTTCDGHRACSTYRTIYRTAYRSPGL 60  
 DB 20 TEHAYRPGRRVCAVAHAGDPVSESFVORVYOPFLTTCDGHRACSTYRTIYRTAYRSPGL 79  
 QY 61 APARRRYACCGWKRISGLPACGAATQPPCRNGSGCVOPGRRCRPAWNGDTCCSDVD 120  
 DB 80 APARRRYACCGWKRISGLPACGAATQPPCRNGSGCVOPGRRCRPAWNGDTCCSDVD 139  
 QY 121 EGSARRGGCPORCVNTAGSYWCQCEGHSLSADGTLCPKGGPRVA PNPVGVDSAMKEE 180  
 DB 140 EGSARRGGCPORCVNTAGSYWCQCEGHSLSADGTLCPKGGPRVA PNPVGVDSAMKEE 199  
 QY 181 VORLQSRVDLLEKQLQVLAFLHSLASQALEHGLPDPGSLVHSPQOLGRIDSLSQISF 240  
 DB 200 VORLQSRVDLLEKQLQVLAFLHSLASQALEHGLPDPGSLVHSPQOLGRIDSLSQISF 259  
 QY 241 LEEQLGSGSCCKKDS 254  
 DB 260 LEEQLGSGSCCKKDS 273  
 RESULT 6  
 AAB24044  
 ID AAB24044 standard; Protein; 273 AA.  
 XX AC AAB24044;  
 XX DT 25-JAN-2001 (first entry)  
 XX DE Human PRO1449 protein sequence SEQ ID NO:8.  
 XX KW Human; tumour; diagnosis; neoplastic disease; identification; cancer;  
 KW tumorigenesis; detection; neoplastic cell growth; proliferation;  
 KW cytostatic; anti-inflammatory; immunomodulatory; inflammatory disorder;  
 KW immunological disorder.  
 XX OS Homo sapiens.  
 XX WO200053754-A1.  
 XX PD 14-SEP-2000.  
 XX PF 06-JAN-2000; 2000WO-US00277.  
 XX PR 08-MAR-1999; 99WO-US05028.  
 XX PR 12-MAR-1999; 99US-0123957.  
 XX PR 29-MAR-1999; 99US-0126773.  
 XX PR 21-APR-1999; 99US-0130232.  
 XX PR 28-APR-1999; 99US-0131445.  
 XX PR 05-OCT-1999; 99WO-US23089.  
 XX PR 30-NOV-1999; 99WO-US28313.  
 XX PR 02-DEC-1999; 99WO-US28565.  
 XX PR 02-DEC-1999; 99WO-US28564.  
 XX PR 30-DEC-1999; 99WO-US31243.  
 XX PR 30-DEC-1999; 99WO-US31274.  
 XX (GETH ) GENENTECH INC.  
 XX PA Baker KP, Desauvage FJ, Goddard A, Gurney AL, Klein RD, Roy MA,  
 PI Wood WI;  
 XX WPI; 2000-572269/53.  
 XX N-PSDB; AAC58228.  
 XX New isolated antibody for use in compositions and methods for the  
 PT diagnosis and treatment of neoplastic cell growth and proliferation in

PT mammals, including humans, and in monitoring tumor treatment -

PS Claim 61; Fig 8; 195pp; English.

XX The present invention describes an isolated antibody (Ab) that binds to  
 CC one of the human proteins (P) designated PRO1330, PRO1449,  
 CC PRO237, PRO324, PRO351, PRO362, PRO615, PRO538, PRO3664, PRO618,  
 CC PRO772, PRO703, PRO792 or PRO474. The Ab can be used in compositions  
 CC and methods for the diagnosis and treatment of neoplastic cell growth  
 CC and proliferation in mammals, including humans. Genes and polypeptides  
 CC encoded by them, that are amplified in the genome of a tumour cell, can  
 CC be identified and are useful targets for the treatment and prevention of  
 CC certain cancers and may be used to monitor tumour treatment. Compounds  
 CC that inhibit the expression or activity of the identified polypeptides  
 CC can be identified and used as antagonists. Benign or malignant tumours,  
 CC inflammatory disorders and immunological disorders can be treated.  
 CC AAC58123 to AAC58224 represent hybridisation probes and PCR primers used  
 CC in the isolation of the human PRO sequences. AAC58225 to AAC58241 and  
 CC AAB24041 to AAB24056 represent human PRO polynucleotide and protein  
 CC sequences given in the exemplification of the present invention.

XX SQ Sequence 273 AA;

Query Match 100.0%; Score 1411; DB 21; Length 273;

Best Local Similarity 100.0%; Pred. No. 3.5e-88;

Matches 254; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TEHAYRFGRRYCAVRAHGDVPVSEFVQRYQPFLLTCDGHRACSTYRTIYRTARRSPGL 60

Db 20 TEHAYRFGRRYCAVRAHGDVPVSEFVQRYQPFLLTCDGHRACSTYRTIYRTARRSPGL 79

Qy 61 APAPRYACCGWRTSGLPACAAACOPPCRNCGSCVQPCRCRCAGWRGTCQSDVD 120

Db 80 APAPRYACCGWRTSGLPACAAACOPPCRNCGSCVQPCRCRCAGWRGTCQSDVD 139

Qy 121 ECSARRGCPORCVNTAGSWCQWEGHLSADGTLCPKGGPPRVAPNPTGVDSAMKEE 180

Db 140 ECSARRGCPORCVNTAGSWCQWEGHLSADGTLCPKGGPPRVAPNPTGVDSAMKEE 199

Qy 181 VORLQSRVLLLEKQLVLAFLHSLASQALEHGLPDPGSLLVHVSFQQLGRIDSLSQISF 240

Db 200 VORLQSRVLLLEKQLVLAFLHSLASQALEHGLPDPGSLLVHVSFQQLGRIDSLSQISF 259

Qy 241 LEEOLGSCSCKKDS 254

Db 260 LEEOLGSCSCKKDS 273

RESULT 7

AAB01376

ID AAB01376 standard; Protein; 273 AA.

XX AAB01376;

XX 20-OCT-2000 (first entry)

XX Neuron-associated protein.

XX Neuron associated protein; NEUAP; neurological disorder; epilepsy;  
 KW ischemic cerebrovascular disease; stroke; cerebral neoplasm;  
 KW Alzheimer's disease; Pick's disease; Huntington's disease;  
 KW dementia; Parkinson's disease; demyelinating disease; meningitis;  
 KW prion disease; kuru; Creutzfeldt-Jakob disease; neurofibromatosis;  
 KW cerebral palsy; muscular dystrophy; central nervous system; CNS;  
 KW peripheral nervous system; PNS; myopathy; schizophrenia;  
 KW actinic keratosis; arteriosclerosis; atherosclerosis; bursitis;  
 KW cirrhosis; hepatitis; mixed connective tissue disease; MCTD;  
 KW myelofibrosis; paroxysmal nocturnal haemoglobinuria; cancer;  
 KW autoimmune disease; inflammation; acquired immunodeficiency syndrome;  
 KW AIDS; Addison's disease; adult respiratory distress syndrome;  
 KW allergy; ankylosing spondylitis; amyloidosis; anaemia; asthma;  
 KW werner syndrome; trauma; human.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 1..19

FT Modified-site 54 /label= Signal peptide

FT Modified-site 64 /note= "Potential phosphorylation site"

FT Modified-site 96 /note= "Potential phosphorylation site"

FT Domain 107..134 /note= "Potential phosphorylation site"

FT Region 130..132 /label= EGF-like domain

FT Modified-site 136 /label= Cell attachment sequence

FT Domain 141..176 /note= "Potential phosphorylation site"

FT Modified-site 142 /label= EGF-like domain

FT Modified-site 152..163 /note= "Potential phosphorylation site"

FT Modified-site 190 /label= Asx hydroxylation site

FT Modified-site 205 /note= "Potential phosphorylation site"

FT Modified-site 252 /note= "Potential phosphorylation site"

FT Modified-site 258 /note= "Potential phosphorylation site"

FT Modified-site 268 /note= "Potential phosphorylation site"

FT Modified-site 273 /note= "Potential phosphorylation site"

XX WO200034477-A2.

XX 15-JUN-2000.

XX 10-DEC-1999; 99WO-US30408.

XX 11-DEC-1998; 98US-0210083.

XX 11-DEC-1998; 98US-9123456.

XX 09-FEB-1999; 99US-0119365.

XX 16-MAR-1999; 99US-0124687.

XX (INCY-) INCYTE PHARM INC.

XX Tang YT, Yue H, Baughn MR, Hillman JL, Lal P, Au-young J, Yang J;

PI Lu DAM, Azimzal Y;

XX WPI; 2000-423423/36.

XX N-PSDB; AAA47417.

XX New human neuron-associated proteins and polynucleotides encoding them,

XX useful for diagnosis, treatment and prevention of cell proliferative

XX disorders including cancer, neuronal and neurological disorders

XX Claim 1; Page 97; 145pp; English.

XX Human neuron-associated proteins (NEUAP) can be used for

XX treating or preventing a disorder associated with decreased

XX expression or activity of NEUAP. Antagonists of NEUAP are useful for

XX treating or preventing disorder associated with increased expression

XX or activity of NEUAP. NEUAP or their fragments or derivatives are

XX useful for treating neurological disorder such as epilepsy, ischemic

XX cerebrovascular disease, stroke, cerebral neoplasms, Alzheimer's

XX disease, Pick's disease, Huntington's disease, dementia and

XX Parkinson's disease. NEUAPs are also useful for treating other

XX demyelinating diseases, bacterial and viral meningitis, prion

XX diseases including kuru, Creutzfeldt-Jakob disease, nutritional and

XX metabolic diseases of the nervous system, neurofibromatosis, other





```

PR 02-JUL-1999; 99JP-0188835.
XX (SAGA) SAGAMI CHEM RES CENT.
PA (PROT-) PROTEGENE INC.
XX Kato S, Kimura T;
XX WPI; 2001-071581/08.
DR N-ESDB; AAF28680, AAF28690.
XX New human proteins with hydrophobic domains, useful for the treatment
XX of immune disorders, tumors, allergic conditions, thrombosis and
XX microbial infection -
XX Claim 1; Pages 97-98; 153pp; English.
XX The present invention relates to human proteins (AAB61608-AAB61617) and
XX their coding sequences (AAF28679-AAF28698). The proteins of the present
XX invention have hydrophobic domains and can be used for the treatment of
XX various immune deficiencies and disorders, such as severe combined
XX immunodeficiency (SCID), multiple sclerosis, rheumatoid arthritis,
XX autoimmune pulmonary inflammation, graft-versus-host disease and
XX Guillain-Barre syndrome. The proteins may also be useful in the treatment
XX of allergic reactions and conditions, such as asthma and in regulation of
XX haematopoiesis or lymphoid cell deficiencies. The proteins may also have
XX utility in compositions used for bone, cartilage, tendon and/or nerve
XX tissue growth or regeneration as well as wound healing and in the
XX treatment of burns. The proteins may be used in the treatment of
XX periodontal disease and in other tooth repair processes. Other uses
XX include treatment of thrombolytic and haemostatic conditions, treatment
XX or prevention of tumours and inhibiting infection by bacteria, viruses,
XX fungi and other parasites.
XX Sequence 273 AA;
XX
Query Match 100.0%; Score 1411; DB 22; Length 273;
Best Local Similarity 100.0%; Pred. No. 3.5e-88;
Matches 254; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TEHAYRPGRRCAVRAHGDVPSESFVQRVYQPFLLTCDGHRACSTYRTYRTAYRRSPGL 60
Db 20 TEHAYRPGRRCAVRAHGDVPSESFVQRVYQPFLLTCDGHRACSTYRTYRTAYRRSPGL 79
Qy 61 APAPRYACCPGKRTSLGPGACGAAICQPPCRNGGSCVQPGRCRCAGWRGTCQSDVD 120
Db 80 APAPRYACCPGKRTSLGPGACGAAICQPPCRNGGSCVQPGRCRCAGWRGTCQSDVD 139
Qy 121 ECSARRGGCPQRCVNTAGSYWCQWEGHLSADGTLCPVKGPPRPVAPNPTGVDSAMKEE 180
Db 140 ECSARRGGCPQRCVNTAGSYWCQWEGHLSADGTLCPVKGPPRPVAPNPTGVDSAMKEE 199
Qy 181 VQRLOSRVLLLEKILQLVLAPLHSLASQALEHGLPDPGSLLVHVSFQQLGRIDSLSEQISF 240
Db 200 VQRLOSRVLLLEKILQLVLAPLHSLASQALEHGLPDPGSLLVHVSFQQLGRIDSLSEQISF 259
Qy 241 LEEQLGSCSKKDS 254
Db 260 LEEQLGSCSKKDS 273
RESULT 10
AAY41769
ID AAY41769 standard; Protein; 273 AA.
XX
XX AAY41769;
AC
XX 07-DEC-1999 (first entry)
DT
XX Human PRO213-1 protein sequence.
DE
XX Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation;
XX probe; blood coagulation disorder; cancer; cellular adhesion disorder;
XX secreted protein; transmembrane protein.
KW

```

```

XX OS Homo sapiens.
XX PN WO9946281-A2.
XX PD 16-SEP-1999.
XX PF 08-MAR-1999;
XX 99WO-US05028.
XX 10-MAR-1998;
PR 98US-0077450.
PR 11-MAR-1998;
PR 98US-0077632.
PR 11-MAR-1998;
PR 98US-0077641.
PR 11-MAR-1998;
PR 98US-0077649.
PR 12-MAR-1998;
PR 98US-0077751.
PR 13-MAR-1998;
PR 98US-0078004.
PR 17-MAR-1998;
PR 98US-0040220.
PR 20-MAR-1998;
PR 98US-0078886.
PR 20-MAR-1998;
PR 98US-0078910.
PR 20-MAR-1998;
PR 98US-0078936.
PR 20-MAR-1998;
PR 98US-0078939.
PR 25-MAR-1998;
PR 98US-0079294.
PR 26-MAR-1998;
PR 98US-0079656.
PR 27-MAR-1998;
PR 98US-0079663.
PR 27-MAR-1998;
PR 98US-0079664.
PR 27-MAR-1998;
PR 98US-0079689.
PR 27-MAR-1998;
PR 98US-0079728.
PR 27-MAR-1998;
PR 98US-0079786.
PR 30-MAR-1998;
PR 98US-0079920.
PR 30-MAR-1998;
PR 98US-0079923.
PR 31-MAR-1998;
PR 98US-0080105.
PR 31-MAR-1998;
PR 98US-0080107.
PR 31-MAR-1998;
PR 98US-0080165.
PR 31-MAR-1998;
PR 98US-0080194.
PR 01-APR-1998;
PR 98US-0080327.
PR 01-APR-1998;
PR 98US-0080328.
PR 01-APR-1998;
PR 98US-0080333.
PR 01-APR-1998;
PR 98US-0080334.
PR 08-APR-1998;
PR 98US-0081049.
PR 08-APR-1998;
PR 98US-0081070.
PR 08-APR-1998;
PR 98US-0081071.
PR 09-APR-1998;
PR 98US-0081195.
PR 09-APR-1998;
PR 98US-0081203.
PR 09-APR-1998;
PR 98US-0081229.
PR 15-APR-1998;
PR 98US-0081817.
PR 15-APR-1998;
PR 98US-0081838.
PR 15-APR-1998;
PR 98US-0081952.
PR 15-APR-1998;
PR 98US-0081955.
PR 21-APR-1998;
PR 98US-0082568.
PR 21-APR-1998;
PR 98US-0082569.
PR 22-APR-1998;
PR 98US-0082700.
PR 22-APR-1998;
PR 98US-0082704.
PR 22-APR-1998;
PR 98US-0082804.
PR 23-APR-1998;
PR 98US-0082767.
PR 23-APR-1998;
PR 98US-0082796.
PR 27-APR-1998;
PR 98US-0083336.
PR 28-APR-1998;
PR 98US-0083322.
PR 29-APR-1998;
PR 98US-0083392.
PR 29-APR-1998;
PR 98US-0083495.
PR 29-APR-1998;
PR 98US-0083496.
PR 29-APR-1998;
PR 98US-0083499.
PR 29-APR-1998;
PR 98US-0083500.
PR 29-APR-1998;
PR 98US-0083545.
PR 29-APR-1998;
PR 98US-0083554.
PR 29-APR-1998;
PR 98US-0083558.
PR 29-APR-1998;
PR 98US-0083559.
PR 30-APR-1998;
PR 98US-0083742.
PR 05-MAY-1998;
PR 98US-0084366.
PR 06-MAY-1998;
PR 98US-0084414.
PR 06-MAY-1998;
PR 98US-0084441.
PR 07-MAY-1998;
PR 98US-0084598.
PR 07-MAY-1998;
PR 98US-0084600.
PR 07-MAY-1998;
PR 98US-0084627.
PR 07-MAY-1998;
PR 98US-0084637.

```



PR 29-APR-1998; 98US-0083392.  
PR 29-APR-1998; 98US-0083495.  
PR 29-APR-1998; 98US-0083496.  
PR 29-APR-1998; 98US-0083499.  
PR 29-APR-1998; 98US-0083500.  
PR 29-APR-1998; 98US-0083545.  
PR 29-APR-1998; 98US-0083545.  
PR 29-APR-1998; 98US-0083554.  
PR 29-APR-1998; 98US-0083558.  
PR 29-APR-1998; 98US-0083559.  
PR 30-APR-1998; 98US-0083742.  
PR 05-MAY-1998; 98US-0084366.  
PR 06-MAY-1998; 98US-0084414.  
PR 06-MAY-1998; 98US-0084441.  
PR 07-MAY-1998; 98US-0084598.  
PR 07-MAY-1998; 98US-0084600.  
PR 07-MAY-1998; 98US-0084627.  
PR 07-MAY-1998; 98US-0084637.  
PR 07-MAY-1998; 98US-0084639.  
PR 07-MAY-1998; 98US-0084640.  
PR 07-MAY-1998; 98US-0084643.  
PR 13-MAY-1998; 98US-0085323.  
PR 13-MAY-1998; 98US-0085338.  
PR 13-MAY-1998; 98US-0085339.  
PR 15-MAY-1998; 98US-0085573.  
PR 15-MAY-1998; 98US-0085579.  
PR 15-MAY-1998; 98US-0085580.  
PR 15-MAY-1998; 98US-0085582.  
PR 15-MAY-1998; 98US-0085582.  
PR 15-MAY-1998; 98US-0085689.  
PR 15-MAY-1998; 98US-0085697.  
PR 15-MAY-1998; 98US-0085704.  
PR 18-MAY-1998; 98US-0086023.  
PR 22-MAY-1998; 98US-0086392.  
PR 22-MAY-1998; 98US-0086414.  
PR 22-MAY-1998; 98US-0086430.  
PR 22-MAY-1998; 98US-0086486.  
PR 28-MAY-1998; 98US-0087098.  
PR 28-MAY-1998; 98US-0087106.  
PR 28-MAY-1998; 98US-0087208.  
PR 30-JUL-1998; 98US-0094651.  
PR 11-SEP-1998; 98US-0100038.  
XX (GETH ) GENENTECH INC.  
XX  
XX Wood WI, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;  
XX WPI; 1999-551358/46.  
XX N-PSDB; AAZ34312.  
XX  
XX New secreted and transmembrane polypeptides and their polynucleotides,  
XX useful for treating blood coagulation disorders, cancers and cellular  
XX adhesion disorders -  
XX  
XX Claim 12; Fig 215; 530pp; English.  
XX  
XX The present invention describes secreted and transmembrane polypeptides  
XX and their polynucleotides. The nucleotide sequences are useful as  
XX sources of probes, primers, for chromosome mapping, and for generation  
XX of antisense sequences. They can also be used to create transgenic  
XX animals. The proteins can be used to treat a variety of diseases and  
XX disorders, depending on their function. Diseases that may be treated  
XX include blood coagulation disorders, cancers and cellular adhesion  
XX disorders. They may also be used to raise antibodies. AAZ33891 to  
XX AAZ34338, and AAY41685 to AAY41774 represent polynucleotide and  
XX polypeptide sequence given in the exemplification of the present  
XX invention.  
XX  
XX Sequence 273 AA;  
XX  
XX Query Match 99.9%; Score 1410; DB 20; Length 273;  
XX Best Local Similarity 99.6%; Pred. No. 4.1e-88;  
XX Matches 253; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TEHAYRPGRRVCAVRAHGDVSESVQVRYQPFLLTTCGHRACSTYRTIYRTAYRRSPGL 60  
Db 20 TEHAYRPGRRVCAVRAHGDVSESVQVRYQPFLLTTCGHRACSTYRTIYRTAYRRSPGL 79  
QY 61 APARPRYACCPGKRTSGLPACGAAIQQPCNRNGSCVQPCRCPCAGWGRDTCQSDVD 120  
Db 80 APARPRYACCPGKRTSGLPACGAAIQQPCNRNGSCVQPCRCPCAGWGRDTCQSDVD 139  
QY 121 ECSARRGCPQRCVNTAGSYWCQWEGHSLSDAGTLCVPGKGPVPAVNPVTGVDAMKEE 180  
Db 140 ECSARRGCPQRCVNTAGSYWCQWEGHSLSDAGTLCVPGKGPVPAVNPVTGVDAMKEE 199  
QY 181 VORLOSRYDLEELQLVLAPLHSLASQALBHLGPDGSLVHSPQQLGRIDSUSEQISF 240  
Db 200 VORLOSRYDLEELQLVLAPLHSLASQALBHLGPDGSLVHSPQQLGRIDSUSEQISF 259  
QY 241 LEEQLGSCCKKDS 254  
Db 260 LEEQLGSCCKKDS 273  
RESULT 12  
AAB44325  
ID AAB44325 standard; Protein; 273 AA.  
XX  
XX AAB44325;  
AC  
XX  
XX 08-FEB-2001 (first entry)  
XX  
XX Human PRO213-1 protein sequence SEQ ID NO:506.  
DE  
XX  
XX Human; secreted protein; transmembrane protein; PRO; EST; cytostatic;  
XX expressed sequence tag; detection; cancer.  
XX  
XX Homo sapiens.  
XX  
XX WO2000053756-A2.  
XX  
XX  
XX 14-SEP-2000.  
XX  
XX  
XX 18-FEB-2000; 2000WO-US04341.  
XX  
XX 08-MAR-1999; 99WO-US05028.  
XX 12-MAR-1999; 99US-0123957.  
XX 29-MAR-1999; 99US-0126773.  
XX 21-APR-1999; 99US-0130232.  
XX 28-APR-1999; 99US-0131445.  
XX 14-MAY-1999; 99US-0134287.  
XX 23-JUN-1999; 99US-0141037.  
XX 26-JUL-1999; 99US-0145698.  
XX 29-OCT-1999; 99US-0162506.  
XX 30-NOV-1999; 99WO-US28313.  
XX 02-DEC-1999; 99WO-US28551.  
XX 02-DEC-1999; 99WO-US28565.  
XX 16-DEC-1999; 99WO-US30095.  
XX 30-DEC-1999; 99WO-US31243.  
XX 30-DEC-1999; 99WO-US31274.  
XX 05-JAN-2000; 2000WO-US00219.  
XX 06-JAN-2000; 2000WO-US00277.  
XX 06-JAN-2000; 2000WO-US00376.  
XX (GETH ) GENENTECH INC.  
XX  
XX Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;  
XX Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;  
XX Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;  
XX Kljavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA;  
XX Shelton DL, Stewart TA, Tumas D, Williams PM, Wood WI;  
XX  
XX WPI; 2000-611443/58.  
XX N-PSDB; AAC78585.  
XX  
XX Novel PRO polypeptides and polynucleotides used in detection methods,

PT to target bioactive molecules to specific cells, and to modulate  
PT cellular activities -  
XX Claim 12, Fig 213; 636pp; English.  
XX  
XX AAC78458 to AAC78599 represent polynucleotide and EST (expressed  
CC sequence tag) sequences which encode secreted or transmembrane PRO  
CC polypeptides. The PRO polynucleotides and polypeptides have cytostatic  
CC activity. The polynucleotides and polypeptides can be used for detecting  
CC the presence of PRO polypeptides in samples, for linking bioactive  
CC molecules to cells and for modulating biological activities of cells,  
CC using the polypeptides for specific targeting. The polypeptide targeting  
CC can be used to kill the target cells, e.g. for the treatment of cancers.  
CC The polypeptide pairs provide specific targeting of bioactive molecules  
CC to cells. AAC78600 to AAC78987 represent PCR primers and probes used in  
CC the isolation of the PRO polynucleotide sequences.  
CC  
XX Sequence 273 AA;  
SQ

Query Match 99.9%; Score 1410; DB 21; Length 273;  
Best Local Similarity 99.6%; Pred. No. 4.1e-88;  
Matches 253; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TEHAYRPGRRVCAVAHAGDPVSESVFVQRYOPFLTTCDGHRACSTYRTTYRTAYRRSPGL 60  
DB 20 TEHAYRPGRRVCAVAHAGDPVSESVFVQRYOPFLTTCDGHRACSTYRTTYRTAYRRSPGL 79  
QY 61 APARPRVACCPGMRKRTSGLPAGCAAIQOPPCRNAGSCVQPRGRCPCPAGMRGDTQSDVD 120  
DB 80 APARPRVACCPGMRKRTSGLPAGCAAIQOPPCRNAGSCVQPRGRCPCPAGMRGDTQSDVD 139  
QY 121 ECSARRGGCPQRCINTAGSYWCQCEGHSLSADGTLCPVKGGPPRVANPTGVDSAMKEE 180  
DB 140 ECSARRGGCPQRCINTAGSYWCQCEGHSLSADGTLCPVKGGPPRVANPTGVDSAMKEE 199  
QY 181 VQRLQSRVDLLEKQLQVLAHPLHSLASQALHGLPDPGSLLVHSPQUGRIDSLSEQISF 240  
DB 200 VQRLQSRVDLLEKQLQVLAHPLHSLASQALHGLPDPGSLLVHSPQUGRIDSLSEQISF 259  
QY 241 LEEQLGSCSCCKKDS 254  
DB 260 LEEQLGSCSCCKKDS 273  
XX

RESULT 13  
AAB44326  
ID AAB44326 standard; Protein; 273 AA.  
AC AAB44326;  
XX  
DT 08-FEB-2001 (first entry)  
XX  
DE Human PRO1330 protein sequence SEQ ID NO:508.  
XX  
KM Human; secreted protein; transmembrane protein; PRO; EST; cytostatic;  
XX expressed sequence tag; detection; cancer.  
OS Homo sapiens.  
XX  
PN WO200053756-A2.  
PD 14-SEP-2000.  
XX  
PF 18-FEB-2000; 2000WO-US04341.  
XX  
PR 08-MAR-1999; 99WO-US05028.  
PR 12-MAR-1999; 99US-0123957.  
PR 29-MAR-1999; 99US-0126773.  
PR 21-APR-1999; 99US-0130232.  
PR 28-APR-1999; 99US-0131445.  
PR 14-MAY-1999; 99US-0134287.  
PR 23-JUN-1999; 99US-0141037.  
PR 26-JUL-1999; 99US-0145698.  
XX

PR 29-OCT-1999; 99US-0162506.  
PR 30-NOV-1999; 99WO-US28313.  
PR 02-DEC-1999; 99WO-US28351.  
PR 02-DEC-1999; 99WO-US28351.  
PR 16-DEC-1999; 99WO-US30095.  
PR 30-DEC-1999; 99WO-US31243.  
PR 30-DEC-1999; 99WO-US31274.  
PR 05-JAN-2000; 2000WO-US00219.  
PR 06-JAN-2000; 2000WO-US00277.  
PR 06-JAN-2000; 2000WO-US00376.  
XX  
XX (GENTH ) GENENTECH INC.  
XX  
XX Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;  
PI Perrera N, Filvaroff E, Fong S, Gao W, Garber H, Gerritsen ME;  
PI Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;  
PI Kijavitt L, Kuo SS, Napier MA, Pan J, Peoni NF, Roy MA;  
PI Shelton DL, Stewart TA, Tumas D, Williams PM, Wood WT;  
XX  
XX MPI; 2000-611443/58.  
XX  
XX N-PSDB; AAC78586.  
XX

PT Novel PRO polypeptides and polynucleotides used in detection methods,  
PT to target bioactive molecules to specific cells, and to modulate  
PT cellular activities -  
XX  
XX Claim 12; Fig 215; 636pp; English.  
XX  
XX AAC78458 to AAC78599 represent polynucleotide and EST (expressed  
CC sequence tag) sequences which encode secreted or transmembrane PRO  
CC polypeptides. The PRO polynucleotides and polypeptides have cytostatic  
CC activity. The polynucleotides and polypeptides can be used for detecting  
CC the presence of PRO polypeptides in samples, for linking bioactive  
CC molecules to cells and for modulating biological activities of cells,  
CC using the polypeptides for specific targeting. The polypeptide targeting  
CC can be used to kill the target cells, e.g. for the treatment of cancers.  
CC The polypeptide pairs provide specific targeting of bioactive molecules  
CC to cells. AAC78600 to AAC78987 represent PCR primers and probes used in  
CC the isolation of the PRO polynucleotide sequences.  
CC  
XX Sequence 273 AA;  
SQ

Query Match 99.9%; Score 1410; DB 21; Length 273;  
Best Local Similarity 99.6%; Pred. No. 4.1e-88;  
Matches 253; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TEHAYRPGRRVCAVAHAGDPVSESVFVQRYOPFLTTCDGHRACSTYRTTYRTAYRRSPGL 60  
DB 20 TEHAYRPGRRVCAVAHAGDPVSESVFVQRYOPFLTTCDGHRACSTYRTTYRTAYRRSPGL 79  
QY 61 APARPRVACCPGMRKRTSGLPAGCAAIQOPPCRNAGSCVQPRGRCPCPAGMRGDTQSDVD 120  
DB 80 APARPRVACCPGMRKRTSGLPAGCAAIQOPPCRNAGSCVQPRGRCPCPAGMRGDTQSDVD 139  
QY 121 ECSARRGGCPQRCINTAGSYWCQCEGHSLSADGTLCPVKGGPPRVANPTGVDSAMKEE 180  
DB 140 ECSARRGGCPQRCINTAGSYWCQCEGHSLSADGTLCPVKGGPPRVANPTGVDSAMKEE 199  
QY 181 VQRLQSRVDLLEKQLQVLAHPLHSLASQALHGLPDPGSLLVHSPQUGRIDSLSEQISF 240  
DB 200 VQRLQSRVDLLEKQLQVLAHPLHSLASQALHGLPDPGSLLVHSPQUGRIDSLSEQISF 259  
QY 241 LEEQLGSCSCCKKDS 254  
DB 260 LEEQLGSCSCCKKDS 273  
XX

RESULT 14  
AAB18673  
ID AAB18673 standard; Protein; 273 AA.  
AC AAB18673;  
XX

22-JAN-2001 (first entry)  
 Amino acid sequence of a human a PRO213 polypeptide.  
 Growth arrest-specific gene 6 protein homologue; PRO320; PRO938; PRO1031;  
 PRO296; PRO13; PRO1449; angiogenesis; cardiovascularisation; PRO1330;  
 cardiovascular disorder; endothelial disorder; angiogenic disorder;  
 cancer; trauma; wound; arteriosclerosis; cardiac hypertrophy.  
 Homo sapiens.

Key Location/Qualifiers  
 Peptide 1..19  
 Modified-site /note= "signal sequence"  
 /note= "N-myristoylation site"  
 Modified-site 26..30  
 /note= "amidation site"  
 Modified-site 78..84  
 /note= "N-myristoylation site"  
 Modified-site 93..97  
 /note= "cAMP- and cGMP-dependent protein kinase phosphorylation site"  
 Modified-site 97..103  
 /note= "N-myristoylation site"  
 Modified-site 100..106  
 /note= "N-myristoylation site"  
 Modified-site 103..109  
 /note= "N-myristoylation site"  
 Region 123..135  
 /note= "EGF-like domain cysteine pattern signature"  
 Region 130..133  
 /note= "cell attachment sequence"  
 Modified-site 152..164  
 /note= "aspartic acid and asparagine hydroxylation site"  
 Modified-site 157..163  
 /note= "N-myristoylation site"  
 Modified-site 191..197  
 /note= "N-myristoylation site"  
 Modified-site 265..271  
 /note= "N-myristoylation site"

WO200053752-A2.  
 14-SEP-2000.  
 30-DEC-1999; 99WO-US31274.  
 08-MAR-1999; 99WO-US05028.  
 21-APR-1999; 99US-0130232.  
 26-APR-1999; 99US-0131022.  
 28-APR-1999; 99US-0131445.  
 14-MAY-1999; 99US-0134287.  
 02-DEC-1999; 99WO-US28565.  
 (GETH ) GENENTECH INC.  
 Baker KP, Ferrara N, Goddard A, Gurney AL, Hillan KJ, Williams PM;  
 Wood WL;  
 WPI; 2000-638138/61.  
 N-PSDB; AAA75702.  
 A composition useful for treatment and diagnosis of a cardiovascular,  
 endothelial or angiogenic disorder, especially cancer, comprises (an  
 agonist or antagonist of) a PRO320, PRO938, PRO1031, PRO296, PRO213,  
 PRO1330 or PRO1449 polypeptide -  
 Claim 67; Fig 10; 152pp; English.  
 The present sequence represents PRO213, a human growth arrest-specific  
 gene 6 protein homologue. The specification describes PRO320, PRO938,  
 PRO1031, PRO296, PRO213, PRO1330 and PRO1449 polypeptides. The

CC polypeptides promoter or inhibit angiogenesis and cardiovascularisation  
 CC in mammals. The polypeptides are used for the treatment and diagnosis  
 CC of a cardiovascular, endothelial or angiogenic disorder, especially  
 CC cancer. Disorders that can be diagnosed, treated or prevented by  
 CC the polypeptides of the invention include trauma such as wounds,  
 CC arteriosclerosis, and cardiac hypertrophy.  
 XX Sequence 273 AA;  
 SQ Query Match 99.9%; Score 1410; DB 21; Length 273;  
 Best Local Similarity 99.6%; Pred. No. 4.le-88;  
 Matches 253; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TEHAYRPGRRVCAVRAHCDPVSESFVQRYQPELTTCGHRACSTYRTIYRTAVRRSPGL 60  
 DB 20 TEHAYRPGRRVCAVRAHCDPVSESFVQRYQPELTTCGHRACSTYRTIYRTAVRRSPGL 79  
 QY 61 APARPRYACCPGWKRTSLPGACGAATCQPPCRNGGSCVQPGRCRCPCAGWRGDTCCSDVD 120  
 DB 80 APARPRYACCPGWKRTSLPGACGAATCQPPCRNGGSCVQPGRCRCPCAGWRGDTCCSDVD 139  
 QY 121 ECSARRGCGPQRCVNTAGSYWCQWEGHSLSDGTLCVPGKGGPRVAPNPTGVDSAMKEE 180  
 DB 140 ECSARRGCGPQRCVNTAGSYWCQWEGHSLSDGTLCVPGKGGPRVAPNPTGVDSAMKEE 199  
 QY 181 VQRLQSRVLLLEEKQLVLAHLPLSLASQALEHGLPDGSLVHVSFQQLGRIDSLSEQLISF 240  
 DB 200 VQRLQSRVLLLEEKQLVLAHLPLSLASQALEHGLPDGSLVHVSFQQLGRIDSLSEQLISF 259  
 QY 241 LEEQLGSCCKKDS 254  
 DB 260 LEEQLGSCCKKDS 273  
 RESULT 15  
 AAB18674  
 ID AAB18674 standard; Protein; 273 AA.  
 XX AAB18674;  
 AC AAB18674;  
 XX 22-JAN-2001 (first entry)  
 DT Amino acid sequence of a human PRO1330 polypeptide.  
 DE Notch 4 homologue; PRO320; PRO938; PRO1031; PRO296; PRO213; PRO1449;  
 XX angiogenesis; cardiovascularisation; PRO1330; cardiovascular disorder;  
 KW endothelial disorder; angiogenic disorder; cancer; trauma; wound;  
 KW arteriosclerosis; cardiac hypertrophy.  
 XX Homo sapiens.  
 OS  
 FH Key Location/Qualifiers  
 FT Peptide 1..19  
 /note= "signal sequence"  
 FT Modified-site 19..25  
 /note= "N-myristoylation site"  
 FT Modified-site 26..30  
 /note= "amidation site"  
 FT Modified-site 78..84  
 /note= "N-myristoylation site"  
 FT Modified-site 93..97  
 /note= "cAMP- and cGMP-dependent protein kinase phosphorylation site"  
 FT Modified-site 97..103  
 /note= "N-myristoylation site"  
 FT Modified-site 100..106  
 /note= "N-myristoylation site"  
 FT Modified-site 103..109  
 /note= "N-myristoylation site"  
 FT Region 123..135  
 /note= "EGF-like domain cysteine pattern signature"  
 FT Region 130..133  
 /note= "cell attachment sequence"

Search completed: December 17, 2002, 10:01:34  
Job time : 31.3643 secs

```

FT Modified-site 152..164
FT /note= "aspartic acid and asparagine hydroxylation site"
FT Modified-site 157..163
FT /note= "N-myristoylation site"
FT Modified-site 191..197
FT /note= "N-myristoylation site"
FT Modified-site 265..271
FT /note= "N-myristoylation site"
XX
XX WO200053752-A2.
XX
XX 14-SEP-2000.
XX
XX 30-DEC-1999; 99WO-US31274.
XX
XX 08-MAR-1999; 99WO-US05028.
XX 21-APR-1999; 99US-0130232.
XX 26-APR-1999; 99US-0131022.
XX 28-APR-1999; 99US-0131445.
XX 14-MAY-1999; 99US-0134287.
XX 02-DEC-1999; 99WO-US28565.
XX
XX (GETH ) GENENTECH INC.
XX
XX Baker KP, Ferrara N, Goddard A, Gurney AL, Hillan KJ, Williams PM;
XX Wood WJ;
XX MPI; 2000-638138/61.
XX N-PSDB; AAA75703.
XX
XX A composition useful for treatment and diagnosis of a cardiovascular,
XX endothelial or angiogenic disorder, especially cancer, comprises (an
XX agonist or antagonist of) a PRO320, PRO938, PRO1031, PRO296, PRO213,
XX PRO1330 or PRO1449 polypeptide -
XX
XX Claim 67; Fig 12; 152pp; English.
XX
XX The present sequence represents PRO1330, a human notch 4 homologue.
XX The specification describes PRO320, PRO938, PRO1031, PRO296, PRO213,
XX PRO1330 and PRO1449 polypeptides. The polypeptides promoter or
XX inhibit angiogenesis and cardiovascularisation in mammals. The
XX polypeptides are used for the treatment and diagnosis of a
XX cardiovascular, endothelial or angiogenic disorder, especially
XX cancer. Disorders that can be diagnosed, treated or prevented by
XX the polypeptides of the invention include trauma such as wounds,
XX atherosclerosis, and cardiac hypertrophy.
XX
XX Sequence 273 AA;
XX
XX Query Match 99.9%; Score 1410; DB 21; Length 273;
XX Best Local Similarity 99.6%; Pred. No. 4..1e-88;
XX Matches 253; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 TEHAYRGRVCAVRAHDPVSEFVQRYVQPLTTCDGHRACSTYRTTIRTAIRSPGL 60
DB 20 TEHAYRGRVCAVRAHDPVSEFVQRYVQPLTTCDGHRACSTYRTTIRTAIRSPGL 79
QY 61 APAPRYACCPGWMRTISGLPGACGAICOPPCRNAGSCVOPGRCPCPAGWRGDTCCSDVD 120
DB 80 APAPRYACCPGWMRTISGLPGACGAICOPPCRNAGSCVOPGRCPCPAGWRGDTCCSDVD 139
QY 121 ECGARRGGCCPQRCVNTAGSYWCQCEGHSLSADGTLCPKGGPPRYVAPNPTGVDSAMKEE 180
DB 140 ECGARRGGCCPQRCVNTAGSYWCQCEGHSLSADGTLCPKGGPPRYVAPNPTGVDSAMKEE 199
QY 181 VQRLQSRVDLLEKTLQVLAFLHSLASQALEHGLPDRGSLVHSPFOQLGRIDLSIQISF 240
DB 200 VQRLQSRVDLLEKTLQVLAFLHSLASQALEHGLPDRGSLVHSPFOQLGRIDLSIQISF 259
QY 241 LEEQLGSCSCCKDS 254
DB 260 LEEQLGSCSCCKDS 273

```





---

; Patent No. 6392018  
; GENERAL INFORMATION:  
; APPLICANT: Ford, John  
; TITLE OF INVENTION: NOVEL EGF MOTIF PROTEIN OBTAINED FROM A CDNA LIBRARY OF FETAL  
; TITLE OF INVENTION: NOVEL EGF MOTIF PROTEIN OBTAINED FROM A CDNA LIBRARY OF FETAL  
; FILE REFERENCE: 24011-727  
; CURRENT APPLICATION NUMBER: US/09/249,697A  
; PRIOR FILING DATE: 1999-02-12  
; PRIOR APPLICATION NUMBER: US 08/968,800  
; PRIOR FILING DATE: 1997-11-22  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 6  
; LENGTH: 553  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: VARIANT  
; LOCATION: (1)...(553)  
; OTHER INFORMATION: Xaa = Any Amino Acid  
US-09-249-697A-6

Query Match 18.1%; Score 255.5; DB 4; Length 553;  
Best Local Similarity 35.1%; Pred. No. 9.2e-13;  
Matches 61; Conservative 20; Mismatches 62; Indels 31; Gaps 7;

QY 20 PVSESFQVQVQPLTTCDGHRACSTYRTIYRTAYRSPGLAPARPRYACCPGWKRTSGL 79  
DB 2 PLPWSLALPLLLPWVAGGFGNAASARHHGLLASA--RQPGVCHYGTKLACCYGWRNRS-- 57  
QY 80 PGACGAATCOPPCRRNGSCVQPGRCRCRCPAGWRGDTCSQSDVDECSARRGGCPQRCVNTAGS 139  
DB 58 KGVC-EATCEPGCK-FGECVGNKCRCPFGYTGKTCSDQVNECGMKPRPCQHRVCNTHGS 115  
QY 140 YMCQWEGHSLSDGTLGV-----PKGGPP-----RVAPN 169  
DB 116 YKCFCLSGHMLMPDAT-CVNSRTCAINQVSCDTEEGPQCLCPSSGLRLAPN 168

RESULT 3  
US-09-363-316B-6  
; Sequence 6, Application US/09363316B  
; Patent No. 6392019  
; GENERAL INFORMATION:  
; APPLICANT: Ford, John  
; TITLE OF INVENTION: EGF MOTIF PROTEIN MATERIALS AND METHODS  
; FILE REFERENCE: 28110/35852  
; CURRENT APPLICATION NUMBER: US/09/363,316B  
; CURRENT FILING DATE: 1999-07-28  
; PRIOR FILING DATE: 1999-02-12  
; PRIOR APPLICATION NUMBER: US 08/968,800  
; PRIOR FILING DATE: 1997-11-22  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 6  
; LENGTH: 553  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (357)  
; OTHER INFORMATION: Xaa = any amino acid  
US-09-363-316B-6

Query Match 18.1%; Score 255.5; DB 4; Length 553;  
Best Local Similarity 35.1%; Pred. No. 9.2e-13;  
Matches 61; Conservative 20; Mismatches 62; Indels 31; Gaps 7;

QY 20 PVSESFQVQVQPLTTCDGHRACSTYRTIYRTAYRSPGLAPARPRYACCPGWKRTSGL 79

DB 2 PLPWSLALPLLLPWVAGGFGNAASARHHGLLASA--RQPGVCHYGTKLACCYGWRNRS-- 57  
QY 80 PGACGAATCOPPCRRNGSCVQPGRCRCRCPAGWRGDTCSQSDVDECSARRGGCPQRCVNTAGS 139  
DB 58 KGVC-EATCEPGCK-FGECVGNKCRCPFGYTGKTCSDQVNECGMKPRPCQHRVCNTHGS 115  
QY 140 YMCQWEGHSLSDGTLGV-----PKGGPP-----RVAPN 169  
DB 116 YKCFCLSGHMLMPDAT-CVNSRTCAINQVSCDTEEGPQCLCPSSGLRLAPN 168

## RESULT 4

US-09-249-697A-19  
; Sequence 19, Application US/09249697A  
; Patent No. 6392018  
; GENERAL INFORMATION:  
; APPLICANT: Ford, John  
; TITLE OF INVENTION: NOVEL EGF MOTIF PROTEIN OBTAINED FROM A CDNA LIBRARY OF FETAL  
; TITLE OF INVENTION: NOVEL EGF MOTIF PROTEIN OBTAINED FROM A CDNA LIBRARY OF FETAL  
; FILE REFERENCE: 24011-727  
; CURRENT APPLICATION NUMBER: US/09/249,697A  
; CURRENT FILING DATE: 1999-02-12  
; PRIOR APPLICATION NUMBER: US 08/968,800  
; PRIOR FILING DATE: 1997-11-22  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 19  
; LENGTH: 553  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-249-697A-19

Query Match 17.9%; Score 252.5; DB 4; Length 553;  
Best Local Similarity 37.4%; Pred. No. 1.6e-12;  
Matches 58; Conservative 16; Mismatches 50; Indels 31; Gaps 7;

QY 39 GHRACSTYRTIYRTAYRSPGLAPARPRYACCPGWKRTSGLPGACGAATCOPPCRRNGSC 98  
DB 21 GNAASARHHGLLASA--RQPGVCHYGTKLACCYGWRNRS--KGVC-EATCEPGCK-FGEC 74  
QY 99 VOPGRCRCRCPAGWRGDTCSQSDVDECSARRGGCPQRCVNTAGSVWCOCWEGHSLSDGTLGV 158  
DB 75 VGNKCRCPFGYTGKTCSDQVNECGMKPRPCQHRVCNTHGSYKFCLSGHMLMPDAT-CV 133  
QY 159 -----PKGGPP-----RVAPN 169  
DB 134 NSRTCAINQVSCDTEEGPQCLCPSSGLRLAPN 168

## RESULT 5

US-09-363-316B-24  
; Sequence 24, Application US/09363316B  
; Patent No. 6392019  
; GENERAL INFORMATION:  
; APPLICANT: Ford, John  
; TITLE OF INVENTION: EGF MOTIF PROTEIN MATERIALS AND METHODS  
; FILE REFERENCE: 28110/35852  
; CURRENT APPLICATION NUMBER: US/09/363,316B  
; CURRENT FILING DATE: 1999-07-28  
; PRIOR FILING DATE: 1999-02-12  
; PRIOR APPLICATION NUMBER: US 08/968,800  
; PRIOR FILING DATE: 1997-11-22  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 24  
; LENGTH: 553  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-363-316B-24



[illegible]

Query Match 13.4%; Score 189; DB 1; Length 678;  
Best Local Similarity 34.2%; Pred. No. 2.3e-07;  
Matches 53; Conservative 8; Mismatches 64; Indels 30; Gaps 8;

QY 27 QRYVQPFLLTCDGH-----RACSTYRTTYRTAYRRSPGLAPRPVACC-----PGWK 74  
DB 47 RRAFOVFEAKQGHLEKRECEBELCS--REARVFEVNDPEIDYFPRYLDCINKKGSPTT 104  
QY 75 RTSG-----LPACGAALICQPPC-RNGGSCVQ--GR--CRCPAGMRGDTQSDVDEC 122  
DB 105 KNSGFATCVQNLDPDC---TPNFCDRKGTQACODLMGNFELCLKAGWGRLCDKDVNEC 160

QY 123 SARRGCPORCVNTAGSYWCQCGWEGHSLSDGTLG 157  
DB 161 SQENGGCLQICHNKPGSFHCSHGFEELSDBGRTG 195

## RESULT 13

US-08-435-434-2  
; Sequence 2, Application US/08435434  
; Patent No. 5714385  
; GENERAL INFORMATION:  
; APPLICANT: Mather, Jennie P.  
; APPLICANT: Li, Ronghao  
; APPLICANT: Chen, Jian  
; TITLE OF INVENTION: ISOLATING AND CULTURING SCHMANN CELLS  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 460 Point San Bruno Blvd  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080

COMPUTER READABLE FORM:  
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: patin (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/435,434  
; FILING DATE: 10-MAY-1995  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lee, Wendy M.  
; REGISTRATION NUMBER: 00,000  
; REFERENCE/DOCKET NUMBER: 946-2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415/225-1994  
; TELEFAX: 415/952-9881  
; TELEX: 910/371-7168  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 678 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
US-08-435-434-2

Query Match 13.4%; Score 189; DB 1; Length 678;  
Best Local Similarity 34.2%; Pred. No. 2.3e-07;  
Matches 53; Conservative 8; Mismatches 64; Indels 30; Gaps 8;

QY 27 QRYVQPFLLTCDGH-----RACSTYRTTYRTAYRRSPGLAPRPVACC-----PGWK 74  
DB 47 RRAFOVFEAKQGHLEKRECEBELCS--REARVFEVNDPEIDYFPRYLDCINKKGSPTT 104  
QY 75 RTSG-----LPACGAALICQPPC-RNGGSCVQ--GR--CRCPAGMRGDTQSDVDEC 122  
DB 105 KNSGFATCVQNLDPDC---TPNFCDRKGTQACODLMGNFELCLKAGWGRLCDKDVNEC 160

QY 123 SARRGCPORCVNTAGSYWCQCGWEGHSLSDGTLG 157  
DB 161 SQENGGCLQICHNKPGSFHCSHGFEELSDBGRTG 195

## RESULT 14

US-08-435-436-2  
; Sequence 2, Application US/08435436  
; Patent No. 5721139  
; GENERAL INFORMATION:  
; APPLICANT: Mather, Jennie P.  
; APPLICANT: Li, Ronghao  
; APPLICANT: Chen, Jian  
; TITLE OF INVENTION: ISOLATING AND CULTURING SCHMANN CELLS  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 460 Point San Bruno Blvd  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080

COMPUTER READABLE FORM:  
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: patin (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/435,436  
; FILING DATE: 10-MAY-1995  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lee, Wendy M.  
; REGISTRATION NUMBER: 00,000  
; REFERENCE/DOCKET NUMBER: 946-3  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415/225-1994  
; TELEFAX: 415/952-9881  
; TELEX: 910/371-7168  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 678 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
US-08-435-436-2

Query Match 13.4%; Score 189; DB 1; Length 678;  
Best Local Similarity 34.2%; Pred. No. 2.3e-07;  
Matches 53; Conservative 8; Mismatches 64; Indels 30; Gaps 8;

QY 27 QRYVQPFLLTCDGH-----RACSTYRTTYRTAYRRSPGLAPRPVACC-----PGWK 74  
DB 47 RRAFOVFEAKQGHLEKRECEBELCS--REARVFEVNDPEIDYFPRYLDCINKKGSPTT 104  
QY 75 RTSG-----LPACGAALICQPPC-RNGGSCVQ--GR--CRCPAGMRGDTQSDVDEC 122  
DB 105 KNSGFATCVQNLDPDC---TPNFCDRKGTQACODLMGNFELCLKAGWGRLCDKDVNEC 160

QY 123 SARRGCPORCVNTAGSYWCQCGWEGHSLSDGTLG 157  
DB 161 SQENGGCLQICHNKPGSFHCSHGFEELSDBGRTG 195

## RESULT 15

US-08-438-863-2  
; Sequence 2, Application US/08438863  
; Patent No. 5849585  
; GENERAL INFORMATION:  
; APPLICANT: Mather, Jennie P.  
; APPLICANT: Ronghao Li

Search completed: December 17, 2002, 10:04:12  
Job time : 14.5313 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 17, 2002, 10:03:07 ; Search time 8.19355 Seconds

(without alignments)  
516.533 Million cell updates/sec

Title: US-09-852-472-3

Perfect score: 1411

Sequence: 1 TEHAYRPGRRVCAVARGDP.....SEQSFLFEQUGSCSCKKDS 254

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 105981 seqs, 16662342 residues

Total number of hits satisfying chosen parameters: 105981

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1411	100.0	273	US-09-978-295A-510	Sequence 510, App
2	1411	100.0	273	US-09-978-697-510	Sequence 510, App
3	1411	100.0	273	US-09-978-192A-510	Sequence 510, App
4	1410	99.9	273	US-09-978-295A-506	Sequence 506, App
5	1410	99.9	273	US-09-978-295A-508	Sequence 506, App
6	1410	99.9	273	US-09-978-697-506	Sequence 506, App
7	1410	99.9	273	US-09-978-697-508	Sequence 506, App
8	1410	99.9	273	US-09-978-192A-506	Sequence 506, App
9	1410	99.9	273	US-09-978-192A-508	Sequence 506, App
10	1410	99.9	273	US-09-790-264-10	Sequence 508, App
11	1392	96.7	251	US-09-790-264-12	Sequence 10, Appl
12	1333	94.5	295	US-09-978-295A-2	Sequence 12, Appl
13	1333	94.5	295	US-09-978-697-2	Sequence 2, Appl
14	1333	94.5	295	US-09-978-697-2	Sequence 2, Appl
15	1139.5	80.8	275	US-09-790-264-15	Sequence 15, Appl
16	945.5	67.0	287	US-09-764-898-218	Sequence 218, App
17	945.5	67.0	288	US-09-764-853-841	Sequence 841, App
18	945.5	67.0	288	US-09-764-898-290	Sequence 290, App
19	945.5	67.0	314	US-09-764-853-670	Sequence 670, App

20	919.5	65.2	247	10	US-09-790-264-20	Sequence 20, Appl
21	255.5	18.1	553	9	US-09-981-649A-6	Sequence 6, Appl
22	252.5	17.9	338	9	US-09-978-295A-119	Sequence 119, Appl
23	252.5	17.9	338	9	US-09-978-697-119	Sequence 119, Appl
24	252.5	17.9	338	9	US-09-978-192A-119	Sequence 119, Appl
25	252.5	17.9	553	10	US-09-981-649A-24	Sequence 24, Appl
26	252.5	17.9	554	10	US-09-981-649A-32	Sequence 32, Appl
27	250.5	17.8	554	10	US-09-981-649A-28	Sequence 30, Appl
28	250.5	17.8	559	9	US-09-981-649A-28	Sequence 28, Appl
29	223	15.8	509	9	US-09-905-291A-315	Sequence 315, App
30	223	15.8	509	10	US-09-909-330-315	Sequence 315, App
31	223	15.8	509	10	US-09-909-088B-315	Sequence 315, App
32	223	15.8	509	12	US-10-052-586-52	Sequence 52, Appl
33	217.5	15.4	502	10	US-09-981-649A-18	Sequence 18, Appl
34	217.5	15.4	537	10	US-09-981-649A-4	Sequence 37, Appl
35	216.5	15.3	100	10	US-09-981-649A-3	Sequence 3, Appl
36	207	14.7	201	10	US-09-764-853-797	Sequence 797, App
37	207	14.7	201	10	US-09-764-898-270	Sequence 270, App
38	184	13.0	652	10	US-09-789-919-96	Sequence 96, Appl
39	183	13.0	810	10	US-09-976-165-34	Sequence 34, Appl
40	181.5	12.9	816	10	US-09-976-165-37	Sequence 37, Appl
41	173.5	12.3	1246	10	US-09-919-497-85	Sequence 85, Appl
42	172	12.2	534	10	US-09-804-156-14	Sequence 14, Appl
43	172	12.2	534	10	US-09-946-633-6	Sequence 6, Appl
44	169	12.0	1055	10	US-09-855-722-2	Sequence 2, Appl
45	166	11.8	1212	10	US-09-855-722-3	Sequence 3, Appl

#### ALIGNMENTS

RESULT 1  
US-09-978-295A-510  
Sequence 510, Application US/09978295A  
Patent No. US2002015606A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Etkin, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillman, Kenneth J.  
APPLICANT: Kijavich, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OR INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630P1C1  
CURRENT APPLICATION NUMBER: US/09/978, 295A  
CURRENT FILING DATE: 2001-10-15  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/064249

1 PRIOR FILING DATE: 1997-11-03  
2 PRIOR APPLICATION NUMBER: 60/065311  
3 PRIOR FILING DATE: 1997-11-13  
4 PRIOR APPLICATION NUMBER: 60/066364  
5 PRIOR FILING DATE: 1997-11-21  
6 PRIOR APPLICATION NUMBER: 60/077450  
7 PRIOR FILING DATE: 1998-03-10  
8 PRIOR APPLICATION NUMBER: 60/077632  
9 PRIOR FILING DATE: 1998-03-11  
10 PRIOR APPLICATION NUMBER: 60/077641  
11 PRIOR FILING DATE: 1998-03-11  
12 PRIOR APPLICATION NUMBER: 60/077649  
13 PRIOR FILING DATE: 1998-03-11  
14 PRIOR APPLICATION NUMBER: 60/077791  
15 PRIOR FILING DATE: 1998-03-12  
16 PRIOR APPLICATION NUMBER: 60/078004  
17 PRIOR FILING DATE: 1998-03-13  
18 PRIOR APPLICATION NUMBER: 60/078886  
19 PRIOR FILING DATE: 1998-03-20  
20 PRIOR APPLICATION NUMBER: 60/078936  
21 PRIOR FILING DATE: 1998-03-20  
22 PRIOR APPLICATION NUMBER: 60/078910  
23 PRIOR FILING DATE: 1998-03-20  
24 PRIOR APPLICATION NUMBER: 60/078939  
25 PRIOR FILING DATE: 1998-03-20  
26 PRIOR APPLICATION NUMBER: 60/079294  
27 PRIOR FILING DATE: 1998-03-25  
28 PRIOR APPLICATION NUMBER: 60/079656  
29 PRIOR FILING DATE: 1998-03-26  
30 PRIOR APPLICATION NUMBER: 60/079664  
31 PRIOR FILING DATE: 1998-03-27  
32 PRIOR APPLICATION NUMBER: 60/079689  
33 PRIOR FILING DATE: 1998-03-27  
34 PRIOR APPLICATION NUMBER: 60/079663  
35 PRIOR FILING DATE: 1998-03-27  
36 PRIOR APPLICATION NUMBER: 60/079728  
37 PRIOR FILING DATE: 1998-03-27  
38 PRIOR APPLICATION NUMBER: 60/079786  
39 PRIOR FILING DATE: 1998-03-27  
40 PRIOR APPLICATION NUMBER: 60/079920  
41 PRIOR FILING DATE: 1998-03-30  
42 PRIOR APPLICATION NUMBER: 60/079923  
43 PRIOR FILING DATE: 1998-03-30  
44 PRIOR APPLICATION NUMBER: 60/080105  
45 PRIOR FILING DATE: 1998-03-31  
46 PRIOR APPLICATION NUMBER: 60/080107  
47 PRIOR FILING DATE: 1998-03-31  
48 PRIOR APPLICATION NUMBER: 60/080165  
49 PRIOR FILING DATE: 1998-03-31  
50 PRIOR APPLICATION NUMBER: 60/080194  
51 PRIOR FILING DATE: 1998-03-31  
52 PRIOR APPLICATION NUMBER: 60/080327  
53 PRIOR FILING DATE: 1998-04-01  
54 PRIOR APPLICATION NUMBER: 60/080328  
55 PRIOR FILING DATE: 1998-04-01  
56 PRIOR APPLICATION NUMBER: 60/080333  
57 PRIOR FILING DATE: 1998-04-01  
58 PRIOR APPLICATION NUMBER: 60/080334  
59 PRIOR FILING DATE: 1998-04-01  
60 PRIOR APPLICATION NUMBER: 60/081070  
61 PRIOR FILING DATE: 1998-04-08  
62 PRIOR APPLICATION NUMBER: 60/081049  
63 PRIOR FILING DATE: 1998-04-08  
64 PRIOR APPLICATION NUMBER: 60/081071  
65 PRIOR FILING DATE: 1998-04-08  
66 PRIOR APPLICATION NUMBER: 60/081195  
67 PRIOR FILING DATE: 1998-04-08  
68 PRIOR APPLICATION NUMBER: 60/081203  
69 PRIOR FILING DATE: 1998-04-09  
70 PRIOR APPLICATION NUMBER: 60/081229  
71 PRIOR FILING DATE: 1998-04-09  
72 PRIOR APPLICATION NUMBER: 60/081955  
73 PRIOR FILING DATE: 1998-04-15

74 PRIOR APPLICATION NUMBER: 60/081817  
75 PRIOR FILING DATE: 1998-04-15  
76 PRIOR APPLICATION NUMBER: 60/081819  
77 PRIOR FILING DATE: 1998-04-15  
78 PRIOR APPLICATION NUMBER: 60/081952  
79 PRIOR FILING DATE: 1998-04-15  
80 PRIOR APPLICATION NUMBER: 60/081838  
81 PRIOR FILING DATE: 1998-04-15  
82 PRIOR APPLICATION NUMBER: 60/082568  
83 PRIOR FILING DATE: 1998-04-21  
84 PRIOR APPLICATION NUMBER: 60/082569  
85 PRIOR FILING DATE: 1998-04-21  
86 PRIOR APPLICATION NUMBER: 60/082704  
87 PRIOR FILING DATE: 1998-04-22  
88 PRIOR APPLICATION NUMBER: 60/082804  
89 PRIOR FILING DATE: 1998-04-22  
90 PRIOR APPLICATION NUMBER: 60/082700  
91 PRIOR FILING DATE: 1998-04-22  
92 PRIOR APPLICATION NUMBER: 60/082797  
93 PRIOR FILING DATE: 1998-04-22  
94 PRIOR APPLICATION NUMBER: 60/082796  
95 PRIOR FILING DATE: 1998-04-23  
96 PRIOR APPLICATION NUMBER: 60/083336  
97 PRIOR FILING DATE: 1998-04-27  
98 PRIOR APPLICATION NUMBER: 60/083322  
99 PRIOR FILING DATE: 1998-04-28  
100 PRIOR APPLICATION NUMBER: 60/083392  
101 PRIOR FILING DATE: 1998-04-29  
102 PRIOR APPLICATION NUMBER: 60/083495  
103 PRIOR FILING DATE: 1998-04-29  
104 PRIOR APPLICATION NUMBER: 60/083496  
105 PRIOR FILING DATE: 1998-04-29  
106 PRIOR APPLICATION NUMBER: 60/083499  
107 PRIOR FILING DATE: 1998-04-29  
108 PRIOR APPLICATION NUMBER: 60/083545  
109 PRIOR FILING DATE: 1998-04-29  
110 PRIOR APPLICATION NUMBER: 60/083554  
111 PRIOR FILING DATE: 1998-04-29  
112 PRIOR APPLICATION NUMBER: 60/083558  
113 PRIOR FILING DATE: 1998-04-29  
114 PRIOR APPLICATION NUMBER: 60/083559  
115 PRIOR FILING DATE: 1998-04-29  
116 PRIOR APPLICATION NUMBER: 60/083500  
117 PRIOR FILING DATE: 1998-04-29  
118 PRIOR APPLICATION NUMBER: 60/083742  
119 PRIOR FILING DATE: 1998-04-30  
120 PRIOR APPLICATION NUMBER: 60/084366  
121 PRIOR FILING DATE: 1998-05-05  
122 PRIOR APPLICATION NUMBER: 60/084414  
123 PRIOR FILING DATE: 1998-05-06  
124 PRIOR APPLICATION NUMBER: 60/084441  
125 PRIOR FILING DATE: 1998-05-06  
126 PRIOR APPLICATION NUMBER: 60/084637  
127 PRIOR FILING DATE: 1998-05-07  
128 PRIOR APPLICATION NUMBER: 60/084639  
129 PRIOR FILING DATE: 1998-05-07  
130 PRIOR APPLICATION NUMBER: 60/084640  
131 PRIOR FILING DATE: 1998-05-07  
132 PRIOR APPLICATION NUMBER: 60/084598  
133 PRIOR FILING DATE: 1998-05-07  
134 PRIOR APPLICATION NUMBER: 60/084600  
135 PRIOR FILING DATE: 1998-05-07  
136 PRIOR APPLICATION NUMBER: 60/084627  
137 PRIOR FILING DATE: 1998-05-07  
138 PRIOR APPLICATION NUMBER: 60/084643  
139 PRIOR FILING DATE: 1998-05-07  
140 PRIOR APPLICATION NUMBER: 60/085339  
141 PRIOR FILING DATE: 1998-05-13  
142 PRIOR APPLICATION NUMBER: 60/085338  
143 PRIOR FILING DATE: 1998-05-13  
144 PRIOR APPLICATION NUMBER: 60/085323  
145 PRIOR FILING DATE: 1998-05-13  
146 PRIOR APPLICATION NUMBER: 60/085582



PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085700  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085689  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085579  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085580  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085573  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085704  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 1411; DB 9; Length 273;  
Best Local Similarity 100.0%; Pred. No. 7, 8e-94;  
Matches 254; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TEHAYRGRVCAVRANGDPVSESFVQRYVQPLTTCDGHRACSTYRTIYRTAYRSPGL 60  
DB 20 TEHAYRGRVCAVRANGDPVSESFVQRYVQPLTTCDGHRACSTYRTIYRTAYRSPGL 79

QY 61 APAPRRACCGWRTSGLPAGCAATCCPCRNCGSCVQPCRCPCAGKREPTCCSDVD 120  
DB 80 APAPRRACCGWRTSGLPAGCAATCCPCRNCGSCVQPCRCPCAGKREPTCCSDVD 139

QY 121 ECSARRGCGQRCVNTAGSYWCQMEGHSLSADDTLCVPCGCPPRVAPNPTGVDSAMKEE 180  
DB 140 ECSARRGCGQRCVNTAGSYWCQMEGHSLSADDTLCVPCGCPPRVAPNPTGVDSAMKEE 199

QY 181 VORIQSVLDLEELQVLVAPLPHSLASQALEHGLPDGSLVHSPQGLRIDSLSQISF 240  
DB 200 VORIQSVLDLEELQVLVAPLPHSLASQALEHGLPDGSLVHSPQGLRIDSLSQISF 259

QY 241 LEBQLGSCGCKXS 254  
DB 260 LEBQLGSCGCKXS 273

RESULT 2  
US-09-978-697-510  
Sequence 510, Application US/09978697  
Patent No. US20020169284A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerltzen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kijavain, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Snelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P263021C27  
CURRENT APPLICATION NUMBER: US/09/978, 697  
CURRENT FILING DATE: 2001-10-16  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/064249  
PRIOR FILING DATE: 1997-11-03  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/066364  
PRIOR FILING DATE: 1997-11-21  
PRIOR APPLICATION NUMBER: 60/077450  
PRIOR FILING DATE: 1998-03-10  
PRIOR APPLICATION NUMBER: 60/077632  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077641  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077649  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077791  
PRIOR FILING DATE: 1998-03-12  
PRIOR APPLICATION NUMBER: 60/078004  
PRIOR FILING DATE: 1998-03-13  
PRIOR APPLICATION NUMBER: 60/078886  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/078936  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/078910  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/078939  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/079294  
PRIOR FILING DATE: 1998-03-25  
PRIOR APPLICATION NUMBER: 60/079656  
PRIOR FILING DATE: 1998-03-26  
PRIOR APPLICATION NUMBER: 60/079664  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/079689  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/079663  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/079728  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/079786  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/079920  
PRIOR FILING DATE: 1998-03-30  
PRIOR APPLICATION NUMBER: 60/079923  
PRIOR FILING DATE: 1998-03-30  
PRIOR APPLICATION NUMBER: 60/080105  
PRIOR FILING DATE: 1998-03-31  
PRIOR APPLICATION NUMBER: 60/080107  
PRIOR FILING DATE: 1998-03-31  
PRIOR APPLICATION NUMBER: 60/080165  
PRIOR FILING DATE: 1998-03-31  
PRIOR APPLICATION NUMBER: 60/080194  
PRIOR FILING DATE: 1998-03-31  
PRIOR APPLICATION NUMBER: 60/080327  
PRIOR FILING DATE: 1998-04-01  
PRIOR APPLICATION NUMBER: 60/080328  
PRIOR FILING DATE: 1998-04-01  
PRIOR APPLICATION NUMBER: 60/080333  
PRIOR FILING DATE: 1998-04-01  
PRIOR APPLICATION NUMBER: 60/080334  
PRIOR FILING DATE: 1998-04-01  
PRIOR APPLICATION NUMBER: 60/081070  
PRIOR FILING DATE: 1998-04-08  
PRIOR APPLICATION NUMBER: 60/081049  
PRIOR FILING DATE: 1998-04-08  
PRIOR APPLICATION NUMBER: 60/081071

; PRIOR FILING DATE: 1998-04-08  
; PRIOR APPLICATION NUMBER: 60/081195  
; PRIOR FILING DATE: 1998-04-08  
; PRIOR APPLICATION NUMBER: 60/081203  
; PRIOR FILING DATE: 1998-04-09  
; PRIOR APPLICATION NUMBER: 60/081229  
; PRIOR FILING DATE: 1998-04-09  
; PRIOR APPLICATION NUMBER: 60/081955  
; PRIOR FILING DATE: 1998-04-15  
; PRIOR APPLICATION NUMBER: 60/081817  
; PRIOR FILING DATE: 1998-04-15  
; PRIOR APPLICATION NUMBER: 60/081819  
; PRIOR FILING DATE: 1998-04-15  
; PRIOR APPLICATION NUMBER: 60/081952  
; PRIOR FILING DATE: 1998-04-15  
; PRIOR APPLICATION NUMBER: 60/081838  
; PRIOR FILING DATE: 1998-04-15  
; PRIOR APPLICATION NUMBER: 60/082568  
; PRIOR FILING DATE: 1998-04-21  
; PRIOR APPLICATION NUMBER: 60/082569  
; PRIOR FILING DATE: 1998-04-21  
; PRIOR APPLICATION NUMBER: 60/082704  
; PRIOR FILING DATE: 1998-04-22  
; PRIOR APPLICATION NUMBER: 60/082804  
; PRIOR FILING DATE: 1998-04-22  
; PRIOR APPLICATION NUMBER: 60/082700  
; PRIOR FILING DATE: 1998-04-22  
; PRIOR APPLICATION NUMBER: 60/082797  
; PRIOR FILING DATE: 1998-04-22  
; PRIOR APPLICATION NUMBER: 60/082796  
; PRIOR FILING DATE: 1998-04-23  
; PRIOR APPLICATION NUMBER: 60/083336  
; PRIOR FILING DATE: 1998-04-27  
; PRIOR APPLICATION NUMBER: 60/083322  
; PRIOR FILING DATE: 1998-04-28  
; PRIOR APPLICATION NUMBER: 60/083392  
; PRIOR FILING DATE: 1998-04-29  
; PRIOR APPLICATION NUMBER: 60/083495  
; PRIOR FILING DATE: 1998-04-29  
; PRIOR APPLICATION NUMBER: 60/083496  
; PRIOR FILING DATE: 1998-04-29  
; PRIOR APPLICATION NUMBER: 60/083499  
; PRIOR FILING DATE: 1998-04-29  
; PRIOR APPLICATION NUMBER: 60/083545  
; PRIOR FILING DATE: 1998-04-29  
; PRIOR APPLICATION NUMBER: 60/083554  
; PRIOR FILING DATE: 1998-04-29  
; PRIOR APPLICATION NUMBER: 60/083558  
; PRIOR FILING DATE: 1998-04-29  
; PRIOR APPLICATION NUMBER: 60/083559  
; PRIOR FILING DATE: 1998-04-29  
; PRIOR APPLICATION NUMBER: 60/083500  
; PRIOR FILING DATE: 1998-04-29  
; PRIOR APPLICATION NUMBER: 60/084414  
; PRIOR FILING DATE: 1998-05-06  
; PRIOR APPLICATION NUMBER: 60/084441  
; PRIOR FILING DATE: 1998-05-06  
; PRIOR APPLICATION NUMBER: 60/084637  
; PRIOR FILING DATE: 1998-05-07  
; PRIOR APPLICATION NUMBER: 60/084639  
; PRIOR FILING DATE: 1998-05-07  
; PRIOR APPLICATION NUMBER: 60/084640  
; PRIOR FILING DATE: 1998-05-07  
; PRIOR APPLICATION NUMBER: 60/084598  
; PRIOR FILING DATE: 1998-05-07  
; PRIOR APPLICATION NUMBER: 60/084600  
; PRIOR FILING DATE: 1998-05-07  
; PRIOR APPLICATION NUMBER: 60/084627  
; PRIOR FILING DATE: 1998-05-07

; PRIOR APPLICATION NUMBER: 60/084643  
; PRIOR FILING DATE: 1998-05-07  
; PRIOR APPLICATION NUMBER: 60/085339  
; PRIOR FILING DATE: 1998-05-13  
; PRIOR APPLICATION NUMBER: 60/085338  
; PRIOR FILING DATE: 1998-05-13  
; PRIOR APPLICATION NUMBER: 60/085323  
; PRIOR FILING DATE: 1998-05-13  
; PRIOR APPLICATION NUMBER: 60/085582  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085700  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085689  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085579  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085580  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085573  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085704  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085697  
; PRIOR APPLICATION NUMBER: 60/085697  
Query Match 100.0%; Score 1411; DB 9; Length 273;  
Best Local Similarity 100.0%; Pred. No. 7.8e-94;  
Matches 254; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TEHAYRPGRRYCAVRAHGDVPSFVQRYOPFLTTCDGHRACSTYRTIYRTAYRRSPGL 60  
DB 20 TEHAYRPGRRYCAVRAHGDVPSFVQRYOPFLTTCDGHRACSTYRTIYRTAYRRSPGL 79  
QY 61 APARYACCPGWKRTSLPGACGAATCOPPCNRNGSCVQPCRCPCAGWGDTCQSDVD 120  
DB 80 APARYACCPGWKRTSLPGACGAATCOPPCNRNGSCVQPCRCPCAGWGDTCQSDVD 139  
QY 121 ECSARRGCPQRCVNTAGSYWCQWEGHSLASADGTLCPVKGPPRPVAPNPPTGVDSAMKEE 180  
DB 140 ECSARRGCPQRCVNTAGSYWCQWEGHSLASADGTLCPVKGPPRPVAPNPPTGVDSAMKEE 199  
QY 181 VQRLQSRVDLLEKQLVLAFLHSLASQALEHGLPDGSLLVHFSFQQLGRIDSLSSEQISF 240  
DB 200 VQRLQSRVDLLEKQLVLAFLHSLASQALEHGLPDGSLLVHFSFQQLGRIDSLSSEQISF 259  
QY 241 LEEQLGSCSKKDS 254  
DB 260 LEEQLGSCSKKDS 273

RESULT 3  
US-09-978-192A-510  
; Sequence 510, Application US/09978192A  
; Patent No. US20020177553A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.

APPLICANT: Pan, James;  
APPLICANT: Pao, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2630P1C9  
CURRENT APPLICATION NUMBER: US/09/978,192A  
PRIOR FILING DATE: 2001-10-15  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/064249  
PRIOR FILING DATE: 1997-11-03  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/066364  
PRIOR FILING DATE: 1997-11-21  
PRIOR APPLICATION NUMBER: 60/077450  
PRIOR FILING DATE: 1998-03-10  
PRIOR APPLICATION NUMBER: 60/077632  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077641  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077649  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077791  
PRIOR FILING DATE: 1998-03-12  
PRIOR APPLICATION NUMBER: 60/078004  
PRIOR FILING DATE: 1998-03-13  
PRIOR APPLICATION NUMBER: 60/078886  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/078936  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/078910  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/078939  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/079294  
PRIOR FILING DATE: 1998-03-25  
PRIOR APPLICATION NUMBER: 60/079656  
PRIOR FILING DATE: 1998-03-26  
PRIOR APPLICATION NUMBER: 60/079664  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/079689  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/079663  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/079728  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/079786  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/079920  
PRIOR FILING DATE: 1998-03-30  
PRIOR APPLICATION NUMBER: 60/079923  
PRIOR FILING DATE: 1998-03-30  
PRIOR APPLICATION NUMBER: 60/080105  
PRIOR FILING DATE: 1998-03-31  
PRIOR APPLICATION NUMBER: 60/080107  
PRIOR FILING DATE: 1998-03-31  
PRIOR APPLICATION NUMBER: 60/080165  
PRIOR FILING DATE: 1998-03-31  
PRIOR APPLICATION NUMBER: 60/080194  
PRIOR FILING DATE: 1998-03-31  
PRIOR APPLICATION NUMBER: 60/080327  
PRIOR FILING DATE: 1998-04-01  
PRIOR APPLICATION NUMBER: 60/080328  
PRIOR FILING DATE: 1998-04-01

PRIOR APPLICATION NUMBER: 60/080333  
PRIOR FILING DATE: 1998-04-01  
PRIOR APPLICATION NUMBER: 60/080334  
PRIOR FILING DATE: 1998-04-01  
PRIOR APPLICATION NUMBER: 60/081070  
PRIOR FILING DATE: 1998-04-08  
PRIOR APPLICATION NUMBER: 60/081049  
PRIOR FILING DATE: 1998-04-08  
PRIOR APPLICATION NUMBER: 60/081071  
PRIOR FILING DATE: 1998-04-08  
PRIOR APPLICATION NUMBER: 60/081195  
PRIOR FILING DATE: 1998-04-08  
PRIOR APPLICATION NUMBER: 60/081203  
PRIOR FILING DATE: 1998-04-09  
PRIOR APPLICATION NUMBER: 60/081229  
PRIOR FILING DATE: 1998-04-09  
PRIOR APPLICATION NUMBER: 60/081955  
PRIOR FILING DATE: 1998-04-15  
PRIOR APPLICATION NUMBER: 60/081817  
PRIOR FILING DATE: 1998-04-15  
PRIOR APPLICATION NUMBER: 60/081819  
PRIOR FILING DATE: 1998-04-15  
PRIOR APPLICATION NUMBER: 60/081952  
PRIOR FILING DATE: 1998-04-15  
PRIOR APPLICATION NUMBER: 60/081838  
PRIOR FILING DATE: 1998-04-15  
PRIOR APPLICATION NUMBER: 60/082568  
PRIOR FILING DATE: 1998-04-21  
PRIOR APPLICATION NUMBER: 60/082569  
PRIOR FILING DATE: 1998-04-21  
PRIOR APPLICATION NUMBER: 60/082704  
PRIOR FILING DATE: 1998-04-22  
PRIOR APPLICATION NUMBER: 60/082804  
PRIOR FILING DATE: 1998-04-22  
PRIOR APPLICATION NUMBER: 60/082700  
PRIOR FILING DATE: 1998-04-22  
PRIOR APPLICATION NUMBER: 60/082797  
PRIOR FILING DATE: 1998-04-22  
PRIOR APPLICATION NUMBER: 60/082796  
PRIOR FILING DATE: 1998-04-23  
PRIOR APPLICATION NUMBER: 60/083336  
PRIOR FILING DATE: 1998-04-27  
PRIOR APPLICATION NUMBER: 60/083322  
PRIOR FILING DATE: 1998-04-28  
PRIOR APPLICATION NUMBER: 60/083392  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083495  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083496  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083499  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083545  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083554  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083558  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083559  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083500  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083742  
PRIOR FILING DATE: 1998-04-30  
PRIOR APPLICATION NUMBER: 60/084366  
PRIOR FILING DATE: 1998-05-05  
PRIOR APPLICATION NUMBER: 60/084414  
PRIOR FILING DATE: 1998-05-06  
PRIOR APPLICATION NUMBER: 60/084441  
PRIOR FILING DATE: 1998-05-06  
PRIOR APPLICATION NUMBER: 60/084637  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/084639



PRIOR FILING DATE: 1998-03-31  
 PRIOR APPLICATION NUMBER: 60/080165  
 PRIOR FILING DATE: 1998-03-31  
 PRIOR APPLICATION NUMBER: 60/080194  
 PRIOR FILING DATE: 1998-03-31  
 PRIOR APPLICATION NUMBER: 60/080327  
 PRIOR FILING DATE: 1998-04-01  
 PRIOR APPLICATION NUMBER: 60/080328  
 PRIOR FILING DATE: 1998-04-01  
 PRIOR APPLICATION NUMBER: 60/080333  
 PRIOR FILING DATE: 1998-04-01  
 PRIOR APPLICATION NUMBER: 60/080334  
 PRIOR FILING DATE: 1998-04-01  
 PRIOR APPLICATION NUMBER: 60/081070  
 PRIOR FILING DATE: 1998-04-08  
 PRIOR APPLICATION NUMBER: 60/081049  
 PRIOR FILING DATE: 1998-04-08  
 PRIOR APPLICATION NUMBER: 60/081071  
 PRIOR FILING DATE: 1998-04-08  
 PRIOR APPLICATION NUMBER: 60/081195  
 PRIOR FILING DATE: 1998-04-08  
 PRIOR APPLICATION NUMBER: 60/081203  
 PRIOR FILING DATE: 1998-04-09  
 PRIOR APPLICATION NUMBER: 60/081229  
 PRIOR FILING DATE: 1998-04-09  
 PRIOR APPLICATION NUMBER: 60/081955  
 PRIOR FILING DATE: 1998-04-15  
 PRIOR APPLICATION NUMBER: 60/081817  
 PRIOR FILING DATE: 1998-04-15  
 PRIOR APPLICATION NUMBER: 60/081819  
 PRIOR FILING DATE: 1998-04-15  
 PRIOR APPLICATION NUMBER: 60/081952  
 PRIOR FILING DATE: 1998-04-15  
 PRIOR APPLICATION NUMBER: 60/081838  
 PRIOR FILING DATE: 1998-04-15  
 PRIOR APPLICATION NUMBER: 60/082568  
 PRIOR FILING DATE: 1998-04-21  
 PRIOR APPLICATION NUMBER: 60/082569  
 PRIOR FILING DATE: 1998-04-21  
 PRIOR APPLICATION NUMBER: 60/082704  
 PRIOR FILING DATE: 1998-04-22  
 PRIOR APPLICATION NUMBER: 60/082804  
 PRIOR FILING DATE: 1998-04-22  
 PRIOR APPLICATION NUMBER: 60/082700  
 PRIOR FILING DATE: 1998-04-22  
 PRIOR APPLICATION NUMBER: 60/082797  
 PRIOR FILING DATE: 1998-04-22  
 PRIOR APPLICATION NUMBER: 60/082796  
 PRIOR FILING DATE: 1998-04-23  
 PRIOR APPLICATION NUMBER: 60/083336  
 PRIOR FILING DATE: 1998-04-27  
 PRIOR APPLICATION NUMBER: 60/083322  
 PRIOR FILING DATE: 1998-04-28  
 PRIOR APPLICATION NUMBER: 60/083392  
 PRIOR FILING DATE: 1998-04-29  
 PRIOR APPLICATION NUMBER: 60/083495  
 PRIOR FILING DATE: 1998-04-29  
 PRIOR APPLICATION NUMBER: 60/083496  
 PRIOR FILING DATE: 1998-04-29  
 PRIOR APPLICATION NUMBER: 60/083499  
 PRIOR FILING DATE: 1998-04-29  
 PRIOR APPLICATION NUMBER: 60/083545  
 PRIOR FILING DATE: 1998-04-29  
 PRIOR APPLICATION NUMBER: 60/083554  
 PRIOR FILING DATE: 1998-04-29  
 PRIOR APPLICATION NUMBER: 60/083558  
 PRIOR FILING DATE: 1998-04-29  
 PRIOR APPLICATION NUMBER: 60/083559  
 PRIOR FILING DATE: 1998-04-29  
 PRIOR APPLICATION NUMBER: 60/083500  
 PRIOR FILING DATE: 1998-04-29  
 PRIOR APPLICATION NUMBER: 60/083742  
 PRIOR FILING DATE: 1998-04-30

PRIOR APPLICATION NUMBER: 60/084366  
 PRIOR FILING DATE: 1998-05-05  
 PRIOR APPLICATION NUMBER: 60/084414  
 PRIOR FILING DATE: 1998-05-06  
 PRIOR APPLICATION NUMBER: 60/084441  
 PRIOR FILING DATE: 1998-05-06  
 PRIOR APPLICATION NUMBER: 60/084637  
 PRIOR FILING DATE: 1998-05-07  
 PRIOR APPLICATION NUMBER: 60/084639  
 PRIOR FILING DATE: 1998-05-07  
 PRIOR APPLICATION NUMBER: 60/084640  
 PRIOR FILING DATE: 1998-05-07  
 PRIOR APPLICATION NUMBER: 60/084598  
 PRIOR FILING DATE: 1998-05-07  
 PRIOR APPLICATION NUMBER: 60/084600  
 PRIOR FILING DATE: 1998-05-07  
 PRIOR APPLICATION NUMBER: 60/084627  
 PRIOR FILING DATE: 1998-05-07  
 PRIOR APPLICATION NUMBER: 60/084643  
 PRIOR FILING DATE: 1998-05-07  
 PRIOR APPLICATION NUMBER: 60/085339  
 PRIOR FILING DATE: 1998-05-13  
 PRIOR APPLICATION NUMBER: 60/085338  
 PRIOR FILING DATE: 1998-05-13  
 PRIOR APPLICATION NUMBER: 60/085323  
 PRIOR FILING DATE: 1998-05-13  
 PRIOR APPLICATION NUMBER: 60/085582  
 PRIOR FILING DATE: 1998-05-15  
 PRIOR APPLICATION NUMBER: 60/085700  
 PRIOR FILING DATE: 1998-05-15  
 PRIOR APPLICATION NUMBER: 60/085689  
 PRIOR FILING DATE: 1998-05-15  
 PRIOR APPLICATION NUMBER: 60/085579  
 PRIOR FILING DATE: 1998-05-15  
 PRIOR APPLICATION NUMBER: 60/085580  
 PRIOR FILING DATE: 1998-05-15  
 PRIOR APPLICATION NUMBER: 60/085573  
 PRIOR FILING DATE: 1998-05-15  
 PRIOR APPLICATION NUMBER: 60/085704  
 PRIOR FILING DATE: 1998-05-15  
 PRIOR APPLICATION NUMBER: 60/085697

Query Match 99.9%; Score 1410; DB 9; Length 273;  
 Best Local Similarity 99.6%; Pred. No. 9.2e-94;  
 Matches 253; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TEHAYRPGRRVCAVAHADPVSESVORVYQPLITTCGHRACSTYRTYRATYRSPGL 60  
 DB 20 TEHAYRPGRRVCAVAHADPVSESVORVYQPLITTCGHRACSTYRTYRATYRSPGL 79  
 QY 61 APARPRVACCPGMRKRTSGLPACGAALICQPPCRNGSCVQDGRCPAGMRGDTCCQSDVD 120  
 DB 80 APARPRVACCPGMRKRTSGLPACGAALICQPPCRNGSCVQDGRCPAGMRGDTCCQSDVD 139  
 QY 121 ECSARRGGCPQRCVNTAGSYWCQCEGHSLSADGTLCTPKGPPRVANPNVCUSAMKEE 180  
 DB 140 ECSARRGGCPQRCVNTAGSYWCQCEGHSLSADGTLCTPKGPPRVANPNVCUSAMKEE 199  
 QY 181 VORLOSRYVDLLEKXQVLYAPLHSLASQALEHGLPDPGSLVHSFOQGRIDSLSQGISF 240  
 DB 200 VORLOSRYVDLLEKXQVLYAPLHSLASQALEHGLPDPGSLVHSFOQGRIDSLSQGISF 259  
 QY 241 LEEQUGSCGCKKDS 254  
 DB 260 LEEQUGSCGCKKDS 273

RESULT 5  
 US-09-978-295A-508  
 ; Sequence 508, Application US/0978295A  
 ; Patent No. US20020156006A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ashkenazi, Avi

APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary B.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630PIC11  
CURRENT APPLICATION NUMBER: US/09/978,295A  
CURRENT FILING DATE: 2001-10-15  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/064249  
PRIOR FILING DATE: 1997-11-03  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/066364  
PRIOR FILING DATE: 1997-11-21  
PRIOR APPLICATION NUMBER: 60/077450  
PRIOR FILING DATE: 1998-03-10  
PRIOR APPLICATION NUMBER: 60/077632  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077641  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077649  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077791  
PRIOR FILING DATE: 1998-03-12  
PRIOR APPLICATION NUMBER: 60/078004  
PRIOR FILING DATE: 1998-03-13  
PRIOR APPLICATION NUMBER: 60/078886  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/078936  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/078910  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/078939  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/079294  
PRIOR FILING DATE: 1998-03-25  
PRIOR APPLICATION NUMBER: 60/079656  
PRIOR FILING DATE: 1998-03-26  
PRIOR APPLICATION NUMBER: 60/079664  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/079689  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/079663  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/079728  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/079786  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/079920  
PRIOR FILING DATE: 1998-03-30  
PRIOR APPLICATION NUMBER: 60/079923  
PRIOR FILING DATE: 1998-03-30  
PRIOR APPLICATION NUMBER: 60/080105  
PRIOR FILING DATE: 1998-03-31  
PRIOR APPLICATION NUMBER: 60/080107  
PRIOR FILING DATE: 1998-03-31  
PRIOR APPLICATION NUMBER: 60/080165  
PRIOR FILING DATE: 1998-03-31  
PRIOR APPLICATION NUMBER: 60/080194  
PRIOR FILING DATE: 1998-03-31  
PRIOR APPLICATION NUMBER: 60/080327  
PRIOR FILING DATE: 1998-04-01  
PRIOR APPLICATION NUMBER: 60/080328  
PRIOR FILING DATE: 1998-04-01  
PRIOR APPLICATION NUMBER: 60/080333  
PRIOR FILING DATE: 1998-04-01  
PRIOR APPLICATION NUMBER: 60/080334  
PRIOR FILING DATE: 1998-04-01  
PRIOR APPLICATION NUMBER: 60/081070  
PRIOR FILING DATE: 1998-04-08  
PRIOR APPLICATION NUMBER: 60/081049  
PRIOR FILING DATE: 1998-04-08  
PRIOR APPLICATION NUMBER: 60/081071  
PRIOR FILING DATE: 1998-04-08  
PRIOR APPLICATION NUMBER: 60/081195  
PRIOR FILING DATE: 1998-04-08  
PRIOR APPLICATION NUMBER: 60/081203  
PRIOR FILING DATE: 1998-04-09  
PRIOR APPLICATION NUMBER: 60/081229  
PRIOR FILING DATE: 1998-04-09  
PRIOR APPLICATION NUMBER: 60/081955  
PRIOR FILING DATE: 1998-04-15  
PRIOR APPLICATION NUMBER: 60/081817  
PRIOR FILING DATE: 1998-04-15  
PRIOR APPLICATION NUMBER: 60/081819  
PRIOR FILING DATE: 1998-04-15  
PRIOR APPLICATION NUMBER: 60/081952  
PRIOR FILING DATE: 1998-04-15  
PRIOR APPLICATION NUMBER: 60/081838  
PRIOR FILING DATE: 1998-04-15  
PRIOR APPLICATION NUMBER: 60/082568  
PRIOR FILING DATE: 1998-04-21  
PRIOR APPLICATION NUMBER: 60/082569  
PRIOR FILING DATE: 1998-04-21  
PRIOR APPLICATION NUMBER: 60/082704  
PRIOR FILING DATE: 1998-04-22  
PRIOR APPLICATION NUMBER: 60/082804  
PRIOR FILING DATE: 1998-04-22  
PRIOR APPLICATION NUMBER: 60/082700  
PRIOR FILING DATE: 1998-04-22  
PRIOR APPLICATION NUMBER: 60/082797  
PRIOR FILING DATE: 1998-04-22  
PRIOR APPLICATION NUMBER: 60/082796  
PRIOR FILING DATE: 1998-04-23  
PRIOR APPLICATION NUMBER: 60/083336  
PRIOR FILING DATE: 1998-04-27  
PRIOR APPLICATION NUMBER: 60/083322  
PRIOR FILING DATE: 1998-04-28  
PRIOR APPLICATION NUMBER: 60/083392  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083495  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083496  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083499  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083545  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083554

PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083558  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083559  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083500  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083742  
PRIOR FILING DATE: 1998-04-30  
PRIOR APPLICATION NUMBER: 60/084366  
PRIOR FILING DATE: 1998-05-05  
PRIOR APPLICATION NUMBER: 60/084414  
PRIOR FILING DATE: 1998-05-06  
PRIOR APPLICATION NUMBER: 60/084441  
PRIOR FILING DATE: 1998-05-06  
PRIOR APPLICATION NUMBER: 60/084637  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/084639  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/084640  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/084598  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/084600  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/084627  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/084643  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/085339  
PRIOR FILING DATE: 1998-05-13  
PRIOR APPLICATION NUMBER: 60/085338  
PRIOR FILING DATE: 1998-05-13  
PRIOR APPLICATION NUMBER: 60/085323  
PRIOR FILING DATE: 1998-05-13  
PRIOR APPLICATION NUMBER: 60/085582  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085700  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085689  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085579  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085580  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085573  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085704  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085697

Query Match 99.94; Score 1410; DB 9; Length 273;  
Best Local Similarity 99.64; Pred. No. 9.2e-94;  
Matches 253; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

1 TEHAYRGRRCVAVRAGDPSVSEFVQVYQPFLLTCDGHRACSTYRTTIRTAVRSSPGL 60  
20 TEHAYRGRRCVAVRAGDPSVSEFVQVYQPFLLTCDGHRACSTYRTTIRTAVRSSPGL 79  
61 AAPAPRYACCPGWRRTSGLPAGCAAIQPPCCRNSSCVQPRGRCRCPAGMRGDTQSDVD 120  
80 AAPAPRYACCPGWRRTSGLPAGCAAIQPPCCRNSSCVQPRGRCRCPAGMRGDTQSDVD 139  
121 ECSARRGGCCPCCNNTGASVWCOCMBGHSLSADGTLGVPGGPPRVAPNPTGVDSANKKE 180  
140 ECSARRGGCCPCCNNTGASVWCOCMBGHSLSADGTLGVPGGPPRVAPNPTGVDSANKKE 199  
181 VQRLQSRVDLLEKTLQVLAPLHSLASQALEHGLPDPGSLVHSGFOQLGRIDSLSEQISF 240  
200 VQRLQSRVDLLEKTLQVLAPLHSLASQALEHGLPDPGSLVHSGFOQLGRIDSLSEQISF 259  
241 LEEQLGSCSCCKDS 254

Db 260 LEEQLGSCSCCKDS 273

RESULT 6  
US-09-978-697-506  
Sequence 506, Application US/09978697  
Patent No. US20020169284A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gertlisen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630P1C27  
CURRENT FILING DATE: 2001-10-16  
CURRENT FILING DATE: 2001-10-16  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/064249  
PRIOR FILING DATE: 1997-11-03  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/066364  
PRIOR FILING DATE: 1997-11-21  
PRIOR APPLICATION NUMBER: 60/077450  
PRIOR FILING DATE: 1998-03-10  
PRIOR APPLICATION NUMBER: 60/077632  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077641  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077649  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077791  
PRIOR FILING DATE: 1998-03-12  
PRIOR APPLICATION NUMBER: 60/078004  
PRIOR FILING DATE: 1998-03-13  
PRIOR APPLICATION NUMBER: 60/078886  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/078936  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/078910  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/078939  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/079294  
PRIOR FILING DATE: 1998-03-25  
PRIOR APPLICATION NUMBER: 60/079656

; PRIOR FILING DATE: 1998-03-26  
 ; PRIOR APPLICATION NUMBER: 60/079664  
 ; PRIOR FILING DATE: 1998-03-27  
 ; PRIOR APPLICATION NUMBER: 60/079689  
 ; PRIOR FILING DATE: 1998-03-27  
 ; PRIOR APPLICATION NUMBER: 60/079663  
 ; PRIOR FILING DATE: 1998-03-27  
 ; PRIOR APPLICATION NUMBER: 60/079728  
 ; PRIOR FILING DATE: 1998-03-27  
 ; PRIOR APPLICATION NUMBER: 60/079786  
 ; PRIOR FILING DATE: 1998-03-27  
 ; PRIOR APPLICATION NUMBER: 60/079920  
 ; PRIOR FILING DATE: 1998-03-30  
 ; PRIOR APPLICATION NUMBER: 60/079923  
 ; PRIOR FILING DATE: 1998-03-30  
 ; PRIOR APPLICATION NUMBER: 60/080105  
 ; PRIOR FILING DATE: 1998-03-31  
 ; PRIOR APPLICATION NUMBER: 60/080107  
 ; PRIOR FILING DATE: 1998-03-31  
 ; PRIOR APPLICATION NUMBER: 60/080165  
 ; PRIOR FILING DATE: 1998-03-31  
 ; PRIOR APPLICATION NUMBER: 60/080194  
 ; PRIOR FILING DATE: 1998-03-31  
 ; PRIOR APPLICATION NUMBER: 60/080327  
 ; PRIOR FILING DATE: 1998-04-01  
 ; PRIOR APPLICATION NUMBER: 60/080328  
 ; PRIOR FILING DATE: 1998-04-01  
 ; PRIOR APPLICATION NUMBER: 60/080333  
 ; PRIOR FILING DATE: 1998-04-01  
 ; PRIOR APPLICATION NUMBER: 60/080334  
 ; PRIOR FILING DATE: 1998-04-01  
 ; PRIOR APPLICATION NUMBER: 60/081070  
 ; PRIOR FILING DATE: 1998-04-08  
 ; PRIOR APPLICATION NUMBER: 60/081049  
 ; PRIOR FILING DATE: 1998-04-08  
 ; PRIOR APPLICATION NUMBER: 60/081071  
 ; PRIOR FILING DATE: 1998-04-08  
 ; PRIOR APPLICATION NUMBER: 60/081195  
 ; PRIOR FILING DATE: 1998-04-08  
 ; PRIOR APPLICATION NUMBER: 60/081203  
 ; PRIOR FILING DATE: 1998-04-09  
 ; PRIOR APPLICATION NUMBER: 60/081229  
 ; PRIOR FILING DATE: 1998-04-09  
 ; PRIOR APPLICATION NUMBER: 60/081955  
 ; PRIOR FILING DATE: 1998-04-15  
 ; PRIOR APPLICATION NUMBER: 60/081817  
 ; PRIOR FILING DATE: 1998-04-15  
 ; PRIOR APPLICATION NUMBER: 60/081819  
 ; PRIOR FILING DATE: 1998-04-15  
 ; PRIOR APPLICATION NUMBER: 60/081952  
 ; PRIOR FILING DATE: 1998-04-15  
 ; PRIOR APPLICATION NUMBER: 60/081838  
 ; PRIOR FILING DATE: 1998-04-15  
 ; PRIOR APPLICATION NUMBER: 60/082568  
 ; PRIOR FILING DATE: 1998-04-21  
 ; PRIOR APPLICATION NUMBER: 60/082569  
 ; PRIOR FILING DATE: 1998-04-21  
 ; PRIOR APPLICATION NUMBER: 60/082704  
 ; PRIOR FILING DATE: 1998-04-22  
 ; PRIOR APPLICATION NUMBER: 60/082804  
 ; PRIOR FILING DATE: 1998-04-22  
 ; PRIOR APPLICATION NUMBER: 60/082700  
 ; PRIOR FILING DATE: 1998-04-22  
 ; PRIOR APPLICATION NUMBER: 60/082797  
 ; PRIOR FILING DATE: 1998-04-22  
 ; PRIOR APPLICATION NUMBER: 60/082796  
 ; PRIOR FILING DATE: 1998-04-23  
 ; PRIOR APPLICATION NUMBER: 60/083336  
 ; PRIOR FILING DATE: 1998-04-27  
 ; PRIOR APPLICATION NUMBER: 60/083322  
 ; PRIOR FILING DATE: 1998-04-28  
 ; PRIOR APPLICATION NUMBER: 60/083392  
 ; PRIOR FILING DATE: 1998-04-29

; PRIOR APPLICATION NUMBER: 60/083495  
 ; PRIOR FILING DATE: 1998-04-29  
 ; PRIOR APPLICATION NUMBER: 60/083496  
 ; PRIOR FILING DATE: 1998-04-29  
 ; PRIOR APPLICATION NUMBER: 60/083499  
 ; PRIOR FILING DATE: 1998-04-29  
 ; PRIOR APPLICATION NUMBER: 60/083545  
 ; PRIOR FILING DATE: 1998-04-29  
 ; PRIOR APPLICATION NUMBER: 60/083554  
 ; PRIOR FILING DATE: 1998-04-29  
 ; PRIOR APPLICATION NUMBER: 60/083558  
 ; PRIOR FILING DATE: 1998-04-29  
 ; PRIOR APPLICATION NUMBER: 60/083559  
 ; PRIOR FILING DATE: 1998-04-29  
 ; PRIOR APPLICATION NUMBER: 60/083500  
 ; PRIOR FILING DATE: 1998-04-29  
 ; PRIOR APPLICATION NUMBER: 60/083742  
 ; PRIOR FILING DATE: 1998-04-30  
 ; PRIOR APPLICATION NUMBER: 60/084366  
 ; PRIOR FILING DATE: 1998-05-05  
 ; PRIOR APPLICATION NUMBER: 60/084414  
 ; PRIOR FILING DATE: 1998-05-06  
 ; PRIOR APPLICATION NUMBER: 60/084441  
 ; PRIOR FILING DATE: 1998-05-06  
 ; PRIOR APPLICATION NUMBER: 60/084637  
 ; PRIOR FILING DATE: 1998-05-07  
 ; PRIOR APPLICATION NUMBER: 60/084639  
 ; PRIOR FILING DATE: 1998-05-07  
 ; PRIOR APPLICATION NUMBER: 60/084640  
 ; PRIOR FILING DATE: 1998-05-07  
 ; PRIOR APPLICATION NUMBER: 60/084598  
 ; PRIOR FILING DATE: 1998-05-07  
 ; PRIOR APPLICATION NUMBER: 60/084600  
 ; PRIOR FILING DATE: 1998-05-07  
 ; PRIOR APPLICATION NUMBER: 60/084627  
 ; PRIOR FILING DATE: 1998-05-07  
 ; PRIOR APPLICATION NUMBER: 60/084643  
 ; PRIOR FILING DATE: 1998-05-07  
 ; PRIOR APPLICATION NUMBER: 60/085339  
 ; PRIOR FILING DATE: 1998-05-13  
 ; PRIOR APPLICATION NUMBER: 60/085338  
 ; PRIOR FILING DATE: 1998-05-13  
 ; PRIOR APPLICATION NUMBER: 60/085323  
 ; PRIOR FILING DATE: 1998-05-13  
 ; PRIOR APPLICATION NUMBER: 60/085582  
 ; PRIOR FILING DATE: 1998-05-15  
 ; PRIOR APPLICATION NUMBER: 60/085700  
 ; PRIOR FILING DATE: 1998-05-15  
 ; PRIOR APPLICATION NUMBER: 60/085689  
 ; PRIOR FILING DATE: 1998-05-15  
 ; PRIOR APPLICATION NUMBER: 60/085579  
 ; PRIOR FILING DATE: 1998-05-15  
 ; PRIOR APPLICATION NUMBER: 60/085580  
 ; PRIOR FILING DATE: 1998-05-15  
 ; PRIOR APPLICATION NUMBER: 60/085573  
 ; PRIOR FILING DATE: 1998-05-15  
 ; PRIOR APPLICATION NUMBER: 60/085704  
 ; PRIOR FILING DATE: 1998-05-15  
 ; PRIOR APPLICATION NUMBER: 60/085697

Query Match 99.9%; Score 1410; DB 9; Length 273;

Best Local Similarity 99.6%; Pred. No. 9.2e-94;

Matches 253; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TEHAYRPGRRVCAVRAHGDVSESVQRYQVYQFLLTTCGHRACSTYRTIYRTAVRRSGL 60  
 Db 20 TEHAYRPGRRVCAVRAHGDVSESVQRYQVYQFLLTTCGHRACSTYRTIYRTAVRRSGL 79  
 QY 61 APARPRYACCPGWKTSGLPGACGAAICQPCNRNGSCVQPCRCPCAGWRGDTCSQSDVD 120  
 Db 80 APARPRYACCPGWKTSGLPGACGAAICQPCNRNGSCVQPCRCPCAGWRGDTCSQSDVD 139  
 QY 121 ECSARRGGCPCQRCVNTAGSYWCQCWEHSLSDADGTLCPKGGPPRVPANPTGVDSAMKEE 180



Db 140 ECARRGCGCRCTNIGSTWCCWEGHSLADGTTLCVPCGPPRVAHPTGVDANKER 199  
QY 181 VORLOSRVDLLEKRLQVLAPLHSLASQALEHGLPPGSLVHSPQOLGRIDSLSEQISF 240  
Db 200 VORLOSRVDLLEKRLQVLAPLHSLASQALEHGLPPGSLVHSPQOLGRIDSLSEQISF 259  
QY 241 LEBOLGSCCKKDS 254  
Db 260 LEBOLGSCCKKDS 273

RESULT 7  
US-09-978-697-508  
Sequence 508, Application US/09978697  
Patent No. US20020169284A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gertlisen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James J.  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630PIC27  
CURRENT APPLICATION NUMBER: US/09/978,697  
CURRENT FILING DATE: 2001-10-16  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/064249  
PRIOR FILING DATE: 1997-11-03  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/066364  
PRIOR FILING DATE: 1997-11-21  
PRIOR APPLICATION NUMBER: 60/077450  
PRIOR FILING DATE: 1998-03-10  
PRIOR APPLICATION NUMBER: 60/077632  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077641  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077649  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077791  
PRIOR FILING DATE: 1998-03-12  
PRIOR APPLICATION NUMBER: 60/078004  
PRIOR FILING DATE: 1998-03-13  
PRIOR APPLICATION NUMBER: 60/078886  
PRIOR FILING DATE: 1998-03-20

PRIOR APPLICATION NUMBER: 60/078936  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/078910  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/078939  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/079294  
PRIOR FILING DATE: 1998-03-25  
PRIOR APPLICATION NUMBER: 60/079656  
PRIOR FILING DATE: 1998-03-26  
PRIOR APPLICATION NUMBER: 60/079664  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/079689  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/079663  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/079728  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/079786  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/079920  
PRIOR FILING DATE: 1998-03-30  
PRIOR APPLICATION NUMBER: 60/079923  
PRIOR FILING DATE: 1998-03-30  
PRIOR APPLICATION NUMBER: 60/080105  
PRIOR FILING DATE: 1998-03-31  
PRIOR APPLICATION NUMBER: 60/080107  
PRIOR FILING DATE: 1998-03-31  
PRIOR APPLICATION NUMBER: 60/080165  
PRIOR FILING DATE: 1998-03-31  
PRIOR APPLICATION NUMBER: 60/080194  
PRIOR FILING DATE: 1998-03-31  
PRIOR APPLICATION NUMBER: 60/080327  
PRIOR FILING DATE: 1998-04-01  
PRIOR APPLICATION NUMBER: 60/080328  
PRIOR FILING DATE: 1998-04-01  
PRIOR APPLICATION NUMBER: 60/080333  
PRIOR FILING DATE: 1998-04-01  
PRIOR APPLICATION NUMBER: 60/080334  
PRIOR FILING DATE: 1998-04-01  
PRIOR APPLICATION NUMBER: 60/081070  
PRIOR FILING DATE: 1998-04-08  
PRIOR APPLICATION NUMBER: 60/081049  
PRIOR FILING DATE: 1998-04-08  
PRIOR APPLICATION NUMBER: 60/081071  
PRIOR FILING DATE: 1998-04-08  
PRIOR APPLICATION NUMBER: 60/081195  
PRIOR FILING DATE: 1998-04-08  
PRIOR APPLICATION NUMBER: 60/081203  
PRIOR FILING DATE: 1998-04-09  
PRIOR APPLICATION NUMBER: 60/081229  
PRIOR FILING DATE: 1998-04-09  
PRIOR APPLICATION NUMBER: 60/081955  
PRIOR FILING DATE: 1998-04-15  
PRIOR APPLICATION NUMBER: 60/081817  
PRIOR FILING DATE: 1998-04-15  
PRIOR APPLICATION NUMBER: 60/081819  
PRIOR FILING DATE: 1998-04-15  
PRIOR APPLICATION NUMBER: 60/081952  
PRIOR FILING DATE: 1998-04-15  
PRIOR APPLICATION NUMBER: 60/081838  
PRIOR FILING DATE: 1998-04-15  
PRIOR APPLICATION NUMBER: 60/082568  
PRIOR FILING DATE: 1998-04-21  
PRIOR APPLICATION NUMBER: 60/082569  
PRIOR FILING DATE: 1998-04-21  
PRIOR APPLICATION NUMBER: 60/082704  
PRIOR FILING DATE: 1998-04-22  
PRIOR APPLICATION NUMBER: 60/082804  
PRIOR FILING DATE: 1998-04-22  
PRIOR APPLICATION NUMBER: 60/082700  
PRIOR FILING DATE: 1998-04-22  
PRIOR APPLICATION NUMBER: 60/082797

; PRIOR FILING DATE: 1998-04-22  
; PRIOR APPLICATION NUMBER: 60/082796  
; PRIOR FILING DATE: 1998-04-23  
; PRIOR APPLICATION NUMBER: 60/083336  
; PRIOR FILING DATE: 1998-04-27  
; PRIOR APPLICATION NUMBER: 60/083322  
; PRIOR FILING DATE: 1998-04-28  
; PRIOR APPLICATION NUMBER: 60/083392  
; PRIOR FILING DATE: 1998-04-29  
; PRIOR APPLICATION NUMBER: 60/083495  
; PRIOR FILING DATE: 1998-04-29  
; PRIOR APPLICATION NUMBER: 60/083496  
; PRIOR FILING DATE: 1998-04-29  
; PRIOR APPLICATION NUMBER: 60/083499  
; PRIOR FILING DATE: 1998-04-29  
; PRIOR APPLICATION NUMBER: 60/083545  
; PRIOR FILING DATE: 1998-04-29  
; PRIOR APPLICATION NUMBER: 60/083554  
; PRIOR FILING DATE: 1998-04-29  
; PRIOR APPLICATION NUMBER: 60/083558  
; PRIOR FILING DATE: 1998-04-29  
; PRIOR APPLICATION NUMBER: 60/083559  
; PRIOR FILING DATE: 1998-04-29  
; PRIOR APPLICATION NUMBER: 60/083500  
; PRIOR FILING DATE: 1998-04-29  
; PRIOR APPLICATION NUMBER: 60/083742  
; PRIOR FILING DATE: 1998-04-30  
; PRIOR APPLICATION NUMBER: 60/084366  
; PRIOR FILING DATE: 1998-05-05  
; PRIOR APPLICATION NUMBER: 60/084414  
; PRIOR FILING DATE: 1998-05-06  
; PRIOR APPLICATION NUMBER: 60/084441  
; PRIOR FILING DATE: 1998-05-06  
; PRIOR APPLICATION NUMBER: 60/084637  
; PRIOR FILING DATE: 1998-05-07  
; PRIOR APPLICATION NUMBER: 60/084639  
; PRIOR FILING DATE: 1998-05-07  
; PRIOR APPLICATION NUMBER: 60/084640  
; PRIOR FILING DATE: 1998-05-07  
; PRIOR APPLICATION NUMBER: 60/084598  
; PRIOR FILING DATE: 1998-05-07  
; PRIOR APPLICATION NUMBER: 60/084600  
; PRIOR FILING DATE: 1998-05-07  
; PRIOR APPLICATION NUMBER: 60/084627  
; PRIOR FILING DATE: 1998-05-07  
; PRIOR APPLICATION NUMBER: 60/084643  
; PRIOR FILING DATE: 1998-05-07  
; PRIOR APPLICATION NUMBER: 60/085339  
; PRIOR FILING DATE: 1998-05-13  
; PRIOR APPLICATION NUMBER: 60/085338  
; PRIOR FILING DATE: 1998-05-13  
; PRIOR APPLICATION NUMBER: 60/085323  
; PRIOR FILING DATE: 1998-05-13  
; PRIOR APPLICATION NUMBER: 60/085582  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085700  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085689  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085579  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085580  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085573  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085704  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 99.9%; Score 1410; DB 9; Length 273;  
Best Local Similarity 99.6%; Pred. No. 9.2e-94;  
Matches 253; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TEHAYRPGRRVCNRAHGDVSESFVQRYVQPLTTCQHRACSTYRTIYRTAYRRSPGL 60  
DB 20 TEHAYRPGRRVCNRAHGDVSESFVQRYVQPLTTCQHRACSTYRTIYRTAYRRSPGL 79  
QY 61 APARPRYACCPGWKRTSGLPAGCAAI COPPCRNCGSCVQPCRCRCAGWRGDTCCSDVD 120  
DB 80 APARPRYACCPGWKRTSGLPAGCAAI COPPCRNCGSCVQPCRCRCAGWRGDTCCSDVD 139  
QY 121 ECSARRGGCPQRCVNTAGSYWCQWEGHSLSDAGTLCVPKGGPPRVAPNPTGVDSAMKEE 180  
DB 140 ECSARRGGCPQRCVNTAGSYWCQWEGHSLSDAGTLCVPKGGPPRVAPNPTGVDSAMKEE 199  
QY 181 VQRLQSRVDLLEKQLVLAPLHSLASQALEHGLDPGSLLVHSPQQLGRDLSLSEQISF 240  
DB 200 VQRLQSRVDLLEKQLVLAPLHSLASQALEHGLDPGSLLVHSPQQLGRDLSLSEQISF 259  
QY 241 LBEQLGSCSKKDS 254  
DB 260 LBEQLGSCSKKDS 273  
RESULT 8  
US-09-978-192A-506  
; Sequence 506 Application US/09978192A  
; Patent No. US20020177553A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Shelton, David L.  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2630PIC9  
; CURRENT APPLICATION NUMBER: US/09/978, 192A  
; CURRENT FILING DATE: 2001-10-15  
; PRIOR APPLICATION NUMBER: 09/918585  
; PRIOR FILING DATE: 2001-07-30  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/064249  
; PRIOR FILING DATE: 1997-11-03  
; PRIOR APPLICATION NUMBER: 60/065311  
; PRIOR FILING DATE: 1997-11-13  
; PRIOR APPLICATION NUMBER: 60/066364  
; PRIOR FILING DATE: 1997-11-21  
; PRIOR APPLICATION NUMBER: 60/077450  
; PRIOR FILING DATE: 1998-03-10  
; PRIOR APPLICATION NUMBER: 60/077632  
; PRIOR FILING DATE: 1998-03-11  
; PRIOR APPLICATION NUMBER: 60/077641



```
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match          99.9%; Score 1410; DB 9; Length 273;
Best Local Similarity 99.8%; Pred. No. 9.2e-94;
Matches 253; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TEHAYRGRVCAVRAGDPVSESFVORVQVPLTTCDDHRACTVYRTYRSPGL 60
Db 20 TEHAYRGRVCAVRAGDPVSESFVORVQVPLTTCDDHRACTVYRTYRSPGL 79
Qy 61 APARPRYACCPGKRTSLGACAAICQPPCRNGSCVQPGRCRCPAGWRGDTQSDVD 120
Db 80 APARPRYACCPGKRTSLGACAAICQPPCRNGSCVQPGRCRCPAGWRGDTQSDVD 139
Qy 121 ECSARRGCGPCRCVNTAGSVWCQWEGHSLSDGTLCPVKGPPRVAPNPTGVDSAMKEE 180
Db 140 ECSARRGCGPCRCVNTAGSVWCQWEGHSLSDGTLCPVKGPPRVAPNPTGVDSAMKEE 199
Qy 181 VORLQSRVDLLEKQLVLAPLHSLAQLEHGLPDPGSLLVHVSFOQLGRIDSLSBQISF 240
Db 200 VORLQSRVDLLEKQLVLAPLHSLAQLEHGLPDPGSLLVHVSFOQLGRIDSLSBQISF 259
Qy 241 LEEQSGSCCKKDS 254
Db 260 LEEQSGSCCKKDS 273

RESULT 9
US-09-978-192A-508
; Sequence 508, Application US/09978192A
; Patent No. US20020177553A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C9
; CURRENT APPLICATION NUMBER: US/09/978.192A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066364
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/077450
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 60/077632
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077641
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077649
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077791
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/078004
; PRIOR FILING DATE: 1998-03-13
; PRIOR APPLICATION NUMBER: 60/078886
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078936
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078939
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079664
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079663
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079786
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079920
; PRIOR FILING DATE: 1998-03-30
; PRIOR APPLICATION NUMBER: 60/079923
; PRIOR FILING DATE: 1998-03-30
; PRIOR APPLICATION NUMBER: 60/080105
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080107
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080165
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080194
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080327
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080328
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080333
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080334
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/081070
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081049
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081071
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081195
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081203
; PRIOR FILING DATE: 1998-04-09
; PRIOR APPLICATION NUMBER: 60/081229
; PRIOR FILING DATE: 1998-04-09
; PRIOR APPLICATION NUMBER: 60/081955
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081817
```

PRIOR FILING DATE: 1998-04-15  
PRIOR APPLICATION NUMBER: 60/081819  
PRIOR FILING DATE: 1998-04-15  
PRIOR APPLICATION NUMBER: 60/081952  
PRIOR FILING DATE: 1998-04-15  
PRIOR APPLICATION NUMBER: 60/081838  
PRIOR FILING DATE: 1998-04-15  
PRIOR APPLICATION NUMBER: 60/082568  
PRIOR FILING DATE: 1998-04-21  
PRIOR APPLICATION NUMBER: 60/082569  
PRIOR FILING DATE: 1998-04-21  
PRIOR APPLICATION NUMBER: 60/082704  
PRIOR FILING DATE: 1998-04-22  
PRIOR APPLICATION NUMBER: 60/082804  
PRIOR FILING DATE: 1998-04-22  
PRIOR APPLICATION NUMBER: 60/082700  
PRIOR FILING DATE: 1998-04-22  
PRIOR APPLICATION NUMBER: 60/082797  
PRIOR FILING DATE: 1998-04-22  
PRIOR APPLICATION NUMBER: 60/082796  
PRIOR FILING DATE: 1998-04-23  
PRIOR APPLICATION NUMBER: 60/083336  
PRIOR FILING DATE: 1998-04-27  
PRIOR APPLICATION NUMBER: 60/083322  
PRIOR FILING DATE: 1998-04-28  
PRIOR APPLICATION NUMBER: 60/083392  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083495  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083496  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083499  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083545  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083554  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083558  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083559  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083500  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083742  
PRIOR FILING DATE: 1998-04-30  
PRIOR APPLICATION NUMBER: 60/084366  
PRIOR FILING DATE: 1998-05-05  
PRIOR APPLICATION NUMBER: 60/084414  
PRIOR FILING DATE: 1998-05-06  
PRIOR APPLICATION NUMBER: 60/084441  
PRIOR FILING DATE: 1998-05-06  
PRIOR APPLICATION NUMBER: 60/084637  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/084639  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/084640  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/084598  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/084600  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/084627  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/084643  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/085339  
PRIOR FILING DATE: 1998-05-13  
PRIOR APPLICATION NUMBER: 60/085338  
PRIOR FILING DATE: 1998-05-13  
PRIOR APPLICATION NUMBER: 60/085323  
PRIOR FILING DATE: 1998-05-13  
PRIOR APPLICATION NUMBER: 60/085582  
PRIOR FILING DATE: 1998-05-15

PRIOR APPLICATION NUMBER: 60/085700  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085689  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085579  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085580  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085573  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085704  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085697

Query Match 99.9%; Score 1410; DB 9; Length 273;  
Best Local Similarity 99.6%; Pred. No. 9.2e-94;  
Matches 253; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TEHAYRGRVCAVRAHGDVSEFVQRYOPLTTCDGRACSTYRTTAYRSPGL 60  
DB 20 TEHAYRGRVCAVRAHGDVSEFVQRYOPLTTCDGRACSTYRTTAYRSPGL 79  
QY 61 APARPRVACCPGMRKTSGLPGACGAICOPPCRNHGSVOVGRCPAGMRGDTCCSDVD 120  
DB 80 APARPRVACCPGMRKTSGLPGACGAICOPPCRNHGSVOVGRCPAGMRGDTCCSDVD 139  
QY 121 ECSARGGCPQRCVNTAGSYWCQCEHGSLSADGTLCPKGGPRVAPNPTGVDSAMKEE 180  
DB 140 ECSARGGCPQRCVNTAGSYWCQCEHGSLSADGTLCPKGGPRVAPNPTGVDSAMKEE 199  
QY 161 VORLOSVDLLEEXLQVLAFLHSLASQALEHGLPDPSGLVHSPFOULGRIDSLSQISF 240  
DB 200 VORLOSVDLLEEXLQVLAFLHSLASQALEHGLPDPSGLVHSPFOULGRIDSLSQISF 259  
QY 241 LEEOLGSCCKKDS 254  
DB 260 LEEOLGSCCKKDS 273

RESULT 10  
US-09-790-264-10  
Sequence 10, Application US/09790264  
Patent No. US20020028508A1  
GENERAL INFORMATION:  
APPLICANT: Holtzman, Douglas A.  
APPLICANT: Goodheart, Andrew D.J.  
TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING  
TITLE OF INVENTION: PROGNASTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER  
FILE REFERENCE: 0734-322001  
CURRENT APPLICATION NUMBER: US/09/790,264  
CURRENT FILING DATE: 2001-02-21  
PRIOR APPLICATION NUMBER: US 09/065,661  
PRIOR FILING DATE: 1998-04-23  
PRIOR APPLICATION NUMBER: US 09/298,531  
PRIOR FILING DATE: 1999-04-23  
PRIOR APPLICATION NUMBER: US 09/065,363  
PRIOR FILING DATE: 1998-04-23  
PRIOR APPLICATION NUMBER: US 09/337,930  
PRIOR FILING DATE: 1999-06-22  
PRIOR APPLICATION NUMBER: US 09/102,705  
PRIOR FILING DATE: 1998-06-22  
PRIOR APPLICATION NUMBER: US 09/363,630  
PRIOR FILING DATE: 1999-07-29  
PRIOR APPLICATION NUMBER: US 09/124,538  
PRIOR FILING DATE: 1998-07-29  
NUMBER OF SEQ ID NOS: 68  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 10  
LENGTH: 273  
TYPE: PRT  
ORGANISM: Homo sapiens

```
;
; NAME/KEY: SIGNAL
; LOCATION: (1)...(22)
US-09-790-264-10

Query Match      99.8%; Score 1410; DB 10; Length 273;
Best Local Similarity 99.6%; Pred. No. 9.2e-94;
Matches 253; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TEHAYRPGRRVCAVRAHGDVPSESFQVRVYQPFLLTTCGHRACSTYRTIYRTAYRRSPGL 60
DB 20 TEHAYRPGRRVCAVRAHGDVPSESFQVRVYQPFLLTTCGHRACSTYRTIYRTAYRRSPGL 79

QY 61 APARPRYACCPGWKRTSGLPGACGAAICQPPCRNGGSCVQPGRCRCPCAGWRGDTCSQSDVD 120
DB 80 APARPRYACCPGWKRTSGLPGACGAAICQPPCRNGGSCVQPGRCRCPCAGWRGDTCSQSDVD 139

QY 121 ECSARGGCPORCVNTAGSYWCQWEGHSLSDAGTLCVPGKGGPPRVAPNPTGVDSAMKEE 180
DB 140 ECSARGGCPORCVNTAGSYWCQWEGHSLSDAGTLCVPGKGGPPRVAPNPTGVDSAMKEE 199

QY 181 VORLQSRVDLLEEKQLVLAPLHSLASQALEHGLPDPGSLLVHVSFQQLGRIDSLSSEQISF 240
DB 200 VORLQSRVDLLEEKQLVLAPLHSLASQALEHGLPDPGSLLVHVSFQQLGRIDSLSSEQISF 259

QY 241 LEEQLGSCCKKDS 254
DB 260 LEEQLGSCCKKDS 273

RESULT 11
US-09-790-264-12
; Sequence 12, Application US/09790264
; Patent No. US20020028508A1
; GENERAL INFORMATION:
; APPLICANT: Holtzman, Douglas A.
; APPLICANT: McCarthy, Sean A.
; APPLICANT: Goodenough, Andrew D.J.
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
; TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
; TITLE OF INVENTION: USES
; FILE REFERENCE: 07334-322001
; CURRENT APPLICATION NUMBER: US/09/790,264
; CURRENT FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: US 09/065,661
; PRIOR FILING DATE: 1998-04-23
; PRIOR APPLICATION NUMBER: US 09/298,531
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: US 09/065,363
; PRIOR FILING DATE: 1998-04-23
; PRIOR APPLICATION NUMBER: US 09/337,930
; PRIOR FILING DATE: 1999-06-22
; PRIOR APPLICATION NUMBER: US 09/102,705
; PRIOR FILING DATE: 1998-06-22
; PRIOR APPLICATION NUMBER: US 09/363,630
; PRIOR FILING DATE: 1999-07-29
; PRIOR APPLICATION NUMBER: US 09/124,538
; PRIOR FILING DATE: 1998-07-29
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-790-264-12

Query Match      98.7%; Score 1392; DB 10; Length 251;
Best Local Similarity 99.6%; Pred. No. 1.6e-92;
Matches 250; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 AYRPGRRVCAVRAHGDVPSESFQVRVYQPFLLTTCGHRACSTYRTIYRTAYRRSPGLAPA 63
DB 1 AYRPGRRVCAVRAHGDVPSESFQVRVYQPFLLTTCGHRACSTYRTIYRTAYRRSPGLAPA 60

;
; NAME/KEY: SIGNAL
; LOCATION: (1)...(22)
US-09-790-264-10

Query Match      99.8%; Score 1410; DB 10; Length 273;
Best Local Similarity 99.6%; Pred. No. 9.2e-94;
Matches 253; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TEHAYRPGRRVCAVRAHGDVPSESFQVRVYQPFLLTTCGHRACSTYRTIYRTAYRRSPGL 60
DB 20 TEHAYRPGRRVCAVRAHGDVPSESFQVRVYQPFLLTTCGHRACSTYRTIYRTAYRRSPGL 79

QY 61 APARPRYACCPGWKRTSGLPGACGAAICQPPCRNGGSCVQPGRCRCPCAGWRGDTCSQSDVD 120
DB 80 APARPRYACCPGWKRTSGLPGACGAAICQPPCRNGGSCVQPGRCRCPCAGWRGDTCSQSDVD 139

QY 121 ECSARGGCPORCVNTAGSYWCQWEGHSLSDAGTLCVPGKGGPPRVAPNPTGVDSAMKEE 180
DB 140 ECSARGGCPORCVNTAGSYWCQWEGHSLSDAGTLCVPGKGGPPRVAPNPTGVDSAMKEE 199

QY 181 VORLQSRVDLLEEKQLVLAPLHSLASQALEHGLPDPGSLLVHVSFQQLGRIDSLSSEQISF 240
DB 200 VORLQSRVDLLEEKQLVLAPLHSLASQALEHGLPDPGSLLVHVSFQQLGRIDSLSSEQISF 259

QY 241 LEEQLGSCCKKDS 254
DB 260 LEEQLGSCCKKDS 273

RESULT 12
US-09-978-295A-2
; Sequence 2, Application US/09978295A
; Patent No. US20020156006A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C11
; CURRENT APPLICATION NUMBER: US/09/978,295A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066364
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/077450
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 60/077632
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077641
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077649
; PRIOR FILING DATE: 1998-03-11
```

1	PRIOR APPLICATION NUMBER: 60/077791
2	PRIOR FILING DATE: 1998-03-12
3	PRIOR APPLICATION NUMBER: 60/078004
4	PRIOR FILING DATE: 1998-03-13
5	PRIOR APPLICATION NUMBER: 60/078886
6	PRIOR FILING DATE: 1998-03-20
7	PRIOR APPLICATION NUMBER: 60/078936
8	PRIOR FILING DATE: 1998-03-20
9	PRIOR APPLICATION NUMBER: 60/078910
10	PRIOR FILING DATE: 1998-03-20
11	PRIOR APPLICATION NUMBER: 60/078939
12	PRIOR FILING DATE: 1998-03-20
13	PRIOR APPLICATION NUMBER: 60/079224
14	PRIOR FILING DATE: 1998-03-25
15	PRIOR APPLICATION NUMBER: 60/079656
16	PRIOR FILING DATE: 1998-03-26
17	PRIOR APPLICATION NUMBER: 60/079664
18	PRIOR FILING DATE: 1998-03-27
19	PRIOR APPLICATION NUMBER: 60/079669
20	PRIOR FILING DATE: 1998-03-27
21	PRIOR APPLICATION NUMBER: 60/079663
22	PRIOR FILING DATE: 1998-03-27
23	PRIOR APPLICATION NUMBER: 60/079728
24	PRIOR FILING DATE: 1998-03-27
25	PRIOR APPLICATION NUMBER: 60/079786
26	PRIOR FILING DATE: 1998-03-27
27	PRIOR APPLICATION NUMBER: 60/079920
28	PRIOR FILING DATE: 1998-03-30
29	PRIOR APPLICATION NUMBER: 60/079923
30	PRIOR FILING DATE: 1998-03-30
31	PRIOR APPLICATION NUMBER: 60/080105
32	PRIOR FILING DATE: 1998-03-31
33	PRIOR APPLICATION NUMBER: 60/080107
34	PRIOR FILING DATE: 1998-03-31
35	PRIOR APPLICATION NUMBER: 60/080165
36	PRIOR FILING DATE: 1998-03-31
37	PRIOR APPLICATION NUMBER: 60/080194
38	PRIOR FILING DATE: 1998-03-31
39	PRIOR APPLICATION NUMBER: 60/080327
40	PRIOR FILING DATE: 1998-04-01
41	PRIOR APPLICATION NUMBER: 60/080328
42	PRIOR FILING DATE: 1998-04-01
43	PRIOR APPLICATION NUMBER: 60/080333
44	PRIOR FILING DATE: 1998-04-01
45	PRIOR APPLICATION NUMBER: 60/080344
46	PRIOR FILING DATE: 1998-04-01
47	PRIOR APPLICATION NUMBER: 60/080107
48	PRIOR FILING DATE: 1998-04-08
49	PRIOR APPLICATION NUMBER: 60/081049
50	PRIOR FILING DATE: 1998-04-08
51	PRIOR APPLICATION NUMBER: 60/081071
52	PRIOR FILING DATE: 1998-04-08
53	PRIOR APPLICATION NUMBER: 60/081195
54	PRIOR FILING DATE: 1998-04-08
55	PRIOR APPLICATION NUMBER: 60/081203
56	PRIOR FILING DATE: 1998-04-09
57	PRIOR APPLICATION NUMBER: 60/081229
58	PRIOR FILING DATE: 1998-04-09
59	PRIOR APPLICATION NUMBER: 60/081955
60	PRIOR FILING DATE: 1998-04-15
61	PRIOR APPLICATION NUMBER: 60/081817
62	PRIOR FILING DATE: 1998-04-15
63	PRIOR APPLICATION NUMBER: 60/081819
64	PRIOR FILING DATE: 1998-04-15
65	PRIOR APPLICATION NUMBER: 60/081952
66	PRIOR FILING DATE: 1998-04-15
67	PRIOR APPLICATION NUMBER: 60/081839
68	PRIOR FILING DATE: 1998-04-15
69	PRIOR APPLICATION NUMBER: 60/082568
70	PRIOR FILING DATE: 1998-04-21
71	PRIOR APPLICATION NUMBER: 60/082566
72	PRIOR FILING DATE: 1998-04-21
73	PRIOR APPLICATION NUMBER: 60/082704

PRIOR FILING DATE:	1998-04-22
PRIOR APPLICATION NUMBER:	60/082804
PRIOR FILING DATE:	1998-04-22
PRIOR APPLICATION NUMBER:	60/082700
PRIOR FILING DATE:	1998-04-22
PRIOR APPLICATION NUMBER:	60/082797
PRIOR FILING DATE:	1998-04-22
PRIOR APPLICATION NUMBER:	60/082796
PRIOR FILING DATE:	1998-04-23
PRIOR APPLICATION NUMBER:	60/083336
PRIOR FILING DATE:	1998-04-27
PRIOR APPLICATION NUMBER:	60/083322
PRIOR FILING DATE:	1998-04-28
PRIOR APPLICATION NUMBER:	60/083392
PRIOR FILING DATE:	1998-04-29
PRIOR APPLICATION NUMBER:	60/083495
PRIOR FILING DATE:	1998-04-29
PRIOR APPLICATION NUMBER:	60/083496
PRIOR FILING DATE:	1998-04-29
PRIOR APPLICATION NUMBER:	60/083499
PRIOR FILING DATE:	1998-04-29
PRIOR APPLICATION NUMBER:	60/083545
PRIOR FILING DATE:	1998-04-29
PRIOR APPLICATION NUMBER:	60/083554
PRIOR FILING DATE:	1998-04-29
PRIOR APPLICATION NUMBER:	60/083558
PRIOR FILING DATE:	1998-04-29
PRIOR APPLICATION NUMBER:	60/083559
PRIOR FILING DATE:	1998-04-30
PRIOR APPLICATION NUMBER:	60/083560
PRIOR FILING DATE:	1998-04-30
PRIOR APPLICATION NUMBER:	60/084414
PRIOR FILING DATE:	1998-05-05
PRIOR APPLICATION NUMBER:	60/084433
PRIOR FILING DATE:	1998-05-06
PRIOR APPLICATION NUMBER:	60/084441
PRIOR FILING DATE:	1998-05-07
PRIOR APPLICATION NUMBER:	60/084460
PRIOR FILING DATE:	1998-05-07
PRIOR APPLICATION NUMBER:	60/084598
PRIOR FILING DATE:	1998-05-07
PRIOR APPLICATION NUMBER:	60/084639
PRIOR FILING DATE:	1998-05-07
PRIOR APPLICATION NUMBER:	60/084627
PRIOR FILING DATE:	1998-05-07
PRIOR APPLICATION NUMBER:	60/084643
PRIOR FILING DATE:	1998-05-07
PRIOR APPLICATION NUMBER:	60/085333
PRIOR FILING DATE:	1998-05-13
PRIOR APPLICATION NUMBER:	60/085582
PRIOR FILING DATE:	1998-05-15
PRIOR APPLICATION NUMBER:	60/085700
PRIOR FILING DATE:	1998-05-15
PRIOR APPLICATION NUMBER:	60/085797
PRIOR FILING DATE:	1998-05-15
PRIOR APPLICATION NUMBER:	60/085800
PRIOR FILING DATE:	1998-05-15
PRIOR APPLICATION NUMBER:	60/085779
PRIOR FILING DATE:	1998-05-15
PRIOR APPLICATION NUMBER:	60/085704
PRIOR FILING DATE:	1998-05-15





PRIOR APPLICATION NUMBER: 60/081952  
PRIOR FILING DATE: 1998-04-15  
PRIOR APPLICATION NUMBER: 60/081838  
PRIOR FILING DATE: 1998-04-15  
PRIOR APPLICATION NUMBER: 60/082568  
PRIOR FILING DATE: 1998-04-21  
PRIOR APPLICATION NUMBER: 60/082569  
PRIOR FILING DATE: 1998-04-21  
PRIOR APPLICATION NUMBER: 60/082704  
PRIOR FILING DATE: 1998-04-22  
PRIOR APPLICATION NUMBER: 60/082804  
PRIOR FILING DATE: 1998-04-22  
PRIOR APPLICATION NUMBER: 60/082700  
PRIOR FILING DATE: 1998-04-22  
PRIOR APPLICATION NUMBER: 60/082797  
PRIOR FILING DATE: 1998-04-22  
PRIOR APPLICATION NUMBER: 60/082796  
PRIOR FILING DATE: 1998-04-23  
PRIOR APPLICATION NUMBER: 60/083336  
PRIOR FILING DATE: 1998-04-27  
PRIOR APPLICATION NUMBER: 60/083322  
PRIOR FILING DATE: 1998-04-28  
PRIOR APPLICATION NUMBER: 60/083392  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083495  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083496  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083499  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083545  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083554  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083558  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083559  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083500  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083742  
PRIOR FILING DATE: 1998-04-30  
PRIOR APPLICATION NUMBER: 60/084366  
PRIOR FILING DATE: 1998-05-05  
PRIOR APPLICATION NUMBER: 60/084414  
PRIOR FILING DATE: 1998-05-06  
PRIOR APPLICATION NUMBER: 60/084441  
PRIOR FILING DATE: 1998-05-06  
PRIOR APPLICATION NUMBER: 60/084637  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/084639  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/084640  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/084598  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/084600  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/084627  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/08463  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/085339  
PRIOR FILING DATE: 1998-05-13  
PRIOR APPLICATION NUMBER: 60/085338  
PRIOR FILING DATE: 1998-05-13  
PRIOR APPLICATION NUMBER: 60/085333  
PRIOR FILING DATE: 1998-05-13  
PRIOR APPLICATION NUMBER: 60/085582  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085700  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085689

PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085579  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085580  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085573  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085704  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085697

Query Match 94.5%; Score 1333; DB 9; Length 295;  
Best Local Similarity 96.8%; Pred. No. 3e-88;  
Matches 242; Conservative 2; Mismatches 4; Indels 2; Gaps 1;

QY 7 PRRVCAV--RAHGDVSESVFORVOPFLTTGHRACSTYRTITYTAARSPGLAPAR 64  
DB 46 PARPLGCVLSRAHGDVSESVFORVOPFLTTGHRACSTYRTITYTAARSPGLAPAR 105  
QY 65 PRVACCPGKRTSGLPAGCAAIQPPCRNGSCVOPRCRCRCPAGWBDTCQSDVDECSA 124  
DB 106 PRVACCPGKRTSGLPAGCAAIQPPCRNGSCVOPRCRCRCPAGWBDTCQSDVDECSA 165  
QY 125 RRGCGPQRCVNTAGSYKQCWEHSLADGTLVCPKGGPPVAVNPTGVDSAMKEEVQRL 184  
DB 166 RRGCGPQRCVNTAGSYKQCWEHSLADGTLVCPKGGPPVAVNPTGVDSAMKEEVQRL 225  
QY 185 OSRVDLLEEKQLVLAFLHSLASQALEHGLPDPGSLVHSPQQLGRIDSLEQISFLEBQ 244  
DB 226 OSRVDLLEEKQLVLAFLHSLASQALEHGLPDPGSLVHSPQQLGRIDSLEQISFLEBQ 285  
QY 245 LGSCSCKKDS 254  
DB 286 LGSCSCKKDS 295

RESULT 14  
US-09-978-192A-2  
Sequence 2, Application US/09978192A  
Patent No. US2002017753A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Deonoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrata, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillman, Kenneth J.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2630PICG  
CURRENT APPLICATION NUMBER: US/09/978,192A  
CURRENT FILING DATE: 2001-10-15

1 PRIOR APPLICATION NUMBER: 09/918585  
2 PRIOR FILING DATE: 2001-07-30  
3 PRIOR APPLICATION NUMBER: 60/062250  
4 PRIOR FILING DATE: 1997-10-17  
5 PRIOR APPLICATION NUMBER: 60/064249  
6 PRIOR FILING DATE: 1997-11-03  
7 PRIOR APPLICATION NUMBER: 60/065311  
8 PRIOR FILING DATE: 1997-11-13  
9 PRIOR APPLICATION NUMBER: 60/066364  
10 PRIOR FILING DATE: 1997-11-21  
11 PRIOR APPLICATION NUMBER: 60/077450  
12 PRIOR FILING DATE: 1998-03-10  
13 PRIOR APPLICATION NUMBER: 60/077632  
14 PRIOR FILING DATE: 1998-03-11  
15 PRIOR APPLICATION NUMBER: 60/077641  
16 PRIOR FILING DATE: 1998-03-11  
17 PRIOR APPLICATION NUMBER: 60/077649  
18 PRIOR FILING DATE: 1998-03-11  
19 PRIOR APPLICATION NUMBER: 60/077791  
20 PRIOR FILING DATE: 1998-03-12  
21 PRIOR APPLICATION NUMBER: 60/078004  
22 PRIOR FILING DATE: 1998-03-13  
23 PRIOR APPLICATION NUMBER: 60/078886  
24 PRIOR FILING DATE: 1998-03-20  
25 PRIOR APPLICATION NUMBER: 60/078936  
26 PRIOR FILING DATE: 1998-03-20  
27 PRIOR APPLICATION NUMBER: 60/078910  
28 PRIOR FILING DATE: 1998-03-20  
29 PRIOR APPLICATION NUMBER: 60/078939  
30 PRIOR FILING DATE: 1998-03-20  
31 PRIOR APPLICATION NUMBER: 60/079294  
32 PRIOR FILING DATE: 1998-03-25  
33 PRIOR APPLICATION NUMBER: 60/079656  
34 PRIOR FILING DATE: 1998-03-26  
35 PRIOR APPLICATION NUMBER: 60/079664  
36 PRIOR FILING DATE: 1998-03-27  
37 PRIOR APPLICATION NUMBER: 60/079689  
38 PRIOR FILING DATE: 1998-03-27  
39 PRIOR APPLICATION NUMBER: 60/079663  
40 PRIOR FILING DATE: 1998-03-27  
41 PRIOR APPLICATION NUMBER: 60/079728  
42 PRIOR FILING DATE: 1998-03-27  
43 PRIOR APPLICATION NUMBER: 60/079786  
44 PRIOR FILING DATE: 1998-03-27  
45 PRIOR APPLICATION NUMBER: 60/079920  
46 PRIOR FILING DATE: 1998-03-30  
47 PRIOR APPLICATION NUMBER: 60/079923  
48 PRIOR FILING DATE: 1998-03-30  
49 PRIOR APPLICATION NUMBER: 60/080105  
50 PRIOR FILING DATE: 1998-03-31  
51 PRIOR APPLICATION NUMBER: 60/080107  
52 PRIOR FILING DATE: 1998-03-31  
53 PRIOR APPLICATION NUMBER: 60/080165  
54 PRIOR FILING DATE: 1998-03-31  
55 PRIOR APPLICATION NUMBER: 60/080194  
56 PRIOR FILING DATE: 1998-03-31  
57 PRIOR APPLICATION NUMBER: 60/080327  
58 PRIOR FILING DATE: 1998-04-01  
59 PRIOR APPLICATION NUMBER: 60/080328  
60 PRIOR FILING DATE: 1998-04-01  
61 PRIOR APPLICATION NUMBER: 60/080333  
62 PRIOR FILING DATE: 1998-04-01  
63 PRIOR APPLICATION NUMBER: 60/080334  
64 PRIOR FILING DATE: 1998-04-01  
65 PRIOR APPLICATION NUMBER: 60/081070  
66 PRIOR FILING DATE: 1998-04-08  
67 PRIOR APPLICATION NUMBER: 60/081049  
68 PRIOR FILING DATE: 1998-04-08  
69 PRIOR APPLICATION NUMBER: 60/081071  
70 PRIOR FILING DATE: 1998-04-08  
71 PRIOR APPLICATION NUMBER: 60/081195  
72 PRIOR FILING DATE: 1998-04-08  
73 PRIOR APPLICATION NUMBER: 60/081203  
74 PRIOR FILING DATE: 1998-04-09  
75 PRIOR APPLICATION NUMBER: 60/081229  
76 PRIOR FILING DATE: 1998-04-09  
77 PRIOR APPLICATION NUMBER: 60/081955  
78 PRIOR FILING DATE: 1998-04-15  
79 PRIOR APPLICATION NUMBER: 60/081817  
80 PRIOR FILING DATE: 1998-04-15  
81 PRIOR APPLICATION NUMBER: 60/081819  
82 PRIOR FILING DATE: 1998-04-15  
83 PRIOR APPLICATION NUMBER: 60/081952  
84 PRIOR FILING DATE: 1998-04-15  
85 PRIOR APPLICATION NUMBER: 60/081838  
86 PRIOR FILING DATE: 1998-04-15  
87 PRIOR APPLICATION NUMBER: 60/082568  
88 PRIOR FILING DATE: 1998-04-21  
89 PRIOR APPLICATION NUMBER: 60/082569  
90 PRIOR FILING DATE: 1998-04-21  
91 PRIOR APPLICATION NUMBER: 60/082704  
92 PRIOR FILING DATE: 1998-04-22  
93 PRIOR APPLICATION NUMBER: 60/082804  
94 PRIOR FILING DATE: 1998-04-22  
95 PRIOR APPLICATION NUMBER: 60/082700  
96 PRIOR FILING DATE: 1998-04-22  
97 PRIOR APPLICATION NUMBER: 60/082797  
98 PRIOR FILING DATE: 1998-04-22  
99 PRIOR APPLICATION NUMBER: 60/082796  
100 PRIOR FILING DATE: 1998-04-23  
101 PRIOR APPLICATION NUMBER: 60/083336  
102 PRIOR FILING DATE: 1998-04-27  
103 PRIOR APPLICATION NUMBER: 60/083322  
104 PRIOR FILING DATE: 1998-04-28  
105 PRIOR APPLICATION NUMBER: 60/083392  
106 PRIOR FILING DATE: 1998-04-29  
107 PRIOR APPLICATION NUMBER: 60/083495  
108 PRIOR FILING DATE: 1998-04-29  
109 PRIOR APPLICATION NUMBER: 60/083496  
110 PRIOR FILING DATE: 1998-04-29  
111 PRIOR APPLICATION NUMBER: 60/083499  
112 PRIOR FILING DATE: 1998-04-29  
113 PRIOR APPLICATION NUMBER: 60/083545  
114 PRIOR FILING DATE: 1998-04-29  
115 PRIOR APPLICATION NUMBER: 60/083554  
116 PRIOR FILING DATE: 1998-04-29  
117 PRIOR APPLICATION NUMBER: 60/083558  
118 PRIOR FILING DATE: 1998-04-29  
119 PRIOR APPLICATION NUMBER: 60/083559  
120 PRIOR FILING DATE: 1998-04-29  
121 PRIOR APPLICATION NUMBER: 60/083500  
122 PRIOR FILING DATE: 1998-04-29  
123 PRIOR APPLICATION NUMBER: 60/083742  
124 PRIOR FILING DATE: 1998-04-30  
125 PRIOR APPLICATION NUMBER: 60/084366  
126 PRIOR FILING DATE: 1998-05-05  
127 PRIOR APPLICATION NUMBER: 60/084414  
128 PRIOR FILING DATE: 1998-05-06  
129 PRIOR APPLICATION NUMBER: 60/084441  
130 PRIOR FILING DATE: 1998-05-06  
131 PRIOR APPLICATION NUMBER: 60/084637  
132 PRIOR FILING DATE: 1998-05-07  
133 PRIOR APPLICATION NUMBER: 60/084639  
134 PRIOR FILING DATE: 1998-05-07  
135 PRIOR APPLICATION NUMBER: 60/084640  
136 PRIOR FILING DATE: 1998-05-07  
137 PRIOR APPLICATION NUMBER: 60/084598  
138 PRIOR FILING DATE: 1998-05-07  
139 PRIOR APPLICATION NUMBER: 60/084600  
140 PRIOR FILING DATE: 1998-05-07  
141 PRIOR APPLICATION NUMBER: 60/084627  
142 PRIOR FILING DATE: 1998-05-07  
143 PRIOR APPLICATION NUMBER: 60/084643  
144 PRIOR FILING DATE: 1998-05-07  
145 PRIOR APPLICATION NUMBER: 60/085339  
146 PRIOR FILING DATE: 1998-05-13

```

; PRIOR APPLICATION NUMBER: 60/085338
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085323
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085582
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085700
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085689
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085580
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

```

```

Query Match          94.5%; Score 1333; DB 9; Length 295;
Best Local Similarity 96.8%; Pred. No. 3e-88;
Matches 242; Conservative 2; Mismatches 4; Indels 2; Gaps 1;

```

```

QY 7  PGRRCAY--RAHGDVSESVFVQRYQPFLLTCGHRACSTYRTTYRTAYRRSPGLAPAR 64
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 46  PARPGCVLSTAHGDPVSESVFVQRYQPFLLTCGHRACSTYRTTYRTAYRRSPGLAPAR 105
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 65  PRVACCPGKRTSGLPAGCGAATCOPPCRNAGSCVOPGRCRCPAGMRGDTGQSDVDCSA 124
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 106  PRVACCPGKRTSGLPAGCGAATCOPPCRNAGSCVOPGRCRCPAGMRGDTGQSDVDCSA 165
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 125  RRGCPQRCVNTAGSYWCQCEHSLSDGTLVCPKGGPRVAPNPPTGVDSAMKEEVQRL 184
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 166  RRGCPQRCVNTAGSYWCQCEHSLSDGTLVCPKGGPRVAPNPPTGVDSAMKEEVQRL 225
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 185  QSRVLLLEBKQLVLAFLHSLASQALEHGLPDPGSLVHSTQQLGRIDSLSSEQISFLEEQ 244
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 226  QSRVLLLEBKQLVLAFLHSLASQALEHGLPDPGSLVHSTQQLGRIDSLSSEQISFLEEQ 285
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 245  LGSCSCCKDS 254
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 286  LGSCSCCKDS 295
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```

```

RESULT 15
US-09-790-264-15
; Sequence 15, Application US/09790264
; Patent No. US20020028508A1
; GENERAL INFORMATION:
; APPLICANT: Holtzman, Douglas A.
; APPLICANT: Goodearl, Andrew D.J.
; APPLICANT: McCarthy, Sean A.
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
; TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
; TITLE OF INVENTION: USGS
; FILE REFERENCE: 07334-322001
; CURRENT APPLICATION NUMBER: US/09/790,264
; CURRENT FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: US 09/065,661
; PRIOR FILING DATE: 1998-04-23
; PRIOR APPLICATION NUMBER: US 09/298,531
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: US 09/065,363
; PRIOR FILING DATE: 1998-04-23
; PRIOR APPLICATION NUMBER: US 09/337,930
; PRIOR FILING DATE: 1999-06-22
; PRIOR APPLICATION NUMBER: US 09/102,705
; PRIOR FILING DATE: 1998-06-22
; PRIOR APPLICATION NUMBER: US 09/363,630
; PRIOR FILING DATE: 1999-07-29
; PRIOR APPLICATION NUMBER: US 09/124,538
; PRIOR FILING DATE: 1998-07-29

```

```

; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 275
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-790-264-15

```

```

Query Match          80.8%; Score 1139.5; DB 10; Length 275;
Best Local Similarity 79.9%; Pred. No. 1.6e-74;
Matches 203; Conservative 16; Mismatches 34; Indels 1; Gaps 1;

```

```

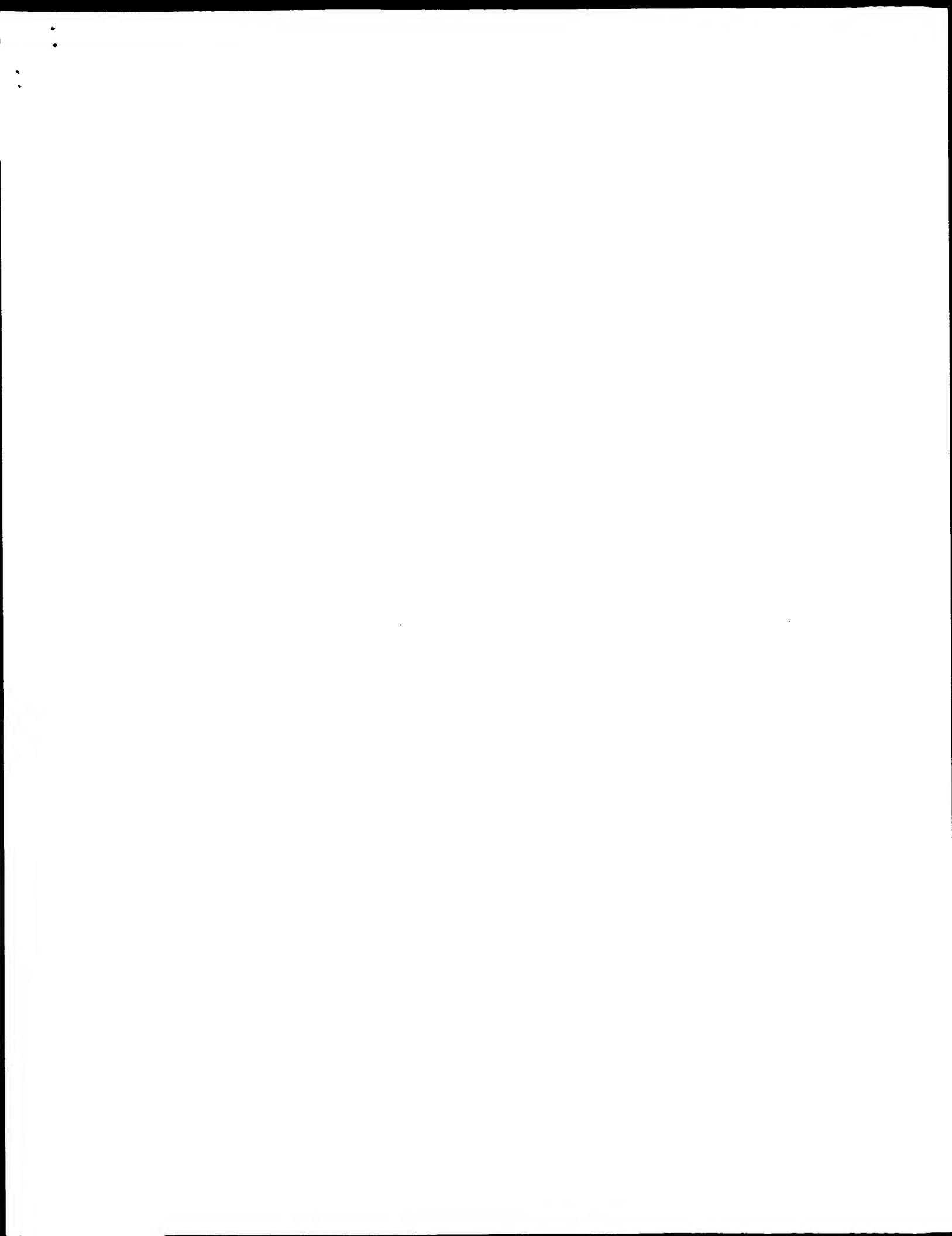
QY 1  TEHAYRPGRRVCAVRAHGDVSESVFVQRYQPFLLTCGHRACSTYRTTYRTAYRRSPGL 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 21  TEHAYRPSRRVCTVGISGSISETFVQRYQPYLTTCGHRACSTYRTTYRTAYRRSPGL 80
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61  APPRPRIACCPGKRTSGLPAGCGAATCOPPCRNAGSCVOPGRCRCPAGMRGDTGQSDVD 120
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 81  TPARPRYACCPGKRTSGLPAGCGAATCOPPCRNAGSCVOPGRCRCPAGMRGDTGQSDVD 140
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 121  ECSARRGGCPQRCVNTAGSYWCQCEHSLSDGTLVCPKGGPRVAPNPPTGVDSAMKE 179
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 141  ECSTGASCPQRCVNTAGSYWCQCEHSLSDGTLVCPKGGPRVAPNPPTGVDSAMKE 200
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 180  EYQRLQSRVLLLEBKQLVLAFLHSLASQALEHGLPDPGSLVHSTQQLGRIDSLSSEQIS 239
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 201  EYVRLQARVDVLEQLQLVLAFLHSLASQALEHGLPDPGSLVHSTQQLGRIDSLSSEQIS 260
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 240  FLEBQLGSCCKKD 253
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 261  FLEBHLGSCCKKD 274
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```

```

Search completed: December 17, 2002, 10:09:46
Job time : 9.1935 secs

```



GenCore version 5.1.3  
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 17, 2002, 10:00:11 ; Search time 13.9772 Seconds  
(without alignments)  
1746.994 Million cell updates/sec

Title: US-09-852-472-3

Perfect score: 1411  
Sequence: 1 THNAVPRGRVCAVARHGP.....SEQISFLEQLGSCSCKKDS 254

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283224 segs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : PIR\_73:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	425	30.1	293	2 T09065	hypothetical prote
2	257	18.2	1574	2 T13954	MEGF6 protein - ra
3	253.5	18.0	558	2 T17324	hypothetical prote
4	219	15.5	1620	2 T27283	hypothetical prote
5	196	13.9	1964	2 T09059	notch4 - mouse
6	189	13.4	678	2 B48089	growth arrest-spec
7	184	13.0	673	2 A48089	growth arrest-spec
8	181	12.8	810	2 T10756	Nel-homolog protein
9	178	12.6	674	2 T55476	growth potentialin
10	175.5	12.4	3002	2 A47221	fibritillin 1 precu
11	175	12.4	2907	2 A57278	fibritillin-2 precu
12	174.5	12.3	2321	2 S78549	notch3 protein - h
13	173.5	12.3	1247	1 M4HUND	notch3 protein - h
14	173	12.3	835	2 JPO076	nidogen precursor
15	172	12.2	2531	2 A46019	Notch-1 protein -
16	171.5	12.2	2871	2 A55624	fibritillin-1 precu
17	170.5	12.1	2871	2 A55624	fibritillin-1 - bovi
18	170	12.0	675	1 KXMS	plasma protein S p
19	169	12.0	2703	1 A24420	notch protein - fr
20	168.5	11.9	2318	2 S45306	notch 3 protein -
21	168	11.9	675	1 KXMS	plasma protein S p
22	168	11.9	833	2 S19087	gene Delta protein
23	165	11.7	832	2 A31246	neurogenic protei
24	165	11.7	880	2 S00670	neurogenic repetit
25	165	11.7	2524	2 A35844	Xotch protein - Af
26	164.5	11.7	2918	2 A54105	fibritillin-2 precu
27	164	11.6	1429	2 S06434	homeotic protein 1
28	164	11.6	2555	2 A40043	notch protein homo
29	163	11.6	3871	2 T22812	hypothetical prote

30	162	11.5	387	2 B49175	Notch A protein -
31	162	11.5	646	2 S38819	plasma protein S -
32	162	11.5	675	1 KXBO	plasma protein S p
33	160.5	11.4	2531	2 S18188	notch protein homo
34	160	11.3	2437	2 S42612	transmembrane prot
35	159.5	11.3	407	1 KFB07	coagulation factor
36	159	11.3	1820	2 A55494	latent transformin
37	158.5	11.2	456	1 KXBO	protein C (activat
38	157	11.1	676	1 KKHUS	plasma protein S p
39	157	11.1	1221	2 A49457	fibulin-2 precu
40	156	11.1	347	2 S53434	plasma protein S p
41	155	11.0	387	2 T38449	extracellular prot
42	155	11.0	1408	2 S16148	gene serrate prote
43	154	10.9	642	2 S53433	plasma protein S p
44	154	10.9	1220	2 A56136	jagged protein pre
45	153.5	10.9	861	2 A48825	Notch homolog Motc

## ALIGNMENTS

## RESULT 1

T09065  
hypothetical protein - mouse

C:Species: Mus musculus (house mouse)

C:Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 11-Jan-2000

C:Accession: T09065

R:Rowen, L.; Mahairas, G.; Qin, S.; Ahearn, M.E.; Dankers, C.; Lasky, S.; Loretz, C.; Sci submitted to the EMBL Data Library, October 1997

A:Description: Sequence of the mouse major histocompatibility locus class III region.

A:Reference number: Z16543

A:Accession: T09065

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-293 <ROM>

A:Cross-references: EMBL:AF030001; NID:G2564945; PID:G2564953

C:Genetics:

A:Map position: 17

A:Insertions: 34/2; 75/2; 112/1; 144/1; 201/1; 228/3; 280/1

C:Superfamily: unassigned EGF-related proteins; EGF homology

F:114-141/Domain: EGF homology <EGF1>

F:148-183/Domain: EGF homology <EGF>

Query Match 30.1%, Score 425; DB 2; Length 293;

Best Local Similarity 37.3%; Pred. No. 4.7e-24;

Matches 103; Conservative 34; Mismatches 95; Indels 44; Gaps 11;

QY	4	AYRPRRVCAVARHGPV--SESFVQRYVOPFTTCDSHRACTYRTTYRAYSPELA 61	
DB	30	SEKESLGVCSKQTLVPRVNESYQPYKPYLTLCAGRRICSTYRTTYRVAHREVREV 89	
QY	62	PAPRYACCPGKRTSGVGAAGA-AIQPCRMGSGVQPCRCAPAGMGDPCCQSDVD 120	
DB	90	P-QTHVCCQGGKKPH--FGALTCDAICSKPCLVGGVCTGDRCECAPGCKCHVDVD 146	
QY	121	ECSSARRGCPQRCVNTAGSYWCQCWEHSLADGTLCPKSGPRVAVNPVGV----- 173	
DB	147	ECRAVLTLCSHCNTLGSFLSCGHPVLVLDGRCA--CGPEE---SPISAILSVAV 201	
QY	174	-----DSMKKEYQLQSRVDLLEKQLVLAPLHSLASQA---LEHGIP-DPGSLIV 222	
DB	202	READEEERARLMEVAEIRGRLEKLEQ-----WATQAGAWRAVLPMPPEIRP 250	
QY	223	HSFOO-----GRISLSQISFLEQLGSCSCKKDS 254	
DB	251	EOVAELMGKGRISLSQVLLLEBRLLGACACEDNS 286	

## RESULT 2

MEGF6 protein - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 21-Jul-2000

C:Accession: T13954  
 R:Nakayama, M.; Nakajima, D.; Nagase, T.; Nomura, N.; Seki, N.; Ohara, O.  
 Genomics 51, 27-34, 1998  
 A:Title: Identification of high-molecular-weight proteins with multiple EGF-like motifs  
 A:Reference number: 214126; MUID:98360089; PMID:9693030  
 A:Accession: T13954  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-1574 <NAK>  
 A:Cross-references: EMBL:AB011532; NID:g3449293; PIDN:BAA32462.1; PID:g3449294  
 A:Experimental source: strain Sprague-Dawley; brain  
 C:Genetics:  
 A:Gene: MEGF6

Query Match 18.2%; Score 257; DB 2; Length 1574;  
 Best Local Similarity 38.5%; Pred. No. 4.1e-11;  
 Matches 65; Conservative 15; Mismatches 61; Indels 28; Gaps 9;  
 QY 11 VCAVR-----AHGDPVSEFVQRYVQPLTTCDGHRAC--STYETIYRTAYRRSPGLAPA 63  
 DB 43 VCAEQLKTLVGHRCQVQAFSRIVPWRRTGCAQAMCIGQERRIVYMSYRQVYA-TEA 101  
 QY 64 RPRVACCPGKRTSLPGA-----CGAAI--CQPPCRN--GGSCVQPGRCRCPCAGWR-- 111  
 DB 102 RTVFRCCFGMSQKPGQEGCLSDVDECAASANGCGPCNTVGGF-----YRCPCPGYQLQ 156  
 QY 112 --GDTCSQDVDECSARRGCGPQRCVNTAGSYWCQCGHLSLSADGTLGV 158  
 DB 157 GDGKTCQ-DVDECAHNGCGQRCVNTPGSYLCECKPGLRHTDGTCL 204

RESULT 3  
 T17324  
 hypothetical protein DKFp564P2063.1 - human (fragment)  
 C:Species: Homo sapiens (man)  
 C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
 C:Accession: T17324  
 R:Duesterhoft, A.; Lauber, J.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.  
 submitted to the Protein Sequence Database, September 1999  
 A:Reference number: Z18727  
 A:Accession: T17324  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-558 <DUE>  
 A:Cross-references: EMBL:AL117610  
 A:Experimental source: fetal brain; clone DKFp564P2063  
 C:Genetics:  
 A:Note: DKFp564P2063.1

Query Match 18.0%; Score 253.5; DB 2; Length 558;  
 Best Local Similarity 37.4%; Pred. No. 3e-11;  
 Matches 58; Conservative 16; Mismatches 50; Indels 31; Gaps 7;  
 QY 39 GHRACSTVTTIYRTAYRRSPGLAPRRYACCPGKRTSLPGACGAAICQPPCRNGGSC 98  
 DB 26 GNAASRRHGLLASA--RQPGVCHYGTKLACYGWRNS--KGVV-EATCEPGCK-FGEC 79  
 QY 99 VQPGRCRCPCAGWRGDTCSQDVDECSARRGCGPQRCVNTAGSYWCQCGHLSLSADGTLGV 158  
 DB 80 VGPNNKRCCLPGVGTGKTSQDVNECGMKPRPCQHRVCVNTGSHYKFCFLSGHMLMPDAT-CV 138  
 QY 159 -----PKGGPP-----RVAEN 169  
 DB 139 YSRTCAMINQVSCEDTEEGPQLCPSPSGLRLAPN 173

RESULT 4  
 T27283  
 hypothetical protein y64G10A.f - Caenorhabditis elegans  
 C:Species: Caenorhabditis elegans  
 C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
 C:Accession: T27283  
 R:Ainscough, R.

submitted to the EMBL Data Library, September 1999  
 A:Reference number: Z20336  
 A:Accession: T27283  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-1620 <WIL>  
 A:Cross-references: EMBL:AL110498; NID:e1542303; PIDN:CAB54471.1; CBSP:Y64G10A.f  
 A:Experimental source: clone Y64G10A  
 C:Genetics:  
 A:Gene: CBSP:Y64G10A.f  
 A:Introns: 77/1; 116/1; 198/1; 282/1; 365/1; 425/1; 466/1; 548/1; 559/1; 601/1; 625/1;

Query Match 15.5%; Score 219; DB 2; Length 1620;  
 Best Local Similarity 41.3%; Pred. No. 2.6e-08;  
 Matches 43; Conservative 8; Mismatches 35; Indels 18; Gaps 4;  
 QY 83 CGAAATCQPPCRNGGSCVQPGR-----CRCPCAGWRGDTCSQDVDECSARRGCGPQRCVNT 136  
 DB 79 CSADL-----CHNGGTCVPSEHNDNEQVCEPCVGTGAKCQYDANECAWNGGCEHCYNT 134  
 QY 137 AGSYWCQCGHLSLSADGTLG-----VPGKG-PPRVAPNPTG 172  
 DB 135 IGTYICRCWPGFELSGDGNCTSDIDECAVSNCGSCDRCVNSPG 178

RESULT 5  
 T09059  
 notch4 - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 11-Jun-2000  
 A:Accession: T09059  
 R:Rowen, L.; Mahairas, G.; Qin, S.; Ahearn, M.E.; Dankers, C.; Lasky, S.; Loretz, C.;  
 submitted to the EMBL Data Library, October 1997  
 A:Description: Sequence of the mouse major histocompatibility locus class III region.  
 A:Reference number: Z16543  
 A:Accession: T09059  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-1964 <ROW>  
 A:Cross-references: EMBL:AF030001; NID:g2564945; PID:g2564947  
 C:Genetics:  
 A:Gene: notch4  
 A:Map position: 17  
 A:Introns: 22/1; 49/2; 148/1; 264/1; 305/1; 384/1; 436/1; 501/1; 539/1; 577/1; 618/1;  
 1679/3; 1729/1; 1761/3  
 C:Superfamily: unassigned EGF-related proteins; EGF homology  
 C:Keywords: receptor; signal transduction  
 F:514-545/Domain: EGF homology <EGF>

Query Match 13.9%; Score 196; DB 2; Length 1964;  
 Best Local Similarity 34.2%; Pred. No. 1.5e-06;  
 Matches 50; Conservative 12; Mismatches 54; Indels 30; Gaps 7;  
 QY 61 APARPRYACCPGKWK-RTSGLPGACGAAICQPPCRNGGSCVQPG---RCRCPCAGWRGDTQ 116  
 DB 134 ASGRQCSCCEPQWTGEQQLRDFCSA----NPCANGVCLATYPQIQRCRPPGEGHTCE 189  
 QY 117 SDVDECSARRGCGPQ--RCVNTAGSYWCQ---WEGHLSLSADGTLGV---KGGPPRVA 167  
 DB 190 RDINECFLEPGPCPQOTSCHNTLSYQCLCPVQGGPQCKLRKGACPPGSCINGGTQCLV 249  
 QY 168 PNP-----TGVDSSMKEE 180  
 DB 250 PEGHSTFHLCLCPPGFTGLDCENMPD 275

RESULT 6  
 B48089  
 growth arrest-specific protein gas6 - human  
 C:Species: Homo sapiens (man)  
 C:Date: 26-May-1994 #sequence\_revision 26-May-1994 #text\_change 05-Nov-1999  
 C:Accession: B48089  
 R:Manfioletti, G.; Brancolini, C.; Avanzi, G.; Schneider, C.

Mol. Cell. Biol. 13, 4976-4985, 1993

A>Title: The protein encoded by a growth arrest-specific gene (gas6) is a new member of

A:Reference number: A48089; MUID:93330291; PMID:8336730

A:Accession: B48089

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-678 <MAN>

C:Cross-references: GB:113720; NID:9401766; PIDN:AAA58494.1; PID:9401767

C:Superfamily: Plasma protein S; EGF homology; GlA domain homology; laminin G repeat hom

F:11-92/Domain: GlA domain homology #status atypical <GLA>

F:120-153/Domain: EGF homology <EG1>

F:160-195/Domain: EGF homology <EG2>

F:201-236/Domain: EGF homology <EG3>

F:242-277/Domain: EGF homology <EG4>

F:311-671/Domain: sex hormone-binding globulin homology <SHB>

F:321-473/Domain: laminin G repeat homology <LGR>

Query Match 13.4%; Score 189; DB 2; Length 678;

Best Local Similarity 34.2%; Pred. No. 1.9e-06;

Matches 53; Conservative 8; Mismatches 64; Indels 30; Gaps 8;

27 QRYVQPEPLTCDG-----RACSTYRTYRTAYRRSPGLAPRRYACC-----PGWK 74

47 RRARVQVEBAKQGLERECVEBELCS--REBARVENDPDTYFYPYIDCINKKYSPT 104

75 RTSG-----LPGACGAICOPPC--RNGSCVQP--GR--CRCPAGMRDTCQSDVDEC 122

105 KNSGFATCVQNLPDQC-----TPNPDCKRTQACQDLMGNFCLCKAKGSRLCDKXVNEC 160

123 SARRGCPQRCVNTAGSYWCQCEGSHSLADGTLG 157

161 SOENGGLQICHNKPGSFHCSHSGFELSSDGRYC 195

RESULT 7

A48089

growth arrest-specific protein gas6 - mouse

C:Species: Mus musculus (house mouse)

C:Date: 26-May-1994 #sequence\_revision 26-May-1994 #text\_change 05-Nov-1999

C:Accession: A48089; S37437

R:Manfioletti, G.; Brancolini, C.; Avanzi, G.; Schneider, C.

Mol. Cell. Biol. 13, 4976-4985, 1993

A>Title: The protein encoded by a growth arrest-specific gene (gas6) is a new member of

A:Reference number: A48089; MUID:93330291; PMID:8336730

A:Accession: A48089

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-673 <MAN>

A:Cross-references: GB:X59846; NID:9407060; PIDN:CAA42507.1; PID:9407061

A>Note: authors translated the codon CCC for residue 424 as Ile

C:Gene: gas6

C:Superfamily: Plasma protein S; EGF homology; GlA domain homology; laminin G repeat hom

F:38-89/Domain: GlA domain homology #status atypical <GLA>

F:117-150/Domain: EGF homology <EG1>

F:157-192/Domain: EGF homology <EG2>

F:198-233/Domain: EGF homology <EG3>

F:239-274/Domain: EGF homology <EG4>

F:308-666/Domain: sex hormone-binding globulin homology <SHB>

F:318-470/Domain: laminin G repeat homology <LGR>

Query Match 13.0%; Score 184; DB 2; Length 673;

Best Local Similarity 31.6%; Pred. No. 4.3e-06;

Matches 50; Conservative 8; Mismatches 64; Indels 36; Gaps 6;

27 QRYVQPEPLTCDG-----RACSTYRTYRTAYRRSPGLAPRRYACC-----70

44 RRARVQVEBAKQGLERECVEBELCS--REBARVENDPDTYFYPYIDCINKKYSPT 101

71 --PGWK--TSGLPAC-----GAICOPPCRNCGSCVQPGRCRCPCAGMRDTCQSDV 119

Db 102 KNPDFAKCVQNLPDQCTPNPCKDKGTHICQDLMGN-----FFCVCTDCKGRLCDKV 154

Qy 120 DECSARRGCPQRCVNTAGSYWCQCEGSHSLADGTLG 157

Db 155 NECVQKNGCGSQVCHNKRKGSFGQACHSGFSLASDQTC 192

RESULT 8

110756

Nel-homolog protein - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 16-Jul-1999

C:Accession: 110756

R:Kuroda, S.; Tokunaga, C.; Kiyohara, Y.; Konishi, H.; Matsubashi, S.; Kikkawa, U.

submitted to the EMBL Data Library, November 1998

A:Description: Protein kinase C-binding protein.

A:Reference number: 217122

A:Accession: 110756

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-810 <KUR>

A:Cross-references: EMBL:U48246; NID:93851179; PID:93851180

A:Experimental source: strain Sprague-Dawley, brain

Query Match 12.8%; Score 181; DB 2; Length 810;

Best Local Similarity 37.5%; Pred. No. 8.4e-06;

Matches 36; Conservative 12; Mismatches 38; Indels 10; Gaps 3;

69 CCRPKRTSGLPAGCAICOPPCRNCGSCVQPGRCRCPCAGMRDTCQSDVDECSARRG 128

Db 504 CQPGVGN-----GTICKAFCEGGRYGTGVAIPKCVCPSSGFTSHCEKIDCEAGFVE 559

Qy 129 CP--ORCVNTAGSYWCQCEGSHSLADGTLG 158

Db 560 CHNYSRCVNLPGWHCEGRSGFHDGTSLSGESCI 595

RESULT 9

155476

growth potentiating factor - rat

C:Species: Rattus sp. (rat)

C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 20-Apr-2001

C:Accession: 155476

R:Nakano, T.; Higashino, K.; Kikuchi, N.; Kishino, J.; Nomura, K.; Fujita, H.; Ohara, O.

J. Biol. Chem. 270, 5702-5705, 1995

A>Title: Vascular smooth muscle cell-derived, GlA-containing growth-potentiating factor

A:Reference number: 155476; MUID:95197586; PMID:7890695

A:Accession: 155476

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-674 <RGS>

A:Cross-references: GB:D42148; NID:91526567; PIDN:BA07719.1; PID:9893402

C:Superfamily: Plasma protein S; EGF homology; GlA domain homology; laminin G repeat hom

F:29-89/Domain: GlA domain homology <GLA>

F:117-150/Domain: EGF homology <EG1>

F:157-192/Domain: EGF homology <EG2>

F:198-233/Domain: EGF homology <EG3>

F:239-274/Domain: EGF homology <EG4>

F:308-667/Domain: sex hormone-binding globulin homology <SHB>

F:318-470/Domain: laminin G repeat homology <LGR>

Query Match 12.6%; Score 178; DB 2; Length 674;

Best Local Similarity 30.4%; Pred. No. 1.2e-05;

Matches 48; Conservative 8; Mismatches 66; Indels 36; Gaps 6;

27 QRYVQPEPLTCDG-----RACSTYRTYRTAYRRSPGLAPRRYACC-----70

44 RRARVQVEBAKQGLERECVEBELCS--REBARVENDPDTYFYPYIDCINKKYSPT 101

Qy 71 --PGWK--TSGLPAC-----GAICOPPCRNCGSCVQPGRCRCPCAGMRDTCQSDV 119

Db 102 KNPDFAKCVQNLPDQCTPNPCKDKGTHICQDLMGN-----FFCLCKDCKGRLCDKV 154

QY 120 DECSARRGCGPQRCYNTAGSYWCQWEGHSLSDGTLTLC 157  
Db 155 NECSQKNGCGSQVCHNKGPSFQACGCHGSLQSDNKC 192

## RESULT 10

A47221  
C:Species: Homo sapiens (man)  
C:Date: 02-Jun-1995 #sequence revision 25-Apr-1997 #text change 02-Aug-2002  
C:Accession: A47221; I54355; S17062; I59574; S17062; S62111; A34198  
R:Corson, G.M.; Chalberg, S.C.; Dietz, H.C.; Charbonneau, N.L.; Sakai, L.Y.  
Genomics 17, 476-484, 1993  
A:Title: Fibrillin binds calcium and is coded by cDNAs that reveal a multidomain structure  
A:Reference number: A47221; MUID:94010947; PMID:7691719  
A:Accession: A47221  
A:Molecule type: mRNA  
A:Residues: 1-337, 'T', 339-1029 <COR>  
A:Cross-references: GB:X63556  
R:Perreira, L.V.; D'Alessio, M.; Ramirez, F.; Lynch, J.; Sykes, B.; Pangilinan, T.; Bonad  
Hum. Mol. Genet. 2, 961-968, 1993  
A:Title: Genomic organization of the sequence coding for fibrillin, the defective gene B  
A:Reference number: I54355; MUID:93372860; PMID:8364578  
A:Accession: I54355  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 132-3002 <PER>  
A:Cross-references: GB:LI3923; NID:G306745; PIDN:AA02036.1; PID:G306746  
R:Maslen, C.L.; Corson, G.M.; Maddox, B.K.; Glanville, R.W.; Sakai, L.Y.  
Nature 352, 334-337, 1991  
A:Title: Partial sequence of a candidate gene for the Marfan syndrome.  
A:Reference number: S17064; MUID:91304568; PMID:1852207  
A:Accession: S17064  
A:Molecule type: mRNA  
A:Residues: 1030-3002 <MAS>  
R:Dietz, H.C.; Valle, D.; Francomano, C.A.; Kendzior, R.J.  
Science 259, 680-683, 1993  
A:Title: The skipping of constitutive exons in vivo induced by nonsense mutations.  
A:Reference number: I59574; MUID:93157831; PMID:8430317  
A:Accession: I59574  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 2217-2298, 'I', 2290-2325 <RES>  
A:Cross-references: GB:S54426; NID:G264860; PIDN:AA025244.1; PID:G264861  
R:Lee, B.; Godfrey, M.; Vitale, E.; Hori, H.; Mattei, M.G.; Sarfarazi, M.; Tsipouras, P.  
Nature 352, 330-334, 1991  
A:Title: Linkage of Marfan syndrome and a phenotypically related disorder to two differe  
A:Reference number: S17062; MUID:91304567; PMID:1852206  
A:Accession: S17062  
A:Molecule type: mRNA  
A:Residues: 'VLVTVVFILSYNKM', 944-1444 <LEE1>  
A:Cross-references: EMBL:X62008; NID:G31398; PIDN:CAB56534.1; PID:G5924015  
A:Accession: S62111  
A:Molecule type: protein  
A:Residues: 1166-1176, 'X', 1178-1180, 'D', 1182-1185 <LEE2>  
R:Maddox, B.K.; Sakai, L.Y.; Keene, D.R.; Glanville, R.W.  
J. Biol. Chem. 264, 21381-21385, 1989  
A:Title: Connective tissue microfibrils. Isolation and characterization of three large p  
A:Reference number: A34198; MUID:90078246; PMID:2512293  
A:Accession: A34198  
A:Molecule type: protein  
A:Residues: 565-575; 1890-1892, 'I', 1894-1900 <MAD>  
C:Comment: Fibrillin is a major component of elastin-associated microfibrils.  
C:Genetics:  
A:Gene: GDB:FBN1  
A:Cross-references: GDB:127115; OMIM:134797; OMIM:154700  
A:Map position: 15q21.1-15q21.1  
A:Introns: 2236/1, 2258/1, 2297/1  
C:Superfamily: fibrillin 1; EGF homology  
C:Keywords: alternative splicing; calcium binding; extracellular matrix; glycoprotein; M  
F:1-3002/Product: fibrillin (5'-region exon A splice form) #status predicted  
F:132-3002/Product: fibrillin (5'-region exon C splice form) #status predicted <MAD>

F:1332-1367/Domain: EGF homology <EGF>  
F:1457-1492/Domain: EGF homology <EGF2>  
F:2262-2295/Domain: EGF homology <EGF1>

Query Match 12.4%; Score 175.5; DB 2; Length 3002;  
Best Local Similarity 18.9%; Pred. No. 6.8e-05;  
Matches 52; Conservative 14; Mismatches 48; Indels 161; Gaps 6;

QY 56 RSFGLAPARPRYACCPGKMTSGLEGA----- 82

Db 185 KGVNCGSYNAYCCPGWKT---LFGNQCIVIPICRHSCGDFCSPNMCTCPSQIAPS 241

QY 83 -----CGAICQPPCHNGSCVQPGRCRCPA 108

Db 242 CGRSIQHCNIRCMNGGSCDDHCLCQKGYITGHCQPVCEGCLNGRCVAPNRCCTY 301

QY 109 GWRGDTCC----- 116

Db 302 GTTGPQCDERTYGTGFTVISNQMQQLSGIVCTKQICCATVGRWHPCEMCPAQPHP 361

QY 117 -----SDVDECSARRGGCP-QRCVNTAGSYWCQWEGHSLSDGTLTLC----- 157

Db 362 CRRGFTPIRTGACQDVDECAIPGLCQCGNCINTVGSFECKPAGHKLNEVSKCEDID 421

QY 158 -----VPKGG-----PPRVAPNPTG 172

Db 422 ECSTIPICEGEGECTNTVSSYFCKCPGFTSPDG 456

## RESULT 11

AS7278

fibrillin-2 precursor - mouse

C:Species: Mus musculus (house mouse)

C:Date: 23-Feb-1996 #sequence\_revision 23-Feb-1996 #text\_change 02-Aug-2002

C:Accession: AS7278

R:Zhang, H.; Hu, W.; Ramirez, F.

J. Cell Biol. 129, 1165-1176, 1995

A:Title: Developmental expression of fibrillin genes suggests heterogeneity of extra

A:Reference number: AS7278; MUID:95263670; PMID:7744963

A:Accession: AS7278

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-2907 <ZHA>

A:Cross-references: GB:L39790; NID:G762830; PIDN:AAA74908.1; PID:G762831

C:Superfamily: fibrillin 1; EGF homology

F:1239-1274/Domain: EGF homology <EGF1>

F:2488-2523/Domain: EGF homology <EGF>

Query Match 12.4%; Score 175; DB 2; Length 2907;

Best Local Similarity 22.9%; Pred. No. 7.1e-05;

Matches 53; Conservative 19; Mismatches 75; Indels 84; Gaps 6;

QY 3 HAY-----RGRVCAVRAHGDVPSFVQVYQPFLLTCDGHRACST--YRTIVRTA 53

Db 94 HSYCCPGKMTLPGNQCIPICRNCSGDFCSR---PNMCTCSSQIISFTGKRSIQCS 150

QY 54 YRSPGLAPARPRYACCPGKMTSGLEGAICQPPCHNGSCVQPGRCRCRCPAGWRGD 113

Db 151 VRCMNGGTCADDHCQCKQGYIGT-----YCGQPVCEGCGNGRCIGENRCACVVGFTGP 205

QY 114 TCQ----- 116

Db 206 QCEDYRTGTGFTQVNNQMQQLTGVCTKLTCCATIGRWHGHPCEMCPAQPCRPGF 265

QY 117 -----SDVDECSARRGGCP-QRCVNTAGSYWCQWEGHSLSDGTLTLC 157

Db 266 IPNIRTGACQDVDECAIPGLCQCGNCINTVGSFECKPAGHKQSETTQKC 316

## RESULT 12

S78549

notch3 protein - human

C:Species: Homo sapiens (man)



C>Date: 24-Jul-1998 #sequence\_revision 24-Jul-1998 #text\_change 02-Aug-2002  
 C/Accession: S76549; S71825  
 R/Jourel, A.; Tournier-Lasserre, E.  
 Submitted to the EMBL data Library, April 1997  
 A/Reference number: S78549  
 A/Accession: S78549  
 A/Molecule type: mRNA  
 A/Residues: 1-2321 <JOU1>  
 A/Cross-references: EMBL:U97669; NID:g2668591; PID:AB91371.1; PID:g2668592  
 R/Jourel, A.; Corpechot, C.; Ducros, A.; Vahedi, K.; Chabrier, H.; Mouton, P.; Alamowitch  
 x, M.M.; Weissbach, J.; Bach, J.F.; Bousser, M.G.; Tournier-Lasserre, E.  
 Nature 383, 707-710, 1996  
 A/Title: Notch mutations in CADASIL, a hereditary adult-onset condition causing stroke  
 A/Reference number: S71825; MUID:97032728; PMID:8878478  
 A/Accession: S71825  
 A/Status: nucleic acid sequence not shown  
 A/Molecule type: DNA  
 A/Residues: 67-113,138-194;268-333,'G',335-346;536-613;716-765;1240-1279;1815-1888 <JOU2  
 A/Cross-references: EMBL:U97669  
 C/Genetics:  
 A:Gene: notch3  
 A:Map position: 19p13.1  
 C/Function:  
 A:Description: may be involved in pathogenesis of CADASIL, causing a type of stroke and  
 C/Superfamily: notch protein; ankyrin repeat homology; EGF homology; laminin-type EGF-1  
 C/Keywords: tandem repeat; transmembrane protein  
 F:123-155/Domain: EGF homology <EGF1>  
 F:162-194/Domain: EGF homology <EGF1>  
 F:240-271/Domain: EGF homology <EGF1>  
 F:318-349/Domain: EGF homology <EGF>  
 F:473-504/Domain: EGF homology <EGF>  
 F:853-884/Domain: EGF homology <EGF3>  
 F:928-959/Domain: EGF homology <EGF4>  
 F:1070-1126/Domain: laminin-type EGF-like homology <LEG>  
 F:11838-1870/Domain: ankyrin repeat homology <AN1>  
 F:11871-1903/Domain: ankyrin repeat homology <AN2>  
 F:1905-1937/Domain: ankyrin repeat homology <AN3>  
 F:1938-1970/Domain: ankyrin repeat homology <AN4>  
 F:1971-2003/Domain: ankyrin repeat homology <AN5>  
 Query Match 12.4%; Score 174.5; DB 2; Length 2321;  
 Best Local Similarity 34.5%; Pred. No. 6,4e-05;  
 Matches 50; Conservative 14; Mismatches 44; Indels 37; Gaps 11;  
 QY 37 CDGHACSTYRTYRTAVRSPGLAPRPRAC-CRGMK-ITSLPGACGAIICPPCR 93  
 Db 87 CAGRGVCS-----SVAGTARPSCKCPRGFGPDCSLPDC---LSSPCA 129  
 QY 94 NGGSC-VDP-GR--CRCPAGWRGDTCCSDVDEC-----SARRGCGPGRCVTAGSYWCQCM 145  
 Db 130 HGARCSVGPDRFLCSPGPGYGRSGSDVDECYGVGRCHG---TCLNTPGSRFCQCP 186  
 QY 146 EGHSLSDGTLCVKGKGPVAVNP 170  
 Db 187 AGYT---GRLCENPAVP--CAPSP 205  
 RESULT 13  
 MATHUND  
 Nidogen precursor - human  
 N/Alternate names: entactin  
 C/Species: Homo sapiens (man)  
 C/Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 20-Oct-2000  
 C/Accession: A33322; A32437; A61367  
 R/Nagayoshi, T.; Sabhorn, D.; Hickok, N.J.; Olsen, D.R.; Fazio, M.J.; Chu, M.L.; Knowlton  
 DNA 8, 581-594, 1989  
 A/Title: Human nidogen: complete amino acid sequence and structural domains deduced from  
 A/Accession: A33322; MUID:90091745; PMID:2574658  
 A/Reference number: A33322  
 A/Molecule type: mRNA  
 A/Residues: 1-1247 <NAG>  
 A/Cross-references: EMBL:M30269  
 R/Olsen, D.R.; Nagayoshi, T.; Fazio, M.; Mattei, M.G.; Passage, E.; Weil, D.; Timpl, R.;

Am. J. Hum. Genet. 44, 876-885, 1989  
 A/Title: Human nidogen: cDNA cloning, cellular expression, and mapping of the gene to chr  
 A/Reference number: A32437; MUID:89270475; PMID:2471408  
 A/Accession: A32437  
 A/Molecule type: mRNA  
 A/Residues: 667-1247 <OLS>  
 A/Cross-references: EMBL:M27445; NID:g602466; PID:AAA57261.1; PID:g602467  
 A/Note: The authors translated the codon AAG for residue 966 as Cys  
 J. Invest. Dermatol. 97, 281-285, 1991  
 A/Title: Human nidogen gene: structural and functional characterization of the 5'-flankir  
 A/Reference number: A61367; MUID:91302882; PMID:1906509  
 A/Accession: A61367  
 A/Molecule type: DNA  
 A/Residues: 1-28 <PAZ>  
 C/Comment: This protein is a basement membrane glycoprotein that forms a complex with lan  
 C/Genetics:  
 A:Gene: GDB:NID  
 A/Cross-references: GDB:120236; OMIM:131390  
 A:Map position: 1q43-1q43  
 C/Superfamily: nidogen; EGF homology; LDL receptor WYTD-containing repeat homology; thyr  
 C/Keywords: basement membrane; beta-hydroxyasparagine; calcium binding; cell binding; cel  
 protein  
 F:1-28/Domain: signal sequence #status predicted <SIG>  
 F:29-1247/Product: nidogen #status predicted <WAT>  
 F:390-425/Domain: EGF homology <EG1>  
 F:672-708/Domain: EGF homology <EG2>  
 F:702-704/Region: cell attachment (R-G-D) motif  
 F:714-750/Domain: EGF homology <EG3>  
 F:762-800/Domain: EGF homology <EG4>  
 F:806-839/Domain: EGF homology <EG5>  
 F:849-919/Domain: thyroglobulin type I repeat homology <THY1>  
 F:990-1032/Domain: LDL receptor WYTD-containing repeat homology <WY1>  
 F:1033-1075/Domain: LDL receptor WYTD-containing repeat homology <WY2>  
 F:1076-1120/Domain: LDL receptor WYTD-containing repeat homology <WY3>  
 F:1121-1160/Domain: LDL receptor WYTD-containing repeat homology <WY4>  
 F:1161-1197/Domain: LDL receptor WYTD-containing repeat homology <WY5>  
 F:1212-1243/Domain: LDL receptor WYTD-containing repeat homology <WY6>  
 F:1289-1296/Binding site: sulfate (Tyr) (covalent) #status predicted  
 F:1729-819/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted  
 F:756/Cross-link: isopeptide (Gln) (interchain to Lys N6-amino of laminin) #status predict  
 F:1137/Binding site: carbonylate (Asn) (covalent) #status predicted  
 Query Match 12.3%; Score 173.5; DB 1; Length 1247;  
 Best Local Similarity 25.8%; Pred. No. 4,4e-05;  
 Matches 80; Conservative 23; Mismatches 98; Indels 109; Gaps 18;  
 QY 1 TEHAYRGRV-----CAVRAH-----DPVSESFVQRYVQPLTTCDGHACSTYR 47  
 Db 681 TNACRGPRTPTCTCECSIGFRDGRTCYDIDECSE-----QP--SVCSHTICNNH- 730  
 QY 48 TIYTAVRSPGLAPRPRACCGWKRTSGLPACGAIICPP--CRNG----- 95  
 Db 731 -----PGRFCEVGEIQPSD--EGTVAVVDRPPIVNCETGLHNCIDIPQR 774  
 QY 96 GSCVQPG---RCRCPAGRGD--TCQSDVDECSARRGGCPQRCVNTAGSYWCQCEGHS 149  
 Db 775 AQCITVGGSSVTCCLPGRSGDQACQ--DVDECQSRCHPDFAFCVNTGSGFTCCQCKPGY- 832  
 QY 150 LQADGTLVCP-----KGAPPVAVNPFG----- 172  
 Db 833 -QGDGFRVCEVEKTRCQHEEHILGAAGADPPRPPIPGILFVECDAGHYAPTCQHG 891  
 QY 173 -----VDSAMEEYQRLQSRVDLLEKGLQVLAFLH--SLASQALEHGLDPPSLVHS 224  
 Db 892 STGYCWCVDRDGR-EVEGRTTRPGMTTPECLSTVAPPIHGGPVPVAVPLP-PGTHLL-- 947  
 QY 225 FQQLGRIDSL 234  
 Db 948 FAQTGKIERL 957  
 RESULT 14

JP0076  
 nel protein - chicken  
 C:Species: Gallus gallus (chicken)  
 C:Date: 24-Feb-1995 #sequence\_revision 24-Feb-1995 #text\_change 13-Aug-1999  
 C:Accession: A38963; JP0076  
 R:Matsumashi, S.; Noji, S.; Koyama, E.; Myokai, F.; Ohuchi, H.; Taniguchi, S.; Hori, K.  
 Dev. Dyn. 203, 212-222, 1995  
 A:Title: New gene, nel, encoding a Mr 93K protein with EGF-like repeats is strongly expressed in the developing chicken embryo  
 A:Reference number: A38963; MUID:95383734; PMID:7655083  
 A:Accession: A38963  
 A:Molecule type: mRNA  
 A:Residues: 1-835 <MAT>  
 A:Cross-references: DDBJ:D45365  
 A:Experimental source: 9-day embryo  
 R:Matsumashi, S.; Noji, S.; Koyama, E.; Myokai, F.; Ohuchi, H.; Taniguchi, S.; Hori, K.  
 submitted to JIPID, January 1995  
 A:Description: A new gene, nel, encoding a Mr 93K protein with EGF-like repeats is strongly expressed in the developing chicken embryo  
 A:Reference number: JP0076  
 A:Accession: JP0076  
 A:Molecule type: mRNA  
 A:Residues: 1-835 <MA2>  
 A:Cross-references: DDBJ:D45365  
 A:Experimental source: 9-day embryo  
 C:Superfamily: von Willebrand factor type C repeat homology; EGF homology  
 F:273-333/Domain: von Willebrand factor type C repeat homology <WVC>  
 F:395-592/Region: EGF-like repeats  
 F:444-480/Region: EGF homology <EGF1>  
 F:486-521/Domain: EGF homology <EGF>  
 F:525-552/Domain: EGF homology <EGF2>

Query Match 12.3%; Score 173; DB 2; Length 835;  
 Best Local Similarity 41.4%; Pred. No. 3.3e-05;  
 Matches 29; Conservative 12; Mismatches 27; Indels 2; Gaps 1;  
 QY 81 GACGAAICPPNNGSCVQPCRCPAGWRCGTCSQDVDECSARRGCGPOR--CVNTPAG 138  
 DB 518 GTVCKAFCKDGRNGACTASNVACPOGFTGSPCETDIIDCSDFVQDSRANCINLPG 577  
 QY 139 SYWCQWEGH 148  
 DB 578 WYHCECRDGY 587

## RESULT 15

A46019  
 Notch-1 protein - mouse  
 N:Alternate names: notch protein  
 C:Species: Mus musculus (house mouse)  
 C:Date: 22-Sep-1993 #sequence\_revision 18-Nov-1994 #text\_change 20-Sep-1999  
 C:Accession: A46019; S25144  
 R:Del Amo, F.F.; Gendron-Maguire, M.; Swiatek, P.J.; Jenkins, N.A.; Copeland, N.G.; Grid  
 Genomics 15, 259-264, 1993  
 A:Title: Cloning, analysis, and chromosomal localization of Notch-1, a mouse homolog of  
 A:Reference number: A46019; MUID:93194170; PMID:8449489  
 A:Accession: A46019  
 A:Status: not compared with conceptual translation  
 A:Molecule type: nucleic acid  
 A:Residues: 1-2531 <DEL>  
 A:Cross-references: GB:Z11886; GB:S47228; MID:9288502; PIDN:CAA77941.1; PID:g288503  
 A:Note: sequence extracted from NCBI backbone (NCBIP:127318)  
 R:Francia del Amo, F.; Smith, D.E.; Swiatek, P.J.; Gendron-Maguire, M.; Greenspan, R.J.;  
 submitted to the EMBL data library, April 1992  
 A:Description: Expression pattern of Notch, a mouse homolog of Drosophila Notch, suggests  
 A:Reference number: S25144  
 A:Accession: S25144  
 A:Molecule type: mRNA  
 A:Residues: 1551-2108, Q', 2110-2114, 'ALP', 2118-2170 <FRA>  
 A:Cross-references: EMBL:Z11886  
 C:Genetics:  
 A:Gene: notch-1  
 A:Map position: 2  
 A:Note: proximal region of chromosome 2  
 C:Superfamily: unassigned ankyrin repeat proteins; ankyrin repeat homology; EGF homology

F:106-138/Domain: EGF homology <EGF1>  
 F:144-175/Domain: EGF homology <EGF1>  
 F:222-254/Domain: EGF homology <EGF2>  
 F:261-292/Domain: EGF homology <EGF2>  
 F:339-370/Domain: EGF homology <EGF3>  
 F:416-449/Domain: EGF homology <EGF3>  
 F:456-487/Domain: EGF homology <EGF4>  
 F:494-525/Domain: EGF homology <EGF5>  
 F:532-563/Domain: EGF homology <EGF6>  
 F:607-638/Domain: EGF homology <EGF7>  
 F:682-713/Domain: EGF homology <EGF8>  
 F:757-788/Domain: EGF homology <EGF9>  
 F:795-826/Domain: EGF homology <EGF10>  
 F:873-904/Domain: EGF homology <EGF11>  
 F:911-942/Domain: EGF homology <EGF12>  
 F:949-980/Domain: EGF homology <EGF13>  
 F:987-1018/Domain: EGF homology <EGF14>  
 F:1025-1056/Domain: EGF homology <EGF15>  
 F:1063-1094/Domain: EGF homology <EGF16>  
 F:1149-1180/Domain: EGF homology <EGF17>  
 F:1187-1218/Domain: EGF homology <EGF18>  
 F:1233-1264/Domain: EGF homology <EGF19>  
 F:1352-1383/Domain: EGF homology <EGF20>  
 F:1391-1425/Domain: EGF homology <EGF21>  
 F:1493-1581/Domain: ankyrin repeat homology <AN1>  
 F:1583-1671/Domain: ankyrin repeat homology <AN2>  
 F:1673-1761/Domain: ankyrin repeat homology <AN3>  
 F:1763-1851/Domain: ankyrin repeat homology <AN4>  
 F:1853-1941/Domain: ankyrin repeat homology <AN5>

Query Match 12.2%; Score 172; DB 2; Length 2531;  
 Best Local Similarity 34.5%; Pred. No. 0.0001;  
 Matches 41; Conservative 37; Mismatches 36; Indels 36; Gaps 5;  
 QY 69 CCFGWKRTSGLFPGAGAAICQP-----PCRNNGSCV---QFGRCPAGWRCGTCSQ 118  
 DB 129 CSFGWSGKS-----CQADPCASNPANGGQCLPFESSYTCRCPPGPHGPTCRD 178  
 QY 119 VDECSARRGCGPQ--PCVNTAGSYWCQWEGH-----SLSADGTLGVKPKG 161  
 DB 179 VNECSQNPGLCRHGHCHNEIGSYRCACCATHTGPHCELPYVPCSPSPQNGATCRPTG 237

Search completed: December 17, 2002, 10:03:40  
 Job time : 16.9772 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 17, 2002, 09:45:16 ; Search time 8.19355 Seconds  
(without alignments)  
1285.766 Million cell updates/sec

Title: US-09-852-472-3  
Perfect score: 1411  
Sequence: 1 TEHAHPRGRVCAVRAHGP.....SEQISFLERQLGSCCKKDS 254

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues  
Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	196	13.9	1964	1 NTG4_MOUSE	P31655 mus musculus
2	188.5	13.4	2003	1 NTG4_HUMAN	O99466 homo sapien
3	184	13.0	816	1 NEI2_MOUSE	O61220 mus musculus
4	183	13.0	810	1 NEI1_HUMAN	O92832 homo sapien
5	181.5	12.9	816	1 NEI2_HUMAN	O99435 homo sapien
6	181	12.8	810	1 NEI1_RAT	O62919 rattus norv
7	179.5	12.7	816	1 NEI2_RAT	O62918 rattus norv
8	176	12.5	652	1 CD93_HUMAN	O90973 homo sapien
9	175.5	12.4	816	1 NEI_CHICK	O90827 gallus gall
10	175.5	12.4	2871	1 FBNI_HUMAN	P35555 homo sapien
11	175	12.4	2907	1 FBNI_MOUSE	O61555 mus musculus
12	174.5	12.4	2321	1 NTG3_HUMAN	O90447 homo sapien
13	173.5	12.3	1247	1 NIDC_HUMAN	P14543 homo sapien
14	172	12.2	2531	1 NTG1_MOUSE	O01705 mus musculus
15	171.5	12.1	2871	1 FBNI_MOUSE	O61554 mus musculus
16	171	12.1	2703	1 NOTC_MOUSE	P07207 drosophila
17	170.5	12.1	2871	1 FBNI_BOVIN	P98133 bos taurus
18	170	12.0	675	1 PRIS_BOVIN	O08761 mus musculus
19	169.5	12.0	2871	1 FBNI_PIG	O91736 sus scrofa
20	168.5	11.9	2318	1 NTG3_MOUSE	O61982 mus musculus
21	168	11.9	675	1 PRIS_RAT	P53813 rattus norv
22	168	11.9	833	1 DL_DROME	O10041 drosophila
23	166	11.8	1238	1 JAG2_HUMAN	O99525 mus musculus
24	166	11.8	1247	1 JAG2_MOUSE	P97607 rattus norv
25	165	11.7	1202	1 JAG2_RAT	P21283 xenopus lae
26	165	11.7	2524	1 NOTC_XENTLA	P35555 mus musculus
27	164.5	11.7	2911	1 FBNI_HUMAN	P14585 caenorhabdi
28	164	11.6	1429	1 LIT2_CAEL	P46531 mus musculus
29	163	11.6	2556	1 NTG1_HUMAN	O89103 mus musculus
30	162	11.5	644	1 CD93_MOUSE	P98118 cryptoleagus
31	162	11.5	675	1 PRIS_RABIT	P07722 bos taurus
32	162	11.5	675	1 PRIS_BOVIN	O91772 rattus norv
33	161.5	11.4	2319	1 NTG3_RAT	

ALIGNMENTS

ID	NTG4_MOUSE	STANDARD	PRT, 1964 AA.	Q9nyj7 homo sapien
AC	P31655; O62389; O62390; O35442; Q9RLW9; O88314; O88316; Q9RLX0;			O9et61 rattus norv
DT	01-JUL-1993 (Rel. 26, Created)			O07008 rattus norv
DT	01-NOV-1997 (Rel. 35, Last sequence update)			P46530 brachydanio
DT	15-NOV-2002 (Rel. 41, Last annotation update)			P22457 bos taurus
DE	Neurogenic locus notch homolog protein 4 precursor (Notch 4)			P00745 bos taurus
DE	[Contains: Transforming protein Int-3].			O9wua1 mus musculus
GN	NOTCH4 OR INT3 OR INT-3.			P37889 homo sapien
OC	Mus musculus (Mouse).			O28520 macaca mula
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			O90y54 brachydanio
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			Q14517 homo sapien
OX	NCBI_TaxID=10090;			
RN	[1]			
RX	SEQUENCE FROM N.A.			
RA	MEDLINE=92194507; PubMed=1312643;			
RT	Robbins J., Blondel B.J., Gallahan D., Callahan R.;			
RT	"Mouse mammary tumor gene int-3: a member of the notch gene family			
RT	transforms mammary epithelial cells.";			
RL	J. Virol. 66:2594-2599(1992).			
RN	[2]			
RX	REVISIONS, SEQUENCE FROM N.A.			
RA	MEDLINE=97294599; PubMed=9150355;			
RT	Gallahan D., Callahan R.;			
RT	"The mouse mammary tumor associated gene INT3 is a unique member of			
RT	the NOTCH gene family (NOTCH4).";			
RL	Oncogene 14:1883-1890(1997).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Lung, and Testis;			
RA	MEDLINE=96281668; PubMed=6681805;			
RT	Uytendaele H., Marazzi G., Wu G., Yan Q., Saassoon D., Kitajewski J.;			
RT	"Notch4/int-3, a mammary proto-oncogene, is an endothelial			
RT	cell-specific mammalian Notch gene.";			
RL	Development 122:2251-2259(1996).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RA	Rosen L., Mahairas G., Qin S., Ahern M.E., Dankers C., Lasky S.,			
RA	Loretz C., Schmidt S., Tipton S., Traicoff R., Zackone K., Hood L.;			
RT	"Sequence of the mouse major histocompatibility locus class III			
RT	region.";			
RL	Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.			
RN	[5]			
RP	SEQUENCE OF 1436-1600 FROM N.A.			
RA	MEDLINE=99252212; PubMed=10233982;			
RT	Lee J.-S., Haruna T., Ishimoto A., Honjo T., Yanagawa S.-I.;			
RT	"Intracisternal type A particle-mediated activation of the Notch4/int3			
RT	gene in a mouse mammary tumor: generation of truncated Notch4/int3			
RT	mRNAs by retroviral splicing events.";			
RL	J. Virol. 73:5166-5171(1999).			
RN	[6]			
RP	FUNCTION.			
RA	MEDLINE=21244657; PubMed=11344305;			
RT	Uytendaele H., Ho J., Rossant J., Kitajewski J.;			
RT	"Vascular patterning defects associated with expression of activated			

RT Notch4 in embryonic endothelium.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 98:5643-5648(2001).  
 RN [7]  
 RP SEQUENCE OF 1463-1964, POST-TRANSLATIONAL PROCESSING, AND MUTAGENESIS  
 RP OF VAL-1463.  
 RA MEDLINE=21523956; PubMed=11518718;  
 RX Saxena M.T., Schroter E.H., Mumm J.S., Kopan R.;  
 RA "Murine notch homologs (NL-4) undergo presenilin-dependent  
 RT proteolysis.";  
 RL J. Biol. Chem. 276:40268-40273(2001).  
 RN [8]  
 RP POST-TRANSLATIONAL PROCESSING  
 RX MEDLINE=21374376; PubMed=11459941;  
 RA Mizutani T., Taniguchi Y., Aoki T., Hashimoto N., Honjo T.;  
 RA "Conservation of the biochemical mechanisms of signal transduction  
 RT among mammalian Notch family members.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 98:9026-9031(2001).  
 CC -!- FUNCTION: Functions as a receptor for membrane-bound ligands  
 CC Jagged1, Jagged2 and Delta to regulate cell-fate determination.  
 CC Upon ligand activation through the released notch intracellular  
 CC domain (NICD) it forms a transcriptional activator complex with  
 CC RBP-J kappa and activates genes of the enhancer of split locus.  
 CC Affects the implementation of differentiation, proliferation and  
 CC apoptotic programs (By similarity). May regulate branching  
 CC morphogenesis in the developing vascular system.  
 CC -!- SUBUNIT: Heterodimer of a C-terminal fragment N(TM) and a N-  
 CC terminal fragment N(EC) which are probably linked by disulfide  
 CC bonds.  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Following  
 CC proteolytical processing NICD is translocated to the nucleus.  
 CC -!- TISSUE SPECIFICITY: Highly expressed in lung, moderately in heart  
 CC kidney, and at lower levels in the ovary and skeletal muscle. A  
 CC very low expression is seen in the brain, intestine, liver and  
 CC testis.  
 CC -!- DEVELOPMENTAL STAGE: Highly expressed in endothelial cells during  
 CC embryonic development from 9.0 d.p.c.  
 CC -!- PTM: Synthesized in the endoplasmic reticulum as an inactive form  
 CC which is proteolytically cleaved by a furin-like convertase in the  
 CC trans-Golgi network before it reaches the plasma membrane to yield  
 CC an active, ligand-accessible form. Cleavage results in a C-  
 CC terminal fragment N(TM) and a N-terminal fragment N(EC). Following  
 CC ligand binding, it is cleaved by TNF-alpha converting enzyme  
 CC (TACE) to yield a membrane-associated intermediate fragment called  
 CC notch extracellular truncation (NEXT). This fragment is then  
 CC cleaved by presenilin dependent gamma-secretase to release a  
 CC notch-derived peptide containing the intracellular domain (NICD)  
 CC from the membrane.  
 CC -!- PTM: Phosphorylated.  
 CC -!- DISEASE: Loss of the extracellular domain causes constitutive  
 CC activation of the Notch protein, which leads to hyperproliferation  
 CC of glandular epithelial tissues and development of mammary  
 CC carcinomas.  
 CC -!- SIMILARITY: BELONGS TO THE NOTCH FAMILY.  
 CC -!- SIMILARITY: CONTAINS 29 EGF-LIKE DOMAINS.  
 CC -!- SIMILARITY: CONTAINS 3 LIN/NOTCH REPEATS.  
 CC -!- SIMILARITY: CONTAINS 5 ANK REPEATS.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL; M80456; AAB38377.1; -;  
 CC EMBL; U43691; AAC52630.1; -;  
 CC EMBL; U43691; AAC52631.1; -;  
 CC EMBL; AF030001; AAB82004.1; -;  
 CC EMBL; AB016771; BAA32281.1; ALT SEQ.  
 CC EMBL; AB016772; BAA32283.1; ALT INIT.  
 CC EMBL; AB016773; BAA32284.1; ALT\_INIT.  
 CC EMBL; AB016774; BAA32285.1; -;

DR PIR: A38072; TMVMT3.  
 DR HSSP; P08709; IBF9.  
 DR MGD; MGI:107471; Notch4.  
 DR InterPro; IPR002110; ANK.  
 DR InterPro; IPR000152; Asx\_hydroxyl.  
 DR InterPro; IPR000561; EGF-like.  
 DR InterPro; IPR000742; EGF\_2.  
 DR InterPro; IPR001881; EGF\_Ca.  
 DR InterPro; IPR001438; EGF\_II.  
 DR InterPro; IPR000800; Notch.  
 DR Pfam; PF00008; EGF; 27.  
 DR Pfam; PF00023; ank; 6.  
 DR Pfam; PF00066; notch; 2.  
 DR PRINTS; PR01415; ANKYRIN.  
 DR PRINTS; PR00010; EGFBLD.  
 DR PRINTS; PR01452; NOTCH.  
 DR SMART; SM00248; ANK; 5.  
 DR SMART; SM00179; EGF\_Ca; 11.  
 DR SMART; SM00001; EGF\_like; 15.  
 DR SMART; SM00004; NL; 2.  
 DR PROSITE; PS50088; ANK\_REPEAT; 5.  
 DR PROSITE; PS50297; ANK\_REPEAT\_REGION; 1.  
 DR PROSITE; PS00010; ASX\_HYDROXYL; 11.  
 DR PROSITE; PS00022; EGF\_1; 28.  
 DR PROSITE; PS01186; EGF\_2; 21.  
 DR PROSITE; PS01187; EGF\_Ca; 9.  
 KW Receptor; Transcription regulation; Activator; Differentiation;  
 KW Developmental protein; Repeat; ANK repeat; EGF-like domain;  
 KW Transmembrane; Glycoprotein; Signal; Phosphorylation; Proto-oncogene.  
 FT SIGNAL 1 20  
 FT CHAIN 21 1964 NEUROGENIC LOCUS NOTCH HOMOLOG PROTEIN 4.  
 FT CHAIN 1411 1964 TRANSFORMING PROTEIN INT-3  
 FT CHAIN 1428 1964 NOTCH EXTRACELLULAR TRUNCATION.  
 FT CHAIN 1463 1964 NOTCH INTRACELLULAR DOMAIN.  
 FT DOMAIN 21 1443 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 1444 1464 POTENTIAL.  
 FT DOMAIN 1465 1964 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 21 60 EGF-LIKE 1.  
 FT DOMAIN 61 112 EGF-LIKE 2.  
 FT DOMAIN 115 152 EGF-LIKE 3.  
 FT DOMAIN 153 189 EGF-LIKE 4.  
 FT DOMAIN 191 229 EGF-LIKE 5. CALCIUM-BINDING (POTENTIAL).  
 FT DOMAIN 231 271 EGF-LIKE 6.  
 FT DOMAIN 273 309 EGF-LIKE 7. CALCIUM-BINDING (POTENTIAL).  
 FT DOMAIN 311 350 EGF-LIKE 8. CALCIUM-BINDING (POTENTIAL).  
 FT DOMAIN 352 388 EGF-LIKE 9. CALCIUM-BINDING (POTENTIAL).  
 FT DOMAIN 389 427 EGF-LIKE 10.  
 FT DOMAIN 429 470 EGF-LIKE 11. CALCIUM-BINDING (POTENTIAL).  
 FT DOMAIN 472 508 EGF-LIKE 12. CALCIUM-BINDING (POTENTIAL).  
 FT DOMAIN 510 546 EGF-LIKE 13. CALCIUM-BINDING (POTENTIAL).  
 FT DOMAIN 548 584 EGF-LIKE 14. CALCIUM-BINDING (POTENTIAL).  
 FT DOMAIN 586 622 EGF-LIKE 15. CALCIUM-BINDING (POTENTIAL).  
 FT DOMAIN 623 656 EGF-LIKE 16.  
 FT DOMAIN 658 686 EGF-LIKE 17.  
 FT DOMAIN 688 724 EGF-LIKE 18.  
 FT DOMAIN 726 762 EGF-LIKE 19.  
 FT DOMAIN 764 800 EGF-LIKE 20.  
 FT DOMAIN 803 839 EGF-LIKE 21.  
 FT DOMAIN 841 877 EGF-LIKE 22.  
 FT DOMAIN 878 924 EGF-LIKE 23.  
 FT DOMAIN 926 962 EGF-LIKE 24.  
 FT DOMAIN 964 1000 EGF-LIKE 25.  
 FT DOMAIN 1002 1040 EGF-LIKE 26.  
 FT DOMAIN 1042 1081 EGF-LIKE 27.  
 FT DOMAIN 1083 1122 EGF-LIKE 28.  
 FT DOMAIN 1126 1167 EGF-LIKE 29.  
 FT DOMAIN 1168 1208 LIN/NOTCH 1.  
 FT REPEAT 1209 1242 LIN/NOTCH 2.  
 FT REPEAT 1243 1282 LIN/NOTCH 3.  
 FT REPEAT 1628 1657 ANK 1.  
 FT REPEAT 1661 1691 ANK 2.  
 FT REPEAT 1695 1724 ANK 3.  
 FT REPEAT 1728 1757 ANK 4.

Query Match 13.9%; Score 196; DB 1; Length 1964;  
 Best Local Similarity 34.2%; Pred. No. 1.9e-07;  
 Matches 50; Conservative 12; Mismatches 54; Indels 30; Gaps 7;

QY 61 APPRPRACCPGK-RTSLPGACGAIICPPRNGSCVQPG---RCRCPRAMRDTQ 116  
 DB 134 ASGRPOCSEPGTGTGRCQQLRDCSA---NPCANGVCLATYPOIQCRCPGFEHGTCE 189  
 QY 117 SDVDECSARRGGPO--RCVNTAGSYWCOC---MEGHSJADGTLVCP---KGGPRVA 167  
 DB 190 RDINECLFEPGPPQGTSCNNTGSIYQCLCPVGQEPQCKLRKACPPSGCLNGTICQLY 249  
 QY 168 PNP-----TGVDANKKEE 180  
 DB 250 PEGHSTPHLCPCPGTGLDCENMPD 275

RESULT 2  
 NT4 HUMAN STANDARD; PRT; 2003 AA.  
 AC 099466; 000306; 099940; 099458; 09H358; 09U119; 09U1J0;  
 DT 15-JUN-2002 (Rel. 41, Created)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Neurogenic locus notch homolog protein 4 precursor (Notch 4)  
 DE (hnc04).  
 GN NOTCH4.  
 OS Homo sapiens (human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OC NCBI TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORM 1), AND POLYMORPHISM OF POLY-LEU.  
 RC TISSUE=Placenta; PubMed=9168133;  
 RA MEDLINE=97311416; PubMed=9168133;  
 RA Sugaya K., Sasamura S.-I., Nohata J., Kimura T., Fukagawa T.,  
 Nakamura Y., Ando A., Inoko H., Ikemura T., Mita K.;  
 "Gene organization of human NOTCH4 and (CTG)n polymorphism in this  
 human counterpart gene of mouse proto-oncogene Int3.";  
 RT Gene 189:235-244 (1997).  
 RL Gene 189:235-244 (1997).  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORMS 1, 2 AND 3).  
 RC TISSUE=Bone marrow, and Heart;  
 RA MEDLINE=98360091; PubMed=9693032;  
 RA Li L., Huang G.M., Banta A.B., Deng Y., Smith T., Dong P.,  
 Friedman C., Chen L., Tresek B.J., Spies T., Rowen L., Hood L.;  
 "Cloning, characterization, and the complete 56.8-kilobase DNA  
 sequence of the human NOTCH4 gene.";  
 RT Genomics 51:45-58 (1998).  
 RL Genomics 51:45-58 (1998).  
 RN [3]  
 RP SEQUENCE OF 1-503 FROM N.A., AND VARIANTS GLN-117 AND GLN-317.  
 RA Miyagawa T., Tokunaga K., Hojo H.;  
 RT "Human notch4 gene variant.";  
 RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP IDENTIFICATION OF LIGANDS.  
 RA MEDLINE=99180765; PubMed=10079256;  
 RA Gray G.E., Mann R.S., Mitsiadis E., Henrique D., Carcangiu M.-L.,  
 Banks A., Leitman J., Ward D., Ish-Horowitz D., Attavanas-Tsakonas S.;  
 "Human ligands of the Notch receptor.";  
 RT Am. J. Pathol. 154:785-794 (1999).  
 RL Am. J. Pathol. 154:785-794 (1999).  
 CC -1- FUNCTION: Functions as a receptor for membrane-bound ligands  
 Jagged1, Jagged2 and Deltal to regulate cell-fate determination.  
 Upon ligand activation through the released notch intracellular  
 domain (NICD) it forms a transcriptional activator complex with  
 RBP-J kappa and activates genes of the enhancer of split locus.  
 Affects the implementation of differentiation, proliferation and  
 apoptotic programs. May regulate branching morphogenesis in the  
 developing vascular system (By similarity).  
 CC -1- SUBUNIT: Heterodimer of a C-terminal fragment N(TM) and a N-  
 terminal fragment N(EC) which are probably linked by disulfide  
 bonds (By similarity).

CC -1- SUBCELLULAR LOCATION: Type I membrane protein. Following  
 CC proteolytical processing NICD is translocated to the nucleus.  
 CC -1- ALTERNATIVE PRODUCTS: 3 isoforms; 1 (shown here), 2 and 3; may be  
 CC produced by alternative splicing.  
 CC -1- TISSUE SPECIFICITY: Highly expressed in the heart, moderately in  
 CC the lung and placenta and at low levels in the liver, skeletal  
 CC muscle, kidney, pancreas, spleen, lymph node, thymus, bone marrow  
 CC and fetal liver. No expression was seen in adult brain or  
 CC peripheral blood leukocytes.  
 CC -1- PTM: Synthesized in the endoplasmic reticulum as an inactive form  
 CC which is proteolytically cleaved by a furin-like convertase in the  
 CC trans-Golgi network before it reaches the plasma membrane to yield  
 CC an active, ligand-accessible form. Cleavage results in a C-  
 CC terminal fragment N(TM) and a N-terminal fragment N(EC). Following  
 CC ligand binding, it is cleaved by TNF-alpha converting enzyme  
 CC (TACE) to yield a membrane-associated intermediate fragment called  
 CC notch extracellular truncation (NEXT). This fragment is then  
 CC cleaved by presentin dependent gamma-secretase to release a  
 CC notch-derived peptide containing the intracellular domain (NICD)  
 CC from the membrane (By similarity).  
 CC -1- PTM: Phosphorylated (By similarity).  
 CC -1- POLYMORPHISM: The poly-Leu region of NOTCH4 (in the signal  
 CC peptide) is polymorphic and the number of Leu varies in the  
 CC population (from 6 to 12).  
 CC -1- SIMILARITY: BELONGS TO THE NOTCH FAMILY.  
 CC -1- SIMILARITY: CONTAINS 28 EGF-LIKE DOMAINS.  
 CC -1- SIMILARITY: CONTAINS 3 LIN/NOTCH REPEATS.  
 CC -1- SIMILARITY: CONTAINS 5 ANK REPEATS.  
 CC -1- CAUTION: Ref.1 sequence differs from that shown due to frameshifts  
 CC in position 1438 to 1463.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.ebi.ac.uk/announcements>  
 CC or send an email to [license@ebi.ac.uk](mailto:license@ebi.ac.uk)).  
 CC -----  
 CC EMBL; D63395; BAA09708.1; ALT\_FRAME.  
 CC EMBL; D65666; BAA13116.1; -.  
 CC EMBL; U95299; AAC32288.1; -.  
 CC EMBL; U89335; AAC63097.1; -.  
 CC EMBL; AB023961; BAB20317.1; -.  
 CC EMBL; AB024520; BAA88951.1; -.  
 CC EMBL; AB024578; BAA88952.1; -.  
 CC HSSP; P08709; 1BP9.  
 CC Genew; HGNC:7884; NOTCH4.  
 CC MIM; 164951; -.  
 CC InterPro; IPR002110; ANK.  
 CC InterPro; IPR000152; Asx\_hydroxyl.  
 CC InterPro; IPR000561; EGF\_1-like.  
 CC InterPro; IPR000742; EGF\_2.  
 CC InterPro; IPR001881; EGF\_Ca.  
 CC InterPro; IPR001388; EGF\_11.  
 CC InterPro; IPR000800; Notch.  
 CC Pfam; PF00008; EGF; 26.  
 CC Pfam; PF00023; ank; 6.  
 CC Pfam; PF00066; notch; 2.  
 CC PRINTS; PR00010; EGFBLD.  
 CC PRINTS; PR00011; EGFAMININ.  
 CC PRINTS; PR00012; ENTPEP.  
 CC SMART; SM00248; ANK; 5.  
 CC SMART; SM00017; EGF\_CA; 11.  
 CC SMART; SM00001; EGF\_1-like; 15.  
 CC SMART; SM00004; NL; 2.  
 CC PROSITE; PS50088; ANK\_REPEAT; 5.  
 CC PROSITE; PS50297; ANK\_REPEAT\_REGION; 1.  
 CC PROSITE; PS00010; ASX\_HYDROXYL; 11.  
 CC PROSITE; PS00022; EGF\_1; 28.  
 CC PROSITE; PS01186; EGF\_2; 21.  
 CC PROSITE; PS01187; EGF\_CA; 9.  
 CC Receptor; Transcription regulation; Activator; Differentiation;



DR Pfam; PF02210; TSPN; 1.  
 DR SMART; SM00179; EGF\_CA; 3.  
 DR SMART; SM00282; LamG; 1.  
 DR SMART; SM00210; TSPN; 1.  
 DR SMART; SM00214; VWC; 2.  
 DR PROSITE; PS00010; ASX\_HYDROXYL; 3.  
 DR PROSITE; PS00022; EGF\_1; 1.  
 DR PROSITE; PS01186; EGF\_2; 3.  
 DR PROSITE; PS01187; EGF\_CA; 3.  
 DR PROSITE; PS01208; VWF; 2.  
 DR Glycoprotein; EGF-like domain; Repeat; Signal.  
 KM SIGNAL; 1 24  
 FT CHAIN; 25 816  
 FT DOMAIN; 30 258  
 FT DOMAIN; 272 331  
 FT DOMAIN; 332 396  
 FT DOMAIN; 397 439  
 FT DOMAIN; 440 481  
 FT DOMAIN; 482 522  
 FT DOMAIN; 521 553  
 FT DOMAIN; 555 601  
 FT DOMAIN; 602 637  
 FT DOMAIN; 638 693  
 FT DOMAIN; 698 756  
 FT DOMAIN; 758 813  
 FT DISULFID; 401 413  
 FT DISULFID; 407 422  
 FT DISULFID; 424 438  
 FT DISULFID; 444 457  
 FT DISULFID; 451 466  
 FT DISULFID; 468 480  
 FT DISULFID; 486 499  
 FT DISULFID; 493 508  
 FT DISULFID; 510 521  
 FT DISULFID; 525 535  
 FT DISULFID; 529 541  
 FT DISULFID; 543 552  
 FT DISULFID; 559 572  
 FT DISULFID; 566 581  
 FT DISULFID; 583 600  
 FT DISULFID; 606 619  
 FT DISULFID; 613 628  
 FT DISULFID; 630 636  
 FT CARBOHYD; 53 55  
 FT CARBOHYD; 225 225  
 FT CARBOHYD; 293 293  
 FT CARBOHYD; 298 298  
 FT CARBOHYD; 517 517  
 FT CARBOHYD; 615 615  
 FT CARBOHYD; 635 635  
 SQ SEQUENCE 816 AA; 91163 MW; SBD00A946F87E7AD CRC64;  
 Query Match 13.0%; Score 184; DB 1; Length 816;  
 Best Local Similarity 28.8%; Pred. No. 6; Ge-07;  
 Matches 46; Conservative 22; Mismatches 64; Indels 28; Gaps 7;  
 QY 7 PGRRAVRAHGDPPSEFVQVYVQPLT---CDGRACSTYRTIYRVRSPGLAPA 63  
 DB 461 PGRMVCVCKT-GYIRIDYSCHEDECLTQHNDENALC--PNTV-----G 504  
 QY 64 RPRYACPGWRTSGLPACAAITCPPCRNAGSCVOPGRCRPAGMRGDTQGVDECS 123  
 DB 505 GHNCCCKGTYGN-----GTTCKAFCKDCRCRAGACIAANVACAPQGFPGSCETDIDCS 560  
 QY 124 ARGGCPR--CVNAGSYMCOQWEGHSLADGTLGVKXG 161  
 DB 561 EGFVQCDSRANCIINPGWYHCECRDGYH--DNGMFAPGG 597

AC Q92832; Q9Y472;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Protein kinase C-binding protein NELL1 precursor (NEL-like protein 1)  
 GN (Nel-related protein 1).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCB1\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=97131504; PubMed=8975702;  
 RA Watanabe T.K., Katagiri T., Suzuki M., Shimizu F., Fujiwara T.,  
 RA Kanemoto N., Nakamura Y., Hirai Y., Maekawa H., Takahashi E.;  
 RT "Cloning and characterization of two novel human cDNAs (NELL1 and  
 RL NELL2) encoding proteins with six EGF-like repeats.";  
 RL Genomics 38:273-276(1996).  
 RP SEQUENCE OF 383-810 FROM N.A.  
 RA Ting K., Vastardis H., Mulliken J.B., Bertolami C., Wen Z.,  
 RA Young M., Tieu A., Kwong E.;  
 RT "Nel homolog gene expression in craniofacial anomalies.";  
 RL Submitted (Sep-1996) to the EMBL/Genbank/DBJ databases.  
 CC -1-SUBUNIT: HOMOTRIMER. BINDS TO PKC BETA-1 (BY SIMILARITY).  
 CC -1-SUBCELLULAR LOCATION: Secreted (By similarity).  
 CC -1-DISEASE: EXPRESSED IN CRANIOFACIAL ANOMALIES.  
 CC -1-SIMILARITY: CONTAINS 5 VWF C-DOMAINS.  
 CC -1-SIMILARITY: CONTAINS 6 EGF-LIKE DOMAINS.  
 CC -1-CAUTION: REF. 2 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO FRAMESHIFTS  
 IN POSITIONS 427 AND 771.  
 CC  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 the European Bioinformatics Institute. There are no restrictions on its  
 use by non-profit institutions as long as its content is in no way  
 modified and this statement is not removed. Usage by and for commercial  
 entities requires a license agreement (See <http://www.ebi.ac.uk/announcements>  
 or send an email to [license@ebi.ac.uk](mailto:license@ebi.ac.uk)).  
 CC  
 DR EMBL; D83017; BA11680.1; -  
 DR EMBL; U57523; AAB06946.1; ALT\_FRAME.  
 DR HSSP; P07204; IADX.  
 DR Genew; HGNC:7750; NELL1.  
 DR MIM; 602319; -  
 DR InterPro; IPR000152; Asx\_hydroxyl.  
 DR InterPro; IPR000561; EGF-like.  
 DR InterPro; IPR001881; EGF\_CA.  
 DR InterPro; IPR001791; Laminin\_G.  
 DR InterPro; IPR003129; TSPN.  
 DR InterPro; IPR001007; VWF\_C.  
 DR Pfam; PF00008; EGF; 4.  
 DR Pfam; PF00093; VWC; 3.  
 DR Pfam; PF02210; TSPN; 1.  
 DR SMART; SM00179; EGF\_CA; 2.  
 DR SMART; SM00001; EGF\_like; 4.  
 DR SMART; SM00282; LamG; 1.  
 DR SMART; SM00210; TSPN; 1.  
 DR SMART; SM00214; VWC; 3.  
 DR PROSITE; PS00010; ASX\_HYDROXYL; 3.  
 DR PROSITE; PS00022; EGF\_1; 1.  
 DR PROSITE; PS01186; EGF\_2; 3.  
 DR PROSITE; PS01187; EGF\_CA; 3.  
 DR PROSITE; PS01208; VWF; 2.  
 KW Glycoprotein; EGF-like domain; Repeat; Signal.  
 FT SIGNAL; 1 16  
 FT CHAIN; 17 810  
 FT DOMAIN; 81 230  
 FT DOMAIN; 273 331  
 FT DOMAIN; 335 390  
 FT DOMAIN; 335 390



FT DOMAIN 391 433  
 FT DOMAIN 434 475  
 FT DOMAIN 476 516  
 FT DOMAIN 515 547  
 FT DOMAIN 549 595  
 FT DOMAIN 596 631  
 FT DOMAIN 632 687  
 FT DOMAIN 692 750  
 FT DOMAIN 752 807  
 FT DISULFID 395 407  
 FT DISULFID 401 416  
 FT DISULFID 418 432  
 FT DISULFID 438 451  
 FT DISULFID 445 460  
 FT DISULFID 462 474  
 FT DISULFID 480 493  
 FT DISULFID 487 502  
 FT DISULFID 504 515  
 FT DISULFID 519 529  
 FT DISULFID 523 535  
 FT DISULFID 537 546  
 FT DISULFID 553 566  
 FT DISULFID 560 575  
 FT DISULFID 577 594  
 FT DISULFID 600 613  
 FT DISULFID 607 622  
 FT DISULFID 624 630  
 FT CARBOHYD 40 40  
 FT CARBOHYD 53 53  
 FT CARBOHYD 83 83  
 FT CARBOHYD 224 224  
 FT CARBOHYD 294 294  
 FT CARBOHYD 372 372  
 FT CARBOHYD 511 511  
 FT CARBOHYD 562 562  
 FT CARBOHYD 609 609  
 FT CARBOHYD 708 708  
 FT CARBOHYD 732 732  
 FT CARBOHYD 758 758  
 FT CONFLICT 383 383  
 FT CONFLICT 573 573  
 FT CONFLICT 626 626  
 SQ SEQUENCE 810 AA; 89606 MW; 549465EA3F7AEED0 CRC64;

Query Match 13.0%; Score 183; DB 1; Length 810;  
 Best Local Similarity 38.5%; Pred. No. 7.8e-07;  
 Matches 37; Conservative 11; Mismatches 38; Indels 10; Gaps 3;

QY 69 CPGWKRTSGLPAGCAIACOPPCNRGSSCVPGRCRCPAGWRGDTCSQSDVDECSARRGG 128  
 Db 504 KPGVGN-----GTTCRAFCEGCRGCGTGVAPNKCVPSCGFTGSHCEKIDECSEGGIE 559  
 QY 129 C--PQRCVNTAGSWCQCEGH-----SLSDAGTGLCV 158  
 Db 560 CHNHSRCVNLPGWYHCECRSGFHDGDTYSLSGSCI 595

RESULT 5  
 ID\_NEL2\_HUMAN STANDARD; PRT; 816 AA.  
 AC Q99435;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE protein kinase C-binding protein NELL2 precursor (NEL-like protein 2)  
 DE (Nel-related protein 2).  
 GN NELL2 OR NRP2.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.

TISSUE-Brain;  
 MEDLINE=97131504; PubMed=8975702;  
 Watanabe T.K., Katagiri T., Suzuki M., Shimizu F., Fujiwara T.,  
 Kanemoto N., Nakamura Y., Hirai Y., Maekawa H., Takahashi E.,  
 "Cloning and characterization of two novel human cDNAs (NELL1 and  
 NELL2) encoding proteins with six EGF-like repeats.",  
 Genomics 38:273-276(1996).  
 [2]  
 TSP N-TERMINAL DOMAIN.  
 MEDLINE=98153258; PubMed=9480764;  
 Beckmann G., Hanke J., Bork P., Reich J.;  
 "Merging extracellular domains: fold prediction for laminin G-like  
 and amino-terminal thrombospondin-like modules based on homology to  
 pentraxins.",  
 J. Mol. Biol. 275:725-730(1998).  
 CC -!- SUBUNIT: HOMOTRIMER. BINDS TO PKC BETA-1 (BY SIMILARITY).  
 CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).  
 CC -!- SIMILARITY: CONTAINS 1 TSP N-TERMINAL DOMAIN.  
 CC -!- SIMILARITY: CONTAINS 5 VWFC DOMAINS.  
 CC -!- SIMILARITY: CONTAINS 6 EGF-LIKE DOMAINS.  
 CC  
 This SWISS-PROT entry is copyright. It is produced through a collaboration  
 between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 the European Bioinformatics Institute. There are no restrictions on its  
 use by non-profit institutions as long as its content is in no way  
 modified and this statement is not removed. Usage by and for commercial  
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 -----  
 EMBL: D83018; BAAL1681.1; -.  
 HSP: P00740; IEDM.  
 Genew; HGNC:7751; NELL2.  
 MIM; 602320; -.  
 InterPro: IPR000152; Asx hydroxyl.  
 InterPro: IPR000561; EGF-like.  
 InterPro: IPR001881; EGF Ca.  
 InterPro: IPR001791; Laminin\_G.  
 InterPro: IPR003129; TSPN.  
 InterPro: IPR001007; VWFC\_C.  
 Pfam: PF00008; EGF; 5.  
 Pfam: PF00093; VWC; 3.  
 Pfam: PF02210; TSPN; 1.  
 SMART; SM00179; EGF\_CA; 3.  
 SMART; SM00001; EGF\_Like; 3.  
 SMART; SM00282; LamG; 1.  
 SMART; SM00210; TSPN; 1.  
 SMART; SM00214; VWC; 3.  
 PROSITE; PS00010; ASX\_HYDROXYL; 3.  
 PROSITE; PS00022; EGF\_1; 1.  
 PROSITE; PS01186; EGF\_2; 4.  
 PROSITE; PS01187; EGF\_CA; 3.  
 PROSITE; PS01208; VWFC; 2.  
 Glycoprotein; EGF-like domain; Repeat; Signal.  
 SIGNAL 1 24  
 POTENTIAL.  
 CHAIN 25 816  
 DOMAIN 30 258  
 TSP N-TERMINAL.  
 VWFC 1.  
 VWFC 2.  
 EGF-LIKE 1. CALCIUM-BINDING (POTENTIAL).  
 EGF-LIKE 2.  
 EGF-LIKE 3.  
 EGF-LIKE 4.  
 EGF-LIKE 5.  
 EGF-LIKE 6. CALCIUM-BINDING (POTENTIAL).  
 VWFC 3.  
 VWFC 4.  
 VWFC 5.  
 BY SIMILARITY.  
 DISULFID 401 413  
 BY SIMILARITY.  
 DISULFID 407 422  
 BY SIMILARITY.  
 DISULFID 424 438  
 BY SIMILARITY.  
 DISULFID 444 457  
 BY SIMILARITY.  
 DISULFID 451 466  
 BY SIMILARITY.  
 DISULFID 468 480  
 BY SIMILARITY.



FT DISULFID 486 499 BY SIMILARITY.  
 FT DISULFID 493 508 BY SIMILARITY.  
 FT DISULFID 510 521 BY SIMILARITY.  
 FT DISULFID 525 535 BY SIMILARITY.  
 FT DISULFID 529 541 BY SIMILARITY.  
 FT DISULFID 543 552 BY SIMILARITY.  
 FT DISULFID 559 572 BY SIMILARITY.  
 FT DISULFID 583 600 BY SIMILARITY.  
 FT DISULFID 606 619 BY SIMILARITY.  
 FT DISULFID 613 628 BY SIMILARITY.  
 FT DISULFID 630 636 BY SIMILARITY.  
 FT CARBOHYD 53 53 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 225 225 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 298 298 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 517 517 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 615 615 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 635 635 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 816 AA; 91346 MW; 89370B987DC7A324 CRC64;

Query Match 12.8%; Score 181.5; DB 1; Length 816;  
 Best Local Similarity 36.8%; Pred. No. 1e-06; Indels 9; Gaps 3;  
 Matches 35; Conservative 14; Mismatches 37;

QY 69 CCGPCKRTSGLPACGAACOPPCRCGSCVOPGRCRCPCAGWRGDTCCSDVDECSARRGG 128  
 DB 510 CKPGYTN-----GTTCKAFPCDGRNGAGACIAANVCAPGFTGSPCETDIDECSDGFVQ 565  
 QY 129 CPOR--CVNTAGSYWCQCGWEGHSLADGTLCPK 161  
 DB 566 CDSRANCINLPGWYHCECRDGYH--DNGMFSPSG 597

RESULT 6  
 ID NEIL RAT STANDARD; PRT; 810 AA.

AC 062919;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Protein kinase C-binding protein NEIL1 precursor (NEIL-like protein 1).  
 GN NEIL1.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Sprague-Dawley; TISSUE=Brain;  
 RX MEDLINE=20017976; PubMed=10548494;  
 RA Kuroda S., Oyasu M., Kawakami M., Kanayama N., Tanizawa K., Saito N.,  
 RA Abe T., Matsubashi S., Ting K.;  
 RT "Biochemical characterization and expression analysis of neural  
 RT chromospondin-1-like proteins NEIL1 and NEIL2."  
 RL Biochem. Biophys. Res. Commun. 265:79-86(1999).  
 CC -1- SUBUNIT: HOMOTRIMER. BINDS TO PKC BETA-1.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- SIMILARITY: CONTAINS 1 TSP N-TERMINAL DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 5 WFEC DOMAINS.  
 CC -1- SIMILARITY: CONTAINS 6 EGF-LIKE DOMAINS.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL; U48246; AAC72252.1; -  
 CC HSSP; P35555; IEMN.  
 CC InterPro; IPR000152; Aex\_hydroxyl.

DR InterPro; IPR000561; EGF-like.  
 DR InterPro; IPR001881; EGF\_Ca.  
 DR InterPro; IPR001791; Laminin\_G.  
 DR InterPro; IPR003129; TSPN.  
 DR InterPro; IPR001007; WFEC\_C.  
 DR Pfam; PF00068; EGF\_4.  
 DR Pfam; PF00093; WFC; 3.  
 DR Pfam; PF02210; TSPN; 1.  
 DR SMART; SM00179; EGF\_Ca; 2.  
 DR SMART; SM00001; EGF-like; 4.  
 DR SMART; SM00282; Lamg; 1.  
 DR SMART; SM00210; TSPN; 1.  
 DR SMART; SM00214; WFC; 1.  
 DR PROSITE; PS00010; ASX\_HYDROXYL; 3.  
 DR PROSITE; PS00022; EGF\_1; 1.  
 DR PROSITE; PS01186; EGF\_2; 3.  
 DR PROSITE; PS01187; EGF\_Ca; 3.  
 DR PROSITE; PS01206; WFEC; 2.  
 KW Glycoprotein; EGF-like domain; Repeat; Signal.  
 FT SIGNAL 1 16  
 FT CHAIN 17 810  
 FT DOMAIN 81 230  
 FT DOMAIN 273 331  
 FT DOMAIN 335 390  
 FT DOMAIN 391 433  
 FT DOMAIN 434 475  
 FT DOMAIN 476 515  
 FT DOMAIN 515 547  
 FT DOMAIN 549 595  
 FT DOMAIN 596 631  
 FT DOMAIN 632 687  
 FT DOMAIN 692 750  
 FT DOMAIN 752 807  
 FT DISULFID 395 407  
 FT DISULFID 401 416  
 FT DISULFID 418 432  
 FT DISULFID 438 451  
 FT DISULFID 445 460  
 FT DISULFID 462 474  
 FT DISULFID 480 493  
 FT DISULFID 487 502  
 FT DISULFID 504 515  
 FT DISULFID 519 529  
 FT DISULFID 523 535  
 FT DISULFID 537 546  
 FT DISULFID 553 566  
 FT DISULFID 560 575  
 FT DISULFID 577 594  
 FT DISULFID 600 613  
 FT DISULFID 607 622  
 FT DISULFID 624 630  
 FT CARBOHYD 40 40  
 FT CARBOHYD 53 53  
 FT CARBOHYD 83 83  
 FT CARBOHYD 224 224  
 FT CARBOHYD 224 294  
 FT CARBOHYD 372 372  
 FT CARBOHYD 372 511  
 FT CARBOHYD 562 562  
 FT CARBOHYD 609 609  
 FT CARBOHYD 708 708  
 SQ SEQUENCE 810 AA; 89212 MW; 46F09C466A9AB0B CRC64;

Query Match 12.8%; Score 181; DB 1; Length 810;  
 Best Local Similarity 37.5%; Pred. No. 1e-06;  
 Matches 36; Conservative 12; Mismatches 38; Indels 10; Gaps 3;

QY 69 CCGPCKRTSGLPACGAACOPPCRCGSCVOPGRCRCPCAGWRGDTCCSDVDECSARRGG 128  
 DB 504 CCGYGVN-----GTTCKAFCEGRCRGYGTVAIPKVCVPSGFTGSHCEKDIDECAGFVE 559  
 QY 129 CP--ORCVNTAGSYWCQCGWEGH-----SLADGTLCP 158

Db 560 CHNYSRCVNLPGWYHCECRSGFDDGTYSLSGESCI 595

## RESULT 7

NEL2\_RAT  
ID NEL2\_RAT STANDARD; PRT; 816 AA.  
AC Q62918;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Protein kinase C-binding protein NELL2 precursor (NEL-like protein 2).  
GN NELL2 OR NEL.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Sprague-Dawley; TISSUE=Brain;  
RX MEDLINE=20017976; PubMed=10548494;  
RA Kuroda S., Oyasu M., Kawakami M., Kanayama N., Tanizawa K., Saito N.,  
RA Abe T., Matsushashi S., Ting K.;  
RT "Biochemical characterization and expression analysis of neural  
RT thrombospondin-1-like proteins NELL1 and NELL2.";  
RL Biochem. Biophys. Res. Commun. 265:79-86(1999).  
RN [2]  
RP TSP N-TERMINAL DOMAIN.  
RX MEDLINE=98153258; PubMed=9480764;  
RA Beckmann G., Hanke J., Bork P., Reich J.;  
RT "Merging extracellular domains: Fold prediction for laminin G-like  
RT and amino-terminal thrombospondin-like modules based on homology to  
RT pentraxins.";  
RL J. Mol. Biol. 275:725-730(1998).  
CC -!- SUBUNIT: HOMOTRIMER. BINDS TO PKC BETA-1.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- SIMILARITY: CONTAINS 1 TSP N-TERMINAL DOMAIN.  
CC -!- SIMILARITY: CONTAINS 5 VWFC DOMAINS.  
CC -!- SIMILARITY: CONTAINS 6 EGF-LIKE DOMAINS.  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
CC EMBL; U48245; AAC72245.1; -.  
CC HSSP; P00740; 1EDM.  
DR InterPro; IPR000152; Asx\_hydroxyl.  
DR InterPro; IPR000561; EGF\_like.  
DR InterPro; IPR001881; EGF\_Ca.  
DR InterPro; IPR001791; Laminin\_G.  
DR InterPro; IPR003129; TSPN.  
DR Pfam; PF00008; EGF; 5.  
DR Pfam; PF00093; Vwc; 3.  
DR Pfam; PF02210; TSPN; 1.  
DR SMART; SM00179; EGF\_CA; 3.  
DR SMART; SM00001; EGF\_like; 3.  
DR SMART; SM00282; LamG; 1.  
DR SMART; SM00210; TSPN; 1.  
DR SMART; SM00214; VWC; 3.  
DR PROSITE; PS00010; ASX\_HYDROXYL; 3.  
DR PROSITE; PS00022; EGF\_1; 1.  
DR PROSITE; PS01186; EGF\_2; 4.  
DR PROSITE; PS01187; EGF\_CA; 3.  
DR PROSITE; PS01208; VWFC; 2.  
KW Glycoprotein; EGF-like domain; Repeat; Signal.  
FT SIGNAL 1 24 POTENTIAL.  
FT CHAIN 25 816 PROTEIN KINASE C-BINDING PROTEIN NELL2.  
FT DOMAIN 30 258 TSP N-TERMINAL.  
FT DOMAIN 272 331 VWFC 1.

FT DOMAIN 332 396  
FT DOMAIN 397 439  
FT DOMAIN 440 481  
FT DOMAIN 482 522  
FT DOMAIN 521 553  
FT DOMAIN 555 601  
FT DOMAIN 602 637  
FT DOMAIN 638 693  
FT DOMAIN 698 756  
FT DOMAIN 758 813  
FT DISULFID 401 413  
FT DISULFID 407 422  
FT DISULFID 424 438  
FT DISULFID 444 457  
FT DISULFID 451 466  
FT DISULFID 468 480  
FT DISULFID 486 499  
FT DISULFID 493 508  
FT DISULFID 510 521  
FT DISULFID 525 535  
FT DISULFID 529 541  
FT DISULFID 543 552  
FT DISULFID 559 572  
FT DISULFID 566 581  
FT DISULFID 583 600  
FT DISULFID 606 619  
FT DISULFID 613 628  
FT DISULFID 630 636  
FT CARBOHYD 53 53  
FT CARBOHYD 225 225  
FT CARBOHYD 233 233  
FT CARBOHYD 238 238  
FT CARBOHYD 517 517  
FT CARBOHYD 615 615  
FT CARBOHYD 635 635  
SQ SEQUENCE 816 AA; 90952 MW; A999F76078060D6B CRC64;  
Query Match 12.7%; Score 179.5; DB 1; Length 816;  
Best Local Similarity 35.8%; Pred. No. 1.5e-06;  
Matches 34; Conservative 15; Mismatches 37; Indels 9; Gaps 3;  
QY 69 CPGKWKRTSLGLPCACMAICQPPCRNGGSCVQPGRCRCPCAGWRGDTQCSDVDQCSARRGG 128  
Db 510 CKEGYTGN---GTTCFAFKDCKGNGACIAANVCAPQSGFTGPGSCETIDICEGSEGVQ 565  
QY 129 CPQR--CVNTAGSYWCQWEGHSLSDGTLCVPKG 161  
Db 566 CDSRANCINLPGWYHCECRDGYH---DNGMFAPGG 597  
RESULT 8  
CD93\_HUMAN  
ID CD93\_HUMAN STANDARD; PRT; 652 AA.  
AC Q9NFY3; O00274;  
DT 15-JUN-2002 (Rel. 41, Created)  
DT 15-JUN-2002 (Rel. 41, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Complement component C1q receptor precursor (Complement component 1, q  
DE subcomponent, receptor 1) (C1qr) (C1qR(p)) (C1q/MBL/SPA receptor)  
DE (CD93 antigen) (CDW93).  
GN C1QR1 OR CD93.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
RX PubMed=9047234;  
RA Nepomuceno R.R., Henschen-Edman A.H., Burgess W.H., Tenner A.J.;  
RT "cDNA cloning and primary structure analysis of C1qR(p), the human  
RT C1q/MBL/SPA receptor that mediates enhanced phagocytosis in vitro.";  
RL Immunity 6:119-129(1997).  
RN [2]

RA SEQUENCE FROM N.A., AND VARIANT ALA-318.  
 RA PubMed=11781389;  
 RA Steinberger P., Szekeres A., Wille S., Stockl J., Selenko N.,  
 RA Prager E., Staffler G., Madic O., Stockinger H., Knapp W.;  
 RT "Identification of human CD93 as the phagocytic C1q receptor (C1qR)  
 RT by expression cloning";  
 RT J. Leukoc. Biol. 71:133-140(2002).  
 RN [3]  
 RN SEQUENCE FROM N.A.  
 RX MEDLINE=21638749; PubMed=11780052;  
 RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,  
 RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,  
 RA Bailey J., Barlow K.F., Bates K.N., Beard L.W., Beare D.W.,  
 RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,  
 RA Black D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,  
 RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,  
 RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,  
 RA Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,  
 RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,  
 RA Grahame D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,  
 RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,  
 RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,  
 RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,  
 RA Leharvalho M.H., Liversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,  
 RA Marsh V.L., Martin S.L., McConachle L.J., McElay A.M., McMurtry A.A.,  
 RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,  
 RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,  
 RA Phillips B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,  
 RA Rice C.M., Rose M.T., Scott C.E., Sehra H.K., Showkneen R., Sims S.,  
 RA Shuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.B.,  
 RA Swann R.M., Symons N., Taylor R., Tee L., Thomas D.W., Thorpe A.,  
 RA Whitehead S.L., Whitlaker P., Willey D.L., Williams L., Williams S.A.,  
 RA Wilmshurst L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,  
 RA Rogers J.;  
 RT "The DNA sequence and comparative analysis of human chromosome 20";  
 RT Nature 414:865-871(2001).  
 RN [4]  
 RN SEQUENCE FROM N.A.  
 RC TISSUE=Leukocyte;  
 RA Strausberg R.;  
 RL Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.  
 RN [5]  
 RN CHARACTERIZATION.  
 RX PubMed=11994479;  
 RA McGreal E.P., Ikegaki N., Akatsu H., Morgan B.P., Gasque P.;  
 RT "Human C1qR is identical with CD93 and the mAb-11 antigen but does  
 RT not bind C1q";  
 RT J. Immunol. 168:5222-5232(2002).  
 RN [6]  
 RN O-GLYCOSYLATION.  
 RX PubMed=10092817;  
 RA Nepomuceno R.R., Ruiz S., Park M., Tenner A.J.;  
 RT "C1qR is a heavily O-glycosylated cell surface protein involved in  
 RT the regulation of phagocytic activity";  
 RT J. Immunol. 162:3583-3589(1999).  
 RN [7]  
 RN FUNCTION: Receptor (or element of a larger receptor complex) for  
 RN C1q, mannose-binding lectin (MBL2) and pulmonary surfactant  
 RN protein A (SPA). May mediate the enhancement of phagocytosis in  
 RN monocytes and macrophages upon interaction with soluble defense  
 RN collagens. May play a role in intercellular adhesion.  
 RN [8]  
 RN SUBCELLULAR LOCATION: Type I membrane protein.  
 RN [9]  
 RN TISSUE SPECIFICITY: Highly expressed in endothelial cells,  
 RN platelets, cells of myeloid origin, such as monocytes and  
 RN neutrophils. Not expressed in cells of lymphoid origin.  
 RN [10]  
 RN PTM: N- and O-glycosylated.  
 RN [11]  
 RN SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.  
 RN [12]  
 RN SIMILARITY: CONTAINS 5 EGF-LIKE DOMAINS.  
 RN [13]  
 RN CAUTION: Has been sometimes referred to as a collectin receptor.  
 RN [14]  
 RN CAUTION: According to Ref.5, C1q is not a ligand for C1QR1.  
 RN [15]  
 RN DATABASE: NAME=PROW; NOTE=PROW 3:1-6(2001);  
 RN WWW="http://www.ncbi.nlm.nih.gov/prow/guide/467246456\_g.htm".

CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation-  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.ebi.ac.uk/announce/>  
 CC or send an email to [license@ebi.ac.uk](mailto:license@ebi.ac.uk)).  
 CC -----  
 CC EMBL; U94333; AAB53110.1; -  
 CC EMBL; AL118508; CAC00597.1; -  
 CC EMBL; BC028075; AAB28075.1; -  
 CC HSSP; P35555; IEMN.  
 CC MIM; 120577; -  
 CC InterPro; IPR000152; Asx\_hydroxy1.  
 CC InterPro; IPR000561; EGF-Like.  
 CC InterPro; IPR001881; EGF Ca.  
 CC InterPro; IPR001304; Lectin C.  
 CC InterPro; IPR001187; Tissue\_factor.  
 CC Pfam; PF00008; EGF; 5.  
 CC Pfam; PF00059; Lectin\_C; 1.  
 CC Pfam; PF01108; Tissue\_fac; 1.  
 CC SMART; SM00034; CLECT; 1.  
 CC SMART; SM00179; EGF\_CA; 3.  
 CC SMART; SM00001; EGF\_Like; 2.  
 CC PROSITE; PS00010; ASX\_HYDROXYL; 3. FALSE\_NEG.  
 CC PROSITE; PS00615; C-TYPE\_LECTIN\_1; 1.  
 CC PROSITE; PS00041; C-TYPE\_LECTIN\_2; 1.  
 CC PROSITE; PS01186; EGF\_2; 3.  
 CC PROSITE; PS01187; EGF\_CA; 3.  
 CC Receptor; EGF-like domain; Signal; Transmembrane; Glycoprotein;  
 CC Repeat; Lectin; Polymorphism.  
 CC SIGNAL 1 21  
 CC CHAIN 22 652  
 CC DOMAIN 24 580  
 CC TRANSMEM 581 601  
 CC DOMAIN 602 652  
 CC DOMAIN 32 174  
 CC DOMAIN 260 301  
 CC DOMAIN 302 344  
 CC DOMAIN 345 384  
 CC DOMAIN 385 426  
 CC DOMAIN 427 468  
 CC DOMAIN 544 601  
 CC DISULFID 264 275  
 CC DISULFID 271 285  
 CC DISULFID 287 300  
 CC DISULFID 306 317  
 CC DISULFID 311 328  
 CC DISULFID 330 343  
 CC DISULFID 349 358  
 CC DISULFID 367 377  
 CC DISULFID 383 393  
 CC DISULFID 389 400  
 CC DISULFID 396 409  
 CC DISULFID 411 425  
 CC DISULFID 431 443  
 CC DISULFID 439 452  
 CC DISULFID 454 467  
 CC CARBOHYD 325 325  
 CC VARIANT 318 318  
 CC CONFLICT 22 22 /FTID=VAR\_013573.  
 CC CONFLICT 36 36 T -> V (IN AA SEQUENCE).  
 CC CONFLICT 38 39 TA -> T (IN AA SEQUENCE).  
 CC CONFLICT 155 155 TA -> RI (IN AA SEQUENCE).  
 CC CONFLICT 186 186 S -> N (IN REF. 1).  
 CC CONFLICT 186 186 G -> A (IN AA SEQUENCE).  
 CC CONFLICT 492 492 S -> A (IN AA SEQUENCE).  
 CC CONFLICT 496 496 R -> Q (IN AA SEQUENCE).  
 CC CONFLICT 504 504 R -> G (IN AA SEQUENCE).  
 CC CONFLICT 541 541 P -> S (IN REF. 1).  
 CC SEQUENCE 652 AA; 68560 MW; EECAP0EAC55FCAC2 CRC64;  
 Query Match 12.5%; Score 176; DB 1; Length 652;



ID FBN1 HUMAN STANDARD; PRT; 2871 AA.  
 AC P3555;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Fibrillin 1 precursor.  
 GN FBN1 OR FBN.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN RP SEQUENCE FROM N.A.  
 RC TISSUE=Placenta;  
 RX MEDLINE=93372860; PubMed=8364578;  
 RA Pereira L.V., D'Alessio M., Ramirez F., Lynch J.R., Sykes B.,  
 RT Pangillan T., Bonadio J.;  
 RT "Genomic organization of the sequence coding for fibrillin, the  
 RT defective gene product in Marfan syndrome.";  
 RL Hum. Mol. Genet. 2:961-968(1993).  
 RN RP SEQUENCE OF 1-932 FROM N.A.  
 RC TISSUE=Placenta, and Fibroblast;  
 RX MEDLINE=94010947; PubMed=7691719;  
 RA Corson G.M., Chabberg S.C., Dietz H.C., Charbonneau N.L., Sakai L.Y.;  
 RT "Fibrillin binds calcium and is coded by cDNAs that reveal a  
 RT multidomain structure and alternatively spliced exons at the 5'  
 RT end.";  
 RL Genomics 17:476-484(1993).  
 RN RP SEQUENCE OF 899-2871 FROM N.A.  
 RX MEDLINE=91304568; PubMed=1852207;  
 RA Maalen C.U., Corson G.M., Maddox B.K., Glanville R.W., Sakai L.Y.;  
 RT "Partial sequence of a candidate gene for the Marfan syndrome.";  
 RL Nature 352:334-337(1991).  
 RN RP SEQUENCE OF 813-1313 FROM N.A.  
 RX MEDLINE=91304567; PubMed=1852206;  
 RA Lee B., Godfrey M., Vitale E., Hori H., Mattei M.-G., Sarfarazi M.,  
 RT Tsipouras P., Ramirez F., Hollister D.W.;  
 RT "Linkage of Marfan syndrome and a phenotypically related disorder to  
 RT two different fibrillin genes.";  
 RL Nature 352:330-334(1991).  
 RN RP CHARACTERIZATION.  
 RX MEDLINE=91317849; PubMed=1860873;  
 RA Sakai L.Y., Keene D.R., Glanville R.W., Bachinger H.P.;  
 RT "Purification and partial characterization of fibrillin, a cysteine-  
 RT rich structural component of connective tissue microfibrils.";  
 RL J Biol. Chem. 266:14763-14770(1991).  
 RN RP STRUCTURE BY NMR OF 2054-2125.  
 RX MEDLINE=96031893; PubMed=9362480;  
 RA Yuan X., Downing A.K., Knott V., Handford P.A.;  
 RT "Solution structure of the transforming growth factor beta-binding  
 RT protein-like module, a domain associated with matrix fibrils.";  
 RL EMO J. 16:6659-6666(1997).  
 RN RP STRUCTURE BY NMR OF 2124-2205.  
 RX MEDLINE=96144829; PubMed=8568869;  
 RA Knott V., Downing A.K., Gardy C.M., Handford P.A.;  
 RT "Calcium binding properties of an epidermal growth factor-like domain  
 RT pair from human fibrillin-1.";  
 RL J. Mol. Biol. 255:22-27(1996).  
 RN RP STRUCTURE BY NMR OF 2124-2205.  
 RX MEDLINE=96222301; PubMed=8653794;  
 RA Downing A.K., Knott V., Werner J.M., Gardy C.M., Campbell I.D.,  
 RT Handford P.A.;  
 RT "Solution structure of a pair of calcium-binding epidermal growth  
 RT factor-like domains: implications for the Marfan syndrome and other  
 RT genetic disorders.";  
 RL Cell 85:597-605(1996).

RN RP REVIEW ON MFS VARIANTS.  
 RX MEDLINE=96174615; PubMed=8594563;  
 RA Colod G., Beroud C., Soussi T., Junien C., Boileau C.;  
 RT "FBN1 gene.";  
 RL FBN1 gene.";  
 RL Nucleic Acids Res. 24:137-141(1996).  
 RN RP REVIEW ON MFS VARIANTS.  
 RX MEDLINE=97169383; PubMed=9016526;  
 RA Colod-Beroud G., Beroud C., Ades L., Black C., Boxer M., Brock D.J.,  
 RA Godfrey M., Hayward C., Karttunen L., Milewicz D., Peltonen L.,  
 RA Richards R.I., Wang W., Junien C., Boileau C.;  
 RT "Marfan Database (second edition): software and database for the  
 RT analysis of mutations in the human FBN1 gene.";  
 RL Nucleic Acids Res. 25:1147-1150(1997).  
 RN RP REVIEW ON VARIANTS.  
 RX MEDLINE=98062175; PubMed=9401003;  
 RA Hayward C., Brock D.J.H.;  
 RT "Fibrillin-1 mutations in Marfan syndrome and other type-1  
 RT fibrillinopathies.";  
 RL Hum. Mutat. 10:415-423(1997).  
 RN RP VARIANT MFS PRO-1137.  
 RX MEDLINE=91304569; PubMed=1852208;  
 RA Dietz H.C., Cutting G.R., Pyeritz R.E., Maslen C.L., Sakai L.Y.,  
 RT Corson G.M., Puffenberger E.G., Hamosh A., Nanthakumar E.J.,  
 RT "Marfan syndrome caused by a recurrent de novo missense mutation in  
 RT the fibrillin gene.";  
 RL Nature 352:337-339(1991).  
 RN RP VARIANTS MFS SER-1249; ARG-1663; SER-2221 AND SER-2307.  
 RX MEDLINE=93250834; PubMed=1301946;  
 RA Dietz H.C., Saraiya J.M., Pyeritz R.E., Cutting G.R., Francmann C.A.;  
 RT "Clustering of fibrillin (FBN1) missense mutations in Marfan syndrome  
 RT patients at cysteine residues in EGF-like domains.";  
 RL Hum. Mutat. 1:366-374(1992).  
 RN RP VARIANT MFS SER-2307.  
 RX MEDLINE=92235290; PubMed=1569206;  
 RA Dietz H.C., Pyeritz R.E., Puffenberger E.G., Kendzior R.J., Jr.,  
 RA Corson G.M., Maslen C.L., Sakai L.Y., Francmann C.A., Cutting G.R.;  
 RT "Marfan phenotype variability in a family segregating a missense  
 RT mutation in the epidermal growth factor-like motif of the fibrillin  
 RT gene.";  
 RL J. Clin. Invest. 89:1674-1680(1992).  
 RN RP VARIANTS MFS ILB-548 AND ALA-723.  
 RX MEDLINE=94010946; PubMed=8406497;  
 RA Dietz H.C., McIntosh I., Sakai L.Y., Corson G.M., Chabberg S.C.,  
 RA Pyeritz R.B., Francmann C.A.;  
 RT "Four novel FBN1 mutations: significance for mutant transcript level  
 RT and EGF-like domain calcium binding in the pathogenesis of Marfan  
 RT syndrome.";  
 RL Genomics 17:468-475(1993).  
 RN RP VARIANTS MFS SER-2144.  
 RX MEDLINE=93278402; PubMed=8504310;  
 RA Hewett D.R., Lynch J.R., Smith R., Sykes B.C.;  
 RT "A novel fibrillin mutation in the Marfan syndrome which could  
 RT disrupt calcium binding of the epidermal growth factor-like module.";  
 RL Hum. Mol. Genet. 2:475-477(1993).  
 RN RP VARIANTS MFS R-862; Y-1117; P-1137 AND F-1589, AND VARIANT A-1148.  
 RX MEDLINE=94108431; PubMed=8281141;  
 RA Tynan K., Comeau K., Pearson M., Wilgenbus P., Levitt D., Gasner C.,  
 RA Berg M.A., Miller D.C., Francke U.;  
 RT "Mutation screening of complete fibrillin-1 coding sequence: report  
 RT of five new mutations, including two in 8-cysteine domains.";  
 RL Hum. Mol. Genet. 2:1813-1821(1993).  
 RN

VARIANTS MFS GYL-217 AND ARG-2627.  
 MEDLINE=95067970; PubMed=7977366;  
 Karttunen L., Raghunath M., Loenqvist L., Peltonen L.;  
 "A compound-heterozygous Marfan patient: two defective fibrillin  
 alleles result in a lethal phenotype";  
 Am. J. Hum. Genet. 55:1083-1091 (1994).  
 [19]  
 VARIANT EL LYS-2447.  
 MEDLINE=94245249; PubMed=8188302;  
 Lonngqvist L., Child A., Kainulainen K., Davidson R., Puhakka L.,  
 Peltonen L.;  
 "A novel mutation of the fibrillin gene causing ectopia lentis";  
 Genomics 19:573-576 (1994).  
 [20]  
 VARIANT MFS CYS-627.  
 MEDLINE=94272487; PubMed=8004112;  
 Hayward C., Rae A.L., Porteous M.E.M., Logie L.J., Brock L.J.;  
 "Two novel mutations and a neutral polymorphism in EGF-like domains  
 of the fibrillin gene (FBN1): SSCP screening of exons 15-21 in Marfan  
 syndrome patients";  
 Hum. Mol. Genet. 3:373-375 (1994).  
 [21]  
 VARIANT MFS CYS-122.  
 MEDLINE=94314977; PubMed=8040326;  
 Stahl-Hallgren C., Ukkonen T., Kainulainen K., Kristofersson U.,  
 Saxne T., Tornqvist K., Peltonen L.;  
 "An extra cysteine in one of the non-calcium-binding epidermal growth  
 factor-like motifs of the FBN1 polypeptide is connected to a novel  
 variant of Marfan syndrome";  
 J. Clin. Invest. 94:709-713 (1994).  
 [22]  
 VARIANT MFS TYR-1223.  
 MEDLINE=94351682; PubMed=8071963;  
 Hewett D.R., Lynch J.R., Child A., Sykes B.C.;  
 "A new missense mutation of fibrillin in a patient with Marfan  
 syndrome";  
 J. Med. Genet. 31:338-339 (1994).  
 [23]  
 VARIANT MFS HIS-1170.  
 MEDLINE=95174777; PubMed=7870075;  
 Hayward C., Porteous M.E.M., Brock D.J.H.;  
 "A novel mutation in the fibrillin gene (FBN1) in familial  
 arachnodactyly";  
 Mol. Cell. Probes 8:325-327 (1994).  
 [24]  
 VARIANTS MFS G-217; N-1023; R-1074; Y-1242; E-2127; W-2151;  
 K-2447 AND R-2511.  
 MEDLINE=94184368; PubMed=8136837;  
 Kainulainen K., Karttunen L., Puhakka L., Sakai L., Peltonen L.;  
 "Mutations in the fibrillin gene responsible for dominant ectopia  
 lentis and neonatal Marfan syndrome";  
 Nat. Genet. 6:64-69 (1994).  
 [25]  
 VARIANT SER-1127.

Query Match 12.4%; Score 175.5; DB 1; Length 2871;  
 Best Local Similarity 18.9%; Pred. NO. 1e-05;  
 Matches 52; Conservative 14; Mismatches 48; Indels 161; Gaps 6;

QY 56 RSPGLAPRPRVACCPGKRTSGLPQA----- 82  
 DB 54 KGNVCGSRYNAYCCFGWKT---LPGNQCIYVICRHSBGDFCSRPNMCTCPSQIAPS 110  
 QY 83 -----CGAICQPPNRNGSCVQPCRCPA 108  
 DB 111 CGSRSIQHCNIRCMNGSGSCDDHCLCQKGYIGTHCGQPVCEGCLNGRCVAPNRCACTY 170  
 QY 109 GWRGDTCC----- 116  
 DB 171 GFTPOCERDYRTGPGFTVISNMCGQLSGIVCTKQLCCATVGRAGWPCMCQAQHP 230  
 QY 117 -----SDVDCSARRGCGP-QRCVNTAGSYWCOCWEGHLSADGTLG----- 157

Db 231 CRGFIPNRTGACQDVDEQAIPLCQGGNCINTVGSFECKCPAGHKLNEVSKCEDID 290  
 QY 158 -----VPKGG-----PRVAPNPTG 172  
 DB 291 ECSTIPGICGEGECTNTVSSYFCKCPGFTVTPDG 325

RESULT 11  
 FBN2\_MOUSE  
 ID FBN2\_MOUSE STANDARD; PRT; 2907 AA.  
 AC Q61555; Q63957;  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Fibrillin 2 precursor.  
 GN FBN2 OR FBN-2.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=95263670; PubMed=7744963;  
 RA Zhang H., Hu W., Ramirez F.;  
 RT "Developmental expression of fibrillin genes suggests heterogeneity  
 of extracellular microfibrils";  
 J. Cell Biol. 129:1165-1176 (1995).  
 RN [2]  
 RP SEQUENCE OF 210-317 FROM N.A.  
 RX MEDLINE=94140368; PubMed=8307578;  
 RA Li X., Pereira L., Zhang H., Sanguinetti C., Ramirez F., Bonadio J.,  
 Francke U.;  
 RT "Fibrillin genes map to regions of conserved mouse/human synteny on  
 mouse chromosomes 2 and 18";  
 Genomics 18:667-672 (1993).  
 RL Genomics 18:667-672 (1993).  
 CC -!- FUNCTION: STRUCTURAL COMPONENT OF CONNECTIVE TISSUE MICROFIBRILS  
 THAT BINDS CALCIUM. FIBRILLIN-1-CONTAINING MICROFIBRILS PROVIDE  
 LONG-TERM FORCE BEARING STRUCTURAL SUPPORT.  
 CC -!- SIMILARITY: CONTAINS 47 EGF-LIKE DOMAINS.  
 CC -!- SIMILARITY: CONTAINS 7 TGF-BETA BINDING PROTEIN DOMAINS.  
 CC  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 the European Bioinformatics Institute. There are no restrictions on its  
 use by non-profit institutions as long as its content is in no way  
 modified and this statement is not removed. Usage by and for commercial  
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 DR EMBL; L39790; AAA74908.1; -.  
 DR EMBL; S69359; AAC60685.1; -.  
 DR HSSP; P35555; 1EMN.  
 DR MGD; MGI:95490; Fbn2.  
 DR InterPro; IPR000152; Asx hydroxyl.  
 DR InterPro; IPR000561; EGF-like.  
 DR InterPro; IPR001881; EGF Ca.  
 DR InterPro; IPR001438; EGF II.  
 DR InterPro; IPR002212; Fibril-assoc.  
 DR Pfam; PF00008; EGF; 46.  
 DR Pfam; PF00683; TB; 9.  
 DR PRINTS; PR00010; EGFBL00D.  
 DR SMART; SM00179; EGF CA; 43.  
 DR SMART; SM00001; EGF-like; 3.  
 DR PROSITE; PS00010; ASX HYDROXYL; 43.  
 DR PROSITE; PS00022; EGF\_1; 2.  
 DR PROSITE; PS01186; EGF\_2; 36.  
 DR PROSITE; PS01187; EGF CA; 43.  
 DR Extracellular matrix; Calcium-binding; Glycoprotein; EGF-like domain;  
 Repeat; Signal; Multigene family.  
 KW Repeat; Signal; Multigene family.  
 FT SIGNAL 1 28 POTENTIAL.  
 FT CHAIN 29 2907 FIBRILLIN 2.  
 FT DOMAIN 111 142 EGF-LIKE 1.  
 FT DOMAIN 145 176 EGF-LIKE 2.

FT	DOMAIN	176	208	EGF-LIKE 3.
FT	DOMAIN	276	317	EGF-LIKE 4, CALCITUM-BINDING.
FT	DOMAIN	318	359	EGF-LIKE 5, CALCITUM-BINDING.
FT	REPEAT	360	426	TGFBP 1.
FT	DOMAIN	487	527	EGF-LIKE 6.
FT	DOMAIN	528	567	EGF-LIKE 7, CALCITUM-BINDING.
FT	DOMAIN	568	609	EGF-LIKE 8, CALCITUM-BINDING.
FT	DOMAIN	610	650	EGF-LIKE 9, CALCITUM-BINDING.
FT	REPEAT	651	691	EGF-LIKE 10, CALCITUM-BINDING.
FT	REPEAT	692	760	TGFBP 2.
FT	DOMAIN	761	802	EGF-LIKE 11, CALCITUM-BINDING.
FT	DOMAIN	803	844	EGF-LIKE 12, CALCITUM-BINDING.
FT	DOMAIN	845	883	EGF-LIKE 13, CALCITUM-BINDING.
FT	DOMAIN	948	989	EGF-LIKE 14, CALCITUM-BINDING.
FT	REPEAT	990	1065	TGFBP 3.
FT	DOMAIN	1066	1107	EGF-LIKE 15, CALCITUM-BINDING.
FT	DOMAIN	1108	1150	EGF-LIKE 16, CALCITUM-BINDING.
FT	DOMAIN	1151	1192	EGF-LIKE 17, CALCITUM-BINDING.
FT	DOMAIN	1193	1234	EGF-LIKE 18, CALCITUM-BINDING.
FT	DOMAIN	1235	1275	EGF-LIKE 19, CALCITUM-BINDING.
FT	DOMAIN	1276	1317	EGF-LIKE 20, CALCITUM-BINDING.
FT	DOMAIN	1318	1359	EGF-LIKE 21, CALCITUM-BINDING.
FT	DOMAIN	1360	1400	EGF-LIKE 22, CALCITUM-BINDING.
FT	DOMAIN	1401	1441	EGF-LIKE 23, CALCITUM-BINDING.
FT	DOMAIN	1442	1483	EGF-LIKE 24, CALCITUM-BINDING.
FT	DOMAIN	1484	1524	EGF-LIKE 25, CALCITUM-BINDING.
FT	DOMAIN	1525	1565	EGF-LIKE 26, CALCITUM-BINDING.
FT	REPEAT	1566	1642	TGFBP 4.
FT	DOMAIN	1643	1684	EGF-LIKE 27, CALCITUM-BINDING.
FT	DOMAIN	1685	1726	EGF-LIKE 28, CALCITUM-BINDING.
FT	REPEAT	1727	1800	TGFBP 5.
FT	DOMAIN	1801	1842	EGF-LIKE 29, CALCITUM-BINDING.
FT	DOMAIN	1843	1884	EGF-LIKE 30, CALCITUM-BINDING.
FT	DOMAIN	1885	1926	EGF-LIKE 31, CALCITUM-BINDING.
FT	DOMAIN	1927	1965	EGF-LIKE 32, CALCITUM-BINDING.
FT	DOMAIN	1966	2008	EGF-LIKE 33, CALCITUM-BINDING.
FT	DOMAIN	2009	2048	EGF-LIKE 34, CALCITUM-BINDING.
FT	DOMAIN	2049	2090	EGF-LIKE 35, CALCITUM-BINDING.
FT	REPEAT	2091	2163	TGFBP 6.
FT	DOMAIN	2164	2205	EGF-LIKE 36, CALCITUM-BINDING.
FT	DOMAIN	2206	2245	EGF-LIKE 37, CALCITUM-BINDING.
FT	DOMAIN	2246	2286	EGF-LIKE 38, CALCITUM-BINDING.
FT	DOMAIN	2287	2330	EGF-LIKE 39, CALCITUM-BINDING.
FT	DOMAIN	2331	2372	EGF-LIKE 40, CALCITUM-BINDING.
FT	REPEAT	2373	2441	TGFBP 7.
FT	DOMAIN	2442	2483	EGF-LIKE 41, CALCITUM-BINDING.
FT	DOMAIN	2484	2524	EGF-LIKE 42, CALCITUM-BINDING.
FT	DOMAIN	2525	2563	EGF-LIKE 43, CALCITUM-BINDING.
FT	DOMAIN	2564	2606	EGF-LIKE 44, CALCITUM-BINDING.
FT	DOMAIN	2607	2646	EGF-LIKE 45, CALCITUM-BINDING.
FT	DOMAIN	2647	2687	EGF-LIKE 46, CALCITUM-BINDING.
FT	DOMAIN	2688	2727	EGF-LIKE 47, CALCITUM-BINDING.
FT	DISULFID	115	124	BY SIMILARITY.
FT	DISULFID	119	130	BY SIMILARITY.
FT	DISULFID	132	141	BY SIMILARITY.
FT	DISULFID	149	159	BY SIMILARITY.
FT	DISULFID	153	164	BY SIMILARITY.
FT	DISULFID	166	175	BY SIMILARITY.
FT	DISULFID	180	190	BY SIMILARITY.
FT	DISULFID	184	196	BY SIMILARITY.
FT	DISULFID	198	207	BY SIMILARITY.
FT	DISULFID	280	292	BY SIMILARITY.
FT	DISULFID	287	301	BY SIMILARITY.
FT	DISULFID	303	316	BY SIMILARITY.
FT	DISULFID	322	334	BY SIMILARITY.
FT	DISULFID	329	343	BY SIMILARITY.
FT	DISULFID	345	358	BY SIMILARITY.
FT	DISULFID	491	503	BY SIMILARITY.
FT	DISULFID	498	512	BY SIMILARITY.
FT	DISULFID	514	526	BY SIMILARITY.
FT	DISULFID	532	542	BY SIMILARITY.
FT	DISULFID	537	551	BY SIMILARITY.
FT	DISULFID	553	566	BY SIMILARITY.

FT	DISULFID	572	584	BY SIMILARITY.
FT	DISULFID	579	593	BY SIMILARITY.
FT	DISULFID	595	608	BY SIMILARITY.
FT	DISULFID	614	625	BY SIMILARITY.
FT	DISULFID	620	634	BY SIMILARITY.
FT	DISULFID	636	649	BY SIMILARITY.
FT	DISULFID	655	666	BY SIMILARITY.
FT	DISULFID	661	675	BY SIMILARITY.
FT	DISULFID	677	690	BY SIMILARITY.
FT	DISULFID	765	777	BY SIMILARITY.
FT	DISULFID	772	786	BY SIMILARITY.
FT	DISULFID	788	801	BY SIMILARITY.
FT	DISULFID	807	819	BY SIMILARITY.
FT	DISULFID	814	828	BY SIMILARITY.
FT	DISULFID	830	843	BY SIMILARITY.
FT	DISULFID	849	859	BY SIMILARITY.
FT	DISULFID	854	868	BY SIMILARITY.
FT	DISULFID	870	883	BY SIMILARITY.
FT	DISULFID	952	964	BY SIMILARITY.
FT	DISULFID	959	973	BY SIMILARITY.
FT	DISULFID	975	988	BY SIMILARITY.
FT	DISULFID	1070	1082	BY SIMILARITY.
FT	DISULFID	1077	1091	BY SIMILARITY.
FT	DISULFID	1093	1106	BY SIMILARITY.
FT	DISULFID	1112	1124	BY SIMILARITY.
FT	DISULFID	1119	1133	BY SIMILARITY.
FT	DISULFID	1135	1149	BY SIMILARITY.
FT	DISULFID	1155	1167	BY SIMILARITY.
FT	DISULFID	1162	1176	BY SIMILARITY.
FT	DISULFID	1178	1191	BY SIMILARITY.
FT	DISULFID	1197	1209	BY SIMILARITY.
FT	DISULFID	1204	1218	BY SIMILARITY.
FT	DISULFID	1220	1233	BY SIMILARITY.
FT	DISULFID	1239	1250	BY SIMILARITY.
FT	DISULFID	1246	1259	BY SIMILARITY.
FT	DISULFID	1261	1274	BY SIMILARITY.
FT	DISULFID	1280	1292	BY SIMILARITY.
FT	DISULFID	1287	1301	BY SIMILARITY.
FT	DISULFID	1303	1316	BY SIMILARITY.
FT	DISULFID	1322	1334	BY SIMILARITY.
FT	DISULFID	1329	1343	BY SIMILARITY.
FT	DISULFID	1345	1358	BY SIMILARITY.
FT	DISULFID	1364	1377	BY SIMILARITY.
FT	DISULFID	1371	1386	BY SIMILARITY.
FT	DISULFID	1388	1399	BY SIMILARITY.
FT	DISULFID	1405	1418	BY SIMILARITY.
FT	DISULFID	1412	1427	BY SIMILARITY.
FT	DISULFID	1429	1440	BY SIMILARITY.
FT	DISULFID	1446	1458	BY SIMILARITY.
FT	DISULFID	1453	1467	BY SIMILARITY.
FT	DISULFID	1469	1482	BY SIMILARITY.
FT	DISULFID	1488	1499	BY SIMILARITY.
FT	DISULFID	1494	1508	BY SIMILARITY.
FT	DISULFID	1510	1523	BY SIMILARITY.
FT	DISULFID	1529	1540	BY SIMILARITY.
FT	DISULFID	1535	1549	BY SIMILARITY.
FT	DISULFID	1551	1564	BY SIMILARITY.
FT	DISULFID	1647	1659	BY SIMILARITY.
FT	DISULFID	1654	1668	BY SIMILARITY.
FT	DISULFID	1670	1683	BY SIMILARITY.
FT	DISULFID	1689	1701	BY SIMILARITY.
FT	DISULFID	1696	1710	BY SIMILARITY.
FT	DISULFID	1712	1725	BY SIMILARITY.

Query Match 12.4%; Score 175; DB 1; Length 2907;  
 Best Local Similarity 22.9%; Pred. No. 1.1e-05;  
 Matches 53; Conservative 19; Mismatches 75; Indels 84; Gaps 6;

QY 3 HAY-----RGRVCAVRAGDPVSEFQRYVOPFLTCDGHCST--YRTIVRTA 53  
 DB 94 HSYCCPGMKITPGSNOCVPIPCRNCSGDFCSR---PMCTCSSGQISPTGGRKSIOQCS 150  
 QY 54 YRSPGLAPARRRYVACPGMKRTSGLPGACGAIIQPPCRNGSCVOPGRCRCPAGWRGD 113



Db 151 VRCWNGTTCADHHCQCKGYIGT-----YCGQPVCEGCGNGRCRGPNRCACVYGTGP 205  
 Qy 114 TCQ----- 116  
 Db 206 QCRDYRTGPGFTQVNNQMGQQLTGIVCTKLCATIGRANGHPCEMCPAQPCRPGRPGF 265  
 Qy 117 -----SDVDECSARRGCP-ORCVNTAGSVMOCWGHLSADGTLIC 157  
 Db 266 IPNIRTAGQDVDECAIPGLCGGNCINTVGSCECRCPAGHKQSETTQRC 316

RESULT 12  
 NTC3 HUMAN  
 ID NTC3 HUMAN STANDARD; PRT; 2321 AA.  
 AC Q9UM47; Q9Y6L8; Q9UPL3; Q9UEB3;  
 DT 15-JUN-2002 (Rel. 41, Created)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Neurogenic locus notch homolog protein 3 precursor (Notch 3).  
 GN NOTCH3.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97032728; PubMed=8878478;  
 RA Joutel A., Corpechot C., Ducros A., Vahedi K., Chabriat H., Mouton P.,  
 RA Alamowitch S., Domenga V., Cecillion M., Marechal E., Maciazek J.,  
 RA Vayssiere C., Cruaud C., Cabanis E.-A., Ruchoux M.M., Weissenbach J.,  
 RA Bach J.-F., Bousser M.-G., Tournier-Lasserre E.;  
 RA "Notch3 mutations in CADASIL, a hereditary adult-onset condition  
 RT causing stroke and dementia.";  
 RL Nature 383:707-710(1996).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Gunel M., Artavanis-Teakonas S.;  
 RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA Lamerding J.E., McCready P.M., Skowronski E., Adamson A.W.,  
 RA Burkhardt-Schultz K., Gordon L., Kyle A., Ramirez M., Stillwagen S.,  
 RA Phan H., Velasco N., Ganes J., Danganan L., Poundstone P.,  
 RA Christensen M., Georgescu A., Avila J., Liu S., Attix C., Andreise T.,  
 RA Frankheim M., Amico-Keller G., Coefield J., Duarte S., Lucas S.,  
 RA Bruce R., Thomas P., Quan G., Kronmiller B., Arellano A.,  
 RA Montgomery M., Ow D., Nolan M., Trong S., Kobayashi A., Olsen A.S.,  
 RA Carrano A.V.;  
 RT "Sequence analysis of an 1.5 Mb olfactory receptor (OLFR) cluster in  
 RT 19p13.1.";  
 RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP VARIANTS CADASIL Y-49; C-71; C-90; C-110; C-133; C-141; R-146; C-153;  
 RP C-169; C-171; C-182; R-185; S-212; G-222; Y-224; C-258; Y-542; C-558;  
 RP C-578; C-728; C-985; C-1006; C-1031; C-1231 AND R-1261, AND VARIANTS  
 RP R-170; L-496; Q-1133; M-1183 AND A-2223.  
 RX MEDLINE=98049753; PubMed=9388399;  
 RA Joutel A., Vahedi K., Corpechot C., Troesch A., Chabriat H.,  
 RA Vayssiere C., Cruaud C., Maciazek J., Weissenbach J., Bousser M.-G.,  
 RA Bach J.-F., Tournier-Lasserre E.;  
 RT "Strong clustering and stereotyped nature of Notch3 mutations in  
 RT CADASIL patients.";  
 RL Lancet 350:1511-1515(1997).  
 RN [5]  
 RP VARIANT CADASIL 114-GLY--PRO-120 DEL.  
 RX MEDLINE=20264473; PubMed=10802807;  
 RA Joutel A., Chabriat H., Vahedi K., Domenga V., Vayssiere C.,  
 RA Ruchoux M.M., Lucas C., Leys D., Bousser M.-G., Tournier-Lasserre E.;  
 RT "Splice site mutation causing a seven amino acid Notch3 in-frame  
 RT deletion in CADASIL.";  
 RL Neurology 54:1874-1875(2000).  
 RN [6]

RP IDENTIFICATION OF LIGANDS.  
 RX MEDLINE=99180763; PubMed=10079256;  
 RA Gray G.E., Mann R.S., Mitsiadis E., Henrique D., Carcangiu M.-L.,  
 RA Banks A., Leiman J., Ward D., Ish-Horowitz D., Artavanis-Teakonas S.,  
 RT "Human ligands of the Notch receptor.";  
 RL Am. J. Pathol. 154:785-794(1999).  
 CC -!- FUNCTION: Functions as a receptor for membrane-bound ligands  
 CC Jagged1, Jagged2 and Delta to regulate cell-fate determination.  
 CC Upon ligand activation through the released notch intracellular  
 CC domain (NICD) it forms a transcriptional activator complex with  
 CC RBP-J kappa and activates genes of the enhancer of split locus.  
 CC Affects the implementation of differentiation, proliferation and  
 CC apoptotic programs (By similarity).  
 CC -!- SUBUNIT: Heterodimer of a C-terminal fragment N(TM) and a N-  
 CC terminal fragment N(EC) which are probably linked by disulfide  
 CC bonds (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Following  
 CC proteolytical processing NICD is translocated to the nucleus.  
 CC -!- TISSUE SPECIFICITY: Ubiquitously expressed in fetal and adult  
 CC tissues.  
 CC -!- PM: Synthesized in the endoplasmic reticulum as an inactive form  
 CC which is proteolytically cleaved by a furin-like convertase in the  
 CC trans-Golgi network before it reaches the plasma membrane to yield  
 CC an active, ligand-accessible form. Cleavage results in a C-  
 CC terminal fragment N(TM) and a N-terminal fragment N(EC). Following  
 CC ligand binding, it is cleaved by TNF-alpha converting enzyme  
 CC (TACE) to yield a membrane-associated intermediate fragment called  
 CC notch extracellular truncation (NEXT). This fragment is then  
 CC cleaved by presenilin dependent gamma-secretase to release a  
 CC notch-derived peptide containing the intracellular domain (NICD)  
 CC from the membrane (By similarity).  
 CC -!- PM: Phosphorylated (By similarity).  
 CC -!- DISEASE: Defects in NOTCH3 are associated with CADASIL (Cerebral  
 CC autosomal dominant arteriopathy with subcortical infarcts and  
 CC leukoencephalopathy) which causes a type of stroke and dementia of  
 CC which key features include recurrent subcortical ischemic events  
 CC and vascular dementia.  
 CC -!- SIMILARITY: BELONGS TO THE NOTCH FAMILY.  
 CC -!- SIMILARITY: CONTAINS 34 EGF-LIKE DOMAINS.  
 CC -!- SIMILARITY: CONTAINS 3 LIN/NOTCH REPEATS.  
 CC -!- SIMILARITY: CONTAINS 5 ANK REPEATS.  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

EMBL; U97669; AAB91371.1; -  
 EMBL; AF058900; AAC14346.1; -  
 EMBL; AF058881; AAC14346.1; JOINED.  
 EMBL; AF058882; AAC14346.1; JOINED.  
 EMBL; AF058883; AAC14346.1; JOINED.  
 EMBL; AF058884; AAC14346.1; JOINED.  
 EMBL; AF058885; AAC14346.1; JOINED.  
 EMBL; AF058886; AAC14346.1; JOINED.  
 EMBL; AF058887; AAC14346.1; JOINED.  
 EMBL; AF058888; AAC14346.1; JOINED.  
 EMBL; AF058889; AAC14346.1; JOINED.  
 EMBL; AF058890; AAC14346.1; JOINED.  
 EMBL; AF058891; AAC14346.1; JOINED.  
 EMBL; AF058892; AAC14346.1; JOINED.  
 EMBL; AF058893; AAC14346.1; JOINED.  
 EMBL; AF058894; AAC14346.1; JOINED.  
 EMBL; AF058895; AAC14346.1; JOINED.  
 EMBL; AF058896; AAC14346.1; JOINED.  
 EMBL; AF058897; AAC14346.1; JOINED.  
 EMBL; AF058898; AAC14346.1; JOINED.  
 EMBL; AF058899; AAC14346.1; JOINED.  
 EMBL; AC004257; AAC04897.1; -  
 EMBL; AC004663; AAC15789.1; ALT\_INIT.



DR HSP; P00740; 1EDM.  
 DR Genew; HGNC:7883; NOTCH3.  
 DR MIM; 600276; .  
 DR MIM; 125310; .  
 DR InterPro; IPR002110; ANK.  
 DR InterPro; IPR000152; Asx\_hydroxyl.  
 DR InterPro; IPR000561; EGF-like.  
 DR InterPro; IPR000742; EGF 2.  
 DR InterPro; IPR001881; EGF-Ca.  
 DR InterPro; IPR001438; EGF-11.  
 DR InterPro; IPR002049; Laminin\_EGF.  
 DR InterPro; IPR000800; Notch.  
 DR Pfam; PF00008; EGF; 34.  
 DR Pfam; PF00023; ank; 6.  
 DR Pfam; PF00066; notch; 3.  
 DR PRINTS; PR00010; EGFBLD.  
 DR PRINTS; PR00011; EGFAMININ.  
 DR PRINTS; PR01452; NOTCH.  
 DR SMART; SM00248; ANK; 5.  
 DR SMART; SM00179; EGF\_CA; 19.  
 DR SMART; SM00004; EGF\_like; 14.  
 DR SMART; SM00004; NL; 3.  
 DR PROSITE; PS50088; ANK\_REPEAT; 4.  
 DR PROSITE; PS50297; ANK\_REPEAT\_REGION; 1.  
 DR PROSITE; PS00010; ASX\_HYDROXYL; 18.  
 DR PROSITE; PS00022; EGF\_1; 33.  
 DR PROSITE; PS01186; EGF\_2; 25.  
 DR PROSITE; PS01187; EGF\_CA; 18.  
 DR Receptor; Transcription regulation; Activator; Differentiation;  
 DR Receptor; Transcription regulation; Repeat; EGF-like domain;  
 DR Transmembrane; Glycoprotein; Signal; Phosphorylation; Polymorphism;  
 DR Disease mutation.  
 FT SIGNAL 1 39  
 FT CHAIN 40 2321  
 FT CHAIN 1629 2321  
 FT CHAIN 1662 2321  
 FT DOMAIN 40 1643  
 FT TRANSMEM 1644 1664  
 FT DOMAIN 1665 2321  
 FT DOMAIN 40 77  
 FT DOMAIN 78 118  
 FT DOMAIN 119 156  
 FT DOMAIN 158 195  
 FT DOMAIN 197 234  
 FT DOMAIN 236 272  
 FT DOMAIN 274 312  
 FT DOMAIN 314 350  
 FT DOMAIN 351 389  
 FT DOMAIN 391 429  
 FT DOMAIN 431 467  
 FT DOMAIN 469 505  
 FT DOMAIN 507 543  
 FT DOMAIN 545 580  
 FT DOMAIN 582 618  
 FT DOMAIN 620 655  
 FT DOMAIN 657 693  
 FT DOMAIN 695 730  
 FT DOMAIN 734 770  
 FT DOMAIN 771 808  
 FT DOMAIN 810 847  
 FT DOMAIN 849 885  
 FT DOMAIN 887 922  
 FT DOMAIN 924 960  
 FT DOMAIN 962 998  
 FT DOMAIN 1000 1034  
 FT DOMAIN 1047 1082

Query Match 12.4%; Score 174.5; DB 1; Length 2321;  
 Best Local Similarity 34.5%; Pred. No. 9.8e-06;  
 Matches 50; Conservative 14; Mismatches 44; Indels 37; Gaps 11;

QY 37 CDGRACSTYRTVITRYAARRSPGIAPARPRVAC-CPEWKR--TSGLPACGAACOPPCR 93  
 DB CAGRGVCCS-----SVVAGTAFFSCRCPRGFRPCSLPDP-----LSSPCA 129  
 QY 94 NGSGC-VQP-CR--CRCPAGRGDTCCSDYDEC-----SARRGGCPQRCVNTAGSYWCQCW 145  
 DB 130 HGARGCVGPDGRFLCSCPPGYGRSCSDVDECRVGEPCRHGG--TCLNTPGSFRQCP 166  
 QY 146 EGHSLADGTLCPKGGPPRYVNP 170  
 DB 187 AGYT-----GLPCENPVP--CAPSP 205

RESULT 13  
 NIDO\_HUMAN STANDARD; PRT; 1247 AA.  
 AC P14543; Q14942;  
 DT 01-JAN-1990 (Rel. 13, Created)  
 DT 01-JAN-1990 (Rel. 13, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Nidogen precursor (Entactin).  
 GN NID.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 OX [1]  
 RP MEDLINE=90091745; PubMed=2574658;  
 RA Nagayoshi T., Saborin D., Hickok N.J., Olsen D.R., Fazio M.J.,  
 Chu M.-L., Knowlton R., Mann K., Deutzmann R., Timpl R., Uitto J.;  
 RT "Human nidogen: complete amino acid sequence and structural domains  
 deduced from cDNAs, and evidence for polymorphism of the gene.";  
 RL DNA 8:581-594(1989).  
 [2]  
 RP MEDLINE=96044428; PubMed=7557988;  
 RA Zimmermann K., Hoischen S., Hattner M., Nischt R.;  
 RT "Genomic sequences and structural organization of the human nidogen  
 gene (NID).";  
 RL Genomics 27:245-250(1995).  
 [3]  
 RP SEQUENCE OF 667-1247 FROM N.A.  
 RC TISSUE=Placenta;  
 RA MEDLINE=89270475; PubMed=2471408;  
 RA Olsen D.R., Nagayoshi T., Fazio M., Mattei M.-G., Passage E., Weil D.,  
 Timpl R., Chu M.-L., Uitto J.;  
 RT "Human nidogen: cDNA cloning, cellular expression, and mapping of the  
 gene to chromosome 1q43.";  
 RL Am. J. Hum. Genet. 44:876-885(1989).  
 CC -!- FUNCTION: SULFATED GLYCOPROTEIN WHICH IS WIDELY DISTRIBUTED IN  
 BASEMENT MEMBRANES AND THAT IS TIGHTLY ASSOCIATED WITH LAMININ.  
 CC ALSO BINDS TO COLLAGEN IV. IT PROBABLY HAS A ROLE IN CELL-  
 EXTRACELLULAR MATRIX INTERACTIONS.  
 CC -!- SUBCELLULAR LOCATION: BASEMENT MEMBRANES.  
 CC -!- PTM: N- AND O-GLYCOSYLATED.  
 CC -!- SIMILARITY: CONTAINS 6 EGF-LIKE DOMAINS.  
 CC -!- SIMILARITY: CONTAINS 1 THYROGLOBULIN TYPE-1 DOMAIN.  
 CC -!- SIMILARITY: CONTAINS 5 LDL-RECEPTOR YWTD DOMAINS.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 the European Bioinformatics Institute. There are no restrictions on its  
 use by non-profit institutions as long as its content is in no way  
 modified and this statement is not removed. Usage by and for commercial  
 entities requires a license agreement (see <http://www.isb.ch/announce/>  
 or send an email to [license@isb.ch](mailto:license@isb.ch)).  
 CC -----  
 CC EMBL; M30269; AAAS9932.1; .  
 DR EMBL; X82245; CAA57709.1; .  
 DR EMBL; X84819; CAA57709.1; JOINED.  
 DR EMBL; X84820; CAA57709.1; JOINED.  
 DR EMBL; X84821; CAA57709.1; JOINED.

DR	EMBL; X84822;	CAA57709.1;	JOINED.	
DR	EMBL; X84823;	CAA57709.1;	JOINED.	
DR	EMBL; X84824;	CAA57709.1;	JOINED.	
DR	EMBL; X84825;	CAA57709.1;	JOINED.	
DR	EMBL; X84826;	CAA57709.1;	JOINED.	
DR	EMBL; X84827;	CAA57709.1;	JOINED.	
DR	EMBL; X84828;	CAA57709.1;	JOINED.	
DR	EMBL; X84829;	CAA57709.1;	JOINED.	
DR	EMBL; X84830;	CAA57709.1;	JOINED.	
DR	EMBL; X84831;	CAA57709.1;	JOINED.	
DR	EMBL; X84832;	CAA57709.1;	JOINED.	
DR	EMBL; X84833;	CAA57709.1;	JOINED.	
DR	EMBL; X84834;	CAA57709.1;	JOINED.	
DR	EMBL; X84835;	CAA57709.1;	JOINED.	
DR	EMBL; X84836;	CAA57709.1;	JOINED.	
DR	EMBL; X84837;	CAA57709.1;	JOINED.	
DR	EMBL; M27445;	AAA57261.1;	-	
DR	PIR; A33322;	MMHUND.		
DR	HSSP; P35555;	LEMN.		
DR	Genew; HGNC:7821;	NID.		
DR	MIM; 131390;	-		
DR	InterPro; IPR000152;	Asx hydroxyl.		
DR	InterPro; IPR000561;	EGF-like.		
DR	InterPro; IPR001881;	EGF-CA.		
DR	InterPro; IPR000033;	Ldl_receptor_rep.		
DR	InterPro; IPR003886;	Nidogen_ext_1.		
DR	InterPro; IPR000716;	Thyroglobulin_1.		
DR	Fram; PF00008;	EGF; 6.		
DR	Fram; PF00058;	ldl_recept_b; 3.		
DR	Fram; PF00086;	thyroglobulin_1; 1.		
DR	SMART; SM00179;	EGF CA; 2.		
DR	SMART; SM00001;	EGF_like; 4.		
DR	SMART; SM00135;	LY_5.		
DR	SMART; SM00539;	NIDO; 1.		
DR	SMART; SMG0211;	TY; 1.		
DR	PROSITE; PS00010;	ASX_HYDROXYL; 3.		
DR	PROSITE; PS00484;	THYROGLOBULIN_1; 1.		
DR	PROSITE; PS00022;	EGF 1; 1.		
DR	PROSITE; PS01186;	EGF-2; 5.		
DR	PROSITE; PS01187;	EGF-CA; 2.		
KW	Basement membrane; Extracellular matrix; Glycoprotein; Sulfation;			
KW	Signal; Calcium-binding; Repeat; EGF-like domain; Cell adhesion.			
FT	SIGNAL	1	28	
FT	CHAIN	29	1247	NIDOGN.
FT	DOMAIN	29	669	I (LARGER GLOBULAR DOMAIN).
FT	DOMAIN	670	917	II (CYSTEINE-RICH).
FT	DOMAIN	918	1247	III (SMALLER GLOBULAR DOMAIN).
FT	DOMAIN	386	426	EGF-LIKE 1.
FT	DOMAIN	668	709	EGF-LIKE 2.
FT	DOMAIN	710	751	EGF-LIKE 3.
FT	DOMAIN	758	801	EGF-LIKE 4.
FT	DOMAIN	802	840	EGF-LIKE 5.
FT	DOMAIN	872	919	THYROGLOBULIN TYPE 1.
FT	DOMAIN	989	1030	LDL-RECEPTOR YWTD MOTIF 1.
FT	DOMAIN	1032	1073	LDL-RECEPTOR YWTD MOTIF 2.
FT	DOMAIN	1075	1118	LDL-RECEPTOR YWTD MOTIF 3.
FT	DOMAIN	1124	1163	LDL-RECEPTOR YWTD MOTIF 4.
FT	DOMAIN	1208	1244	EGF-LIKE 6.
FT	MOD_RES	289	289	SULFATION (POTENTIAL).
FT	MOD_RES	296	296	SULFATION (POTENTIAL).
FT	DISULFID	672	685	BY SIMILARITY.
FT	DISULFID	679	695	BY SIMILARITY.
FT	DISULFID	697	708	BY SIMILARITY.
FT	DISULFID	714	727	BY SIMILARITY.
FT	DISULFID	721	736	BY SIMILARITY.
FT	DISULFID	738	750	BY SIMILARITY.
FT	DISULFID	762	777	BY SIMILARITY.
FT	DISULFID	769	787	BY SIMILARITY.
FT	DISULFID	789	800	BY SIMILARITY.
FT	DISULFID	806	817	BY SIMILARITY.
FT	DISULFID	811	826	BY SIMILARITY.
FT	DISULFID	828	839	BY SIMILARITY.
FT	DISULFID	1212	1223	BY SIMILARITY.

FT	DISULFID	1219	1232	BY SIMILARITY.
FT	DISULFID	1234	1243	BY SIMILARITY.
FT	SITE	702	704	CELL ATTACHMENT SITE.
FT	CARBOHYD	1137	1137	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CONFLICT	33	34	EL -> SS (IN REF. 2).
FT	CONFLICT	37	42	FGPGQG -> SAPDR (IN REF. 2).
FT	CONFLICT	1115	1115	H -> T (IN REF. 3).
SQ	SEQUENCE	1247 AA;	136488 MW;	4681B5B3CEC1575B CRC64;

Query Match	12.3%;	Score 173.5;	DB 1;	Length 1247;
Best Local Similarity	25.8%;	Pred. No. 6.4e-06;		
Matches	80;	Conservative	23;	Mismatches 98; Indels 109; Gaps

Qy	1	TEHAYRRGRRV-----CAVRAHG-----DPVSSSFQVRVYQVPLTTCDGHRACSTYR	47
Db	681	TNAACREGPRQTQTCSCIGFRGDRTCYDIECSE-----QP--SVCGSHITCNNH-	730
Qy	48	TIYNTAVRRSPGLAPARPRVYACCPGKRTSGLPGACGAALCOPP-----CRNG-----	95
Db	731	-----PGTFRCCEVEGQFSD--EGTCVAVVDQRPINVCETGLHNCIDIPOR	774
Qy	96	GSCVQPG-----RCRCPAGWRGD--TCQSDVDECSARRGCGPCRCVNTAGSYWCQWEGHS	149
Db	775	AQIYTGSSSYTCCLPGFGSDGQAQ--DVDEQCPSRCHPDACFYNTPGSFCTQCKPGY-	832
Qy	150	LSADGTLCPV-----KGGPRVAPNPTG-----	172
Db	833	-QGDGFRCVPEGEVEKTRCOHERHILGAAGATDQRPPIPGFLVPECDAGHYAPTQCHG	891
Qy	173	-----VDSAMKEEYQRLQSRVDLLEEKQLVLAPLH--SLASQALEHGLPDPGSLLVHS	224
Db	892	STGYCWCVDNRGR-EVEGTRTRPGMTTPCCLSTVAPPIHQGPVAVTAVPLP-PGTHLL--	947
Qy	225	FQQLGRIDSL	234
Db	948	FAOTGKIERL	957

RESULT 14			
NTCL MOUSE			
ID	NTCL_MOUSE	STANDARD;	PRT; 2531 AA.
AC	Q01705; Q9QW58; Q99UC2; Q06007; Q61905; Q9R0X7;		
DT	01-NOV-1995 (Rel. 32, Created)		
DT	01-FEB-1996 (Rel. 33, Last sequence update)		
DT	15-JUN-2002 (Rel. 41, Last annotation update)		
DE	Neurogenic locus notch homolog protein 1 precursor (Notch 1) (Motch A		
DE	(nt14) (p300)		
GN	NOTCH1 OR NOTCH.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
NCBI_TaxID	10090;		
[1]	SEQUENCE FROM N.A. (ISOFORM 1).		
RP	TISSUE=Embryo;		
RC	MEDLINE=93194170; PubMed=8449489;		
RX	Francello del Amo F., Gendron-Maguire M., Swiatek P.J., Jenkins N.A.,		
RA	Copeland N.G., Gridley T.;		
RA	"Cloning, analysis, and chromosomal localization of Notch-1, a mouse		
RT	homolog of Drosophila Notch.";		
RT	Genomics 15:259-264(1993).		
RN	[2]		
RC	SEQUENCE OF 731-1899 FROM N.A. (ISOFORM 2), AND DEVELOPMENTAL STAGE.		
RP	STRAIN=CD-1; TISSUE=Embryo;		
RC	MEDLINE=93050801; PubMed=1426644;		
RX	Reaume A.G., Conlon R.A., Zirngibl R., Yamauchi T.P., Roseant J.;		
RT	"Expression analysis of a Notch homologue in the mouse embryo.";		
RT	Dev. Biol. 154:377-387(1992).		
RN	[3]		
RC	SEQUENCE OF 1551-1647 FROM N.A. (ISOFORM 1), AND DEVELOPMENTAL STAGE.		
RP	TISSUE=Embryo;		
RX	MEDLINE=93048835; PubMed=1425352;		
RX	Francello del Amo F., Smith D.E., Swiatek P.J., Gendron-Maguire M.		

RA Greenspan R.U., McMahon A.P., Gridley T.;  
RT "Expression pattern of Notch, a mouse homolog of Drosophila Notch,  
RT suggests an important role in early postimplantation mouse  
RT development.";  
RL Development 115:737-744(1992).  
[4]  
RN SEQUENCE OF 1161-1547 FROM N.A.  
RC STRAIN=C57BL/6 X CBA; TISSUE=Embryo;  
RX MEDLINE=93178563; PubMed=8440332;  
RA Lardelli M., Lendahl U.;  
RT "Notch A and Notch B-two mouse Notch homologues coexpressed in a  
RT wide variety of tissues.";  
RL Exp. Cell Res. 204:364-372(1993).  
[5]  
RN SEQUENCE OF 1659-1673 FROM N.A.  
RX MEDLINE=9364499; PubMed=10437787;  
RA Lee J.S., Ishimoto A., Yanagawa S.I.;  
RT "Murine leukemia provirus-mediated activation of the Notch1 gene leads  
RT to induction of HES-1 in a mouse T lymphoma cell line, DU-3.";  
RL FEBS Lett. 455:276-280(1999).  
[6]  
RN SEQUENCE OF 1950-2201 FROM N.A.  
RX MEDLINE=98029496; PubMed=9384671;  
RA Messierle M., Folio M., Nehls M., Eggert H., Boehm T.;  
RT "Dynamic changes in gene expression during in vitro differentiation of  
RT mouse embryonic stem cells.";  
RL Cytokines Cell. Mol. Ther. 1:139-143(1995).  
[7]  
RN SEQUENCE OF 1655-1659, CLEAVAGE BY FURIN-LIKE CONVERTASE, AND  
RN NOTAGENESIS OF 1651-ARG-GLN-ARG-ARG-1654.  
RX MEDLINE=98318619; PubMed=9653148;  
RA Logeat F., Bessia C., Brou C., Leball O., Jarrault S., Seidah N.G.,  
RA Israel A.;  
RT "The Notch1 receptor is cleaved constitutively by a furin-like  
RT convertase.";  
RL Proc. Natl. Acad. Sci. U.S.A. 95:8108-8112(1998).  
[8]  
RN PARTIAL SEQUENCE, AND POST-TRANSLATIONAL PROCESSING.  
RX MEDLINE=91523956; PubMed=11518718;  
RA Saxena M.T., Schroeter E.H., Mumm J.S., Kopan R.;  
RT "Murine notch homologs (NL-4) undergo presenilin-dependent  
RT proteolysis.";  
RL J. Biol. Chem. 276:40268-40273(2001).  
[9]  
RN POST-TRANSLATIONAL PROCESSING.  
RX MEDLINE=21374376; PubMed=11459941;  
RA Mizutani T., Taniguchi Y., Aoki T., Hashimoto N., Honjo T.;  
RT "Conservation of the biochemical mechanisms of signal transduction  
RT among mammalian Notch family members.";  
RL Proc. Natl. Acad. Sci. U.S.A. 98:9026-9031(2001).  
[10]  
RN FUNCTION: Functions as a receptor for membrane-bound ligands  
RN Jagged1, Jagged2 and Delta1 to regulate cell-fate determination.  
RN Upon ligand activation through the released notch intracellular  
RN domain (NICD) it forms a transcriptional activator complex with  
RN RBP-J kappa and activates genes of the enhancer of split locus.  
RN Affects the implementation of differentiation, proliferation and  
RN apoptotic programs (by similarity). May play an essential role in  
RN postimplantation development, probably in some aspect of cell  
RN specification and/or differentiation. May be involved in mesoderm  
RN development, somitogenesis and neurogenesis. Involved in the  
RN maturation of both CD4+ and CD8+ cells in the thymus.  
RN [11]  
RN SUBUNIT: Heterodimer of a C-terminal fragment N(TM) and a N-  
RN terminal fragment N(EC) which are probably linked by disulfide  
RN bonds.  
RN [12]  
RN SURCELLULAR LOCATION: Type I membrane protein. Following  
RN proteolytic processing, NICD is translocated to the nucleus.  
RN [13]  
RN ALTERNATIVE PRODUCTS: 2 isoforms, 1 (shown here) and 2; may be  
RN produced by alternative splicing.  
RN [14]  
RN TISSUE SPECIFICITY: Highly expressed in the brain, lung and  
RN thymus. Expressed at lower levels in the spleen, bone-marrow,  
RN spinal cord, eyes, mammary gland, liver, intestine, skeletal  
RN muscle, kidney and heart.  
RN [15]  
RN DEVELOPMENTAL STAGE: First detected in the mesoderm at 7.5 d.p.c.

CC By 8.5 d.p.c. highly expressed in presomitic mesoderm, mesenchyme  
CC and endodermal cells, while much lower levels are seen in the  
CC neuroepithelium. Between 9.5-10.5 d.p.c. expressed at high levels  
CC in the neuroepithelium. At 13.5 d.p.c. expressed in the surface  
CC ectoderm, eye and developing whisker follicles.  
CC [16]  
CC P-TM: Synthesized in the endoplasmic reticulum as an inactive form  
CC which is proteolytically cleaved by a furin-like convertase in the  
CC trans-Golgi network before it reaches the plasma membrane to yield  
CC an active, ligand-accessible form. Cleavage results in a C-  
CC terminal fragment N(TM) and a N-terminal fragment N(EC). Following  
CC ligand binding, it is cleaved by TNF-alpha converting enzyme  
CC (TACE) to yield a membrane-associated intermediate fragment called  
CC notch extracellular truncation (NEXT). This fragment is then  
CC cleaved by presenilin dependent gamma-secretase to release a  
CC notch-derived peptide containing the intracellular domain (NICD)  
CC from the membrane.  
CC [17]  
CC P-TM: Phosphorylated.  
CC [18]  
CC -1- SIMILARITY: BELONGS TO THE NOTCH FAMILY.  
CC -1- SIMILARITY: CONTAINS 36 EGF-LIKE DOMAINS.  
CC -1- SIMILARITY: CONTAINS 3 LIN/NOTCH REPEATS.  
CC -1- SIMILARITY: CONTAINS 5 ANK REPEATS.  
CC [19]  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation  
CC in the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
CC EMBL: Z1186; CAAT7941.1; -  
CC EMBL: L02613; AAK14898.1; -  
CC EMBL: X68278; CAA48339.1; -  
CC EMBL: AJ238029; CAB40733.1; -  
CC EMBL: X82562; CAA57909.1; -  
CC HSSP: P00740; IEDM.  
CC MGD: MGI:97363; Notch1.  
CC InterPro: IPR002110; ANK.  
CC InterPro: IPR000152; Asx hydroxy1.  
CC InterPro: IPR000561; EGF-like.  
CC InterPro: IPR000742; EGF 2.  
CC InterPro: IPR001881; EGF\_Ca.  
CC InterPro: IPR001438; EGF\_IT.  
CC InterPro: IPR000800; Notch.  
CC Pfam: PF00008; EGF; 35.  
CC Pfam: PF00023; ank; 7.  
CC Pfam: PF00065; notch; 3.  
CC PRINTS: PR00010; EGRBLOOD.  
CC PRINTS: PR01452; NOTCH.  
CC SMART: SM00248; ANK; 3.  
CC SMART: SM00179; EGF\_CA; 23.  
CC SMART: SM00001; EGF\_Like; 11.  
CC SMART: SM00004; NL; 2.  
CC PROSITE: PS50086; ANK\_REPEAT; 2.  
CC PROSITE: PS50297; ANK\_REPEAT\_REGION; 1.  
CC PROSITE: PS00010; ASX\_HYDROXYL; 22.  
CC PROSITE: PS00022; EGF\_1; 34.  
CC PROSITE: PS01186; EGF\_2; 27.  
CC PROSITE: PS01187; EGF\_CA; 21.  
CC Receptor; Transcription regulation; Activator; Differentiation;  
CC Developmental protein; Repeat; ANK repeat; EGF-like domain;  
CC Transmembrane; Glycoprotein; Signal; Phosphorylation;  
CC [20]  
CC ALTERNATIVE SPLICING.  
CC [21]  
CC SIGNAL: 1  
CC CHAIN: 19 2531  
CC CHAIN: 1711 2531  
CC CHAIN: 1744 2531  
CC DOMAIN: 19 1725  
CC DOMAIN: 1726 1746  
CC TRANSMEM: 1747 2531  
CC DOMAIN: 1747 2531  
CC DOMAIN: 20 58  
CC DOMAIN: 59 99  
CC DOMAIN: 102 139  
CC [22]  
CC POTENTIAL.  
CC NEUROGENIC LOCUS NOTCH HOMOLOG PROTEIN 1.  
CC NOTCH EXTRACELLULAR TRUNCATION.  
CC NOTCH INTRACELLULAR DOMAIN.  
CC EXTRACELLULAR (POTENTIAL).  
CC POTENTIAL.  
CC CYTOPLASMIC (POTENTIAL).  
CC EGF-LIKE 1.  
CC EGF-LIKE 2.  
CC EGF-LIKE 3.

FT DOMAIN 140 176 EGF-LIKE 4. CALCIUM-BINDING (POTENTIAL).

FT DOMAIN 178 216 EGF-LIKE 5. CALCIUM-BINDING (POTENTIAL).

FT DOMAIN 218 255 EGF-LIKE 6. CALCIUM-BINDING (POTENTIAL).

FT DOMAIN 257 293 EGF-LIKE 7. CALCIUM-BINDING (POTENTIAL).

FT DOMAIN 295 333 EGF-LIKE 8. CALCIUM-BINDING (POTENTIAL).

FT DOMAIN 335 371 EGF-LIKE 9. CALCIUM-BINDING (POTENTIAL).

FT DOMAIN 372 410 EGF-LIKE 10. CALCIUM-BINDING (POTENTIAL).

FT DOMAIN 412 450 EGF-LIKE 11. CALCIUM-BINDING (POTENTIAL).

FT DOMAIN 452 488 EGF-LIKE 12. CALCIUM-BINDING (POTENTIAL).

FT DOMAIN 490 526 EGF-LIKE 13. CALCIUM-BINDING (POTENTIAL).

FT DOMAIN 528 564 EGF-LIKE 14. CALCIUM-BINDING (POTENTIAL).

FT DOMAIN 566 601 EGF-LIKE 15. CALCIUM-BINDING (POTENTIAL).

FT DOMAIN 603 639 EGF-LIKE 16. CALCIUM-BINDING (POTENTIAL).

FT DOMAIN 641 676 EGF-LIKE 17. CALCIUM-BINDING (POTENTIAL).

FT DOMAIN 678 714 EGF-LIKE 18. CALCIUM-BINDING (POTENTIAL).

FT DOMAIN 716 751 EGF-LIKE 19. CALCIUM-BINDING (POTENTIAL).

FT DOMAIN 753 789 EGF-LIKE 20. CALCIUM-BINDING (POTENTIAL).

FT DOMAIN 791 827 EGF-LIKE 21. CALCIUM-BINDING (POTENTIAL).

FT DOMAIN 829 867 EGF-LIKE 22. CALCIUM-BINDING (POTENTIAL).

FT DOMAIN 869 905 EGF-LIKE 23. CALCIUM-BINDING (POTENTIAL).

FT DOMAIN 907 943 EGF-LIKE 24. CALCIUM-BINDING (POTENTIAL).

Query Match 12.2%; Score 172; DB 1; Length 2531;  
 Best Local Similarity 34.5%; Pred. No. 1.7e-05;  
 Matches 41; Conservative 5; Mismatches 37; Indels 36; Gaps 5;

QY 69 CPGWRTSLPACGAATCP-----PCRNQSGCV---QFGRCRCPAGWRGDTQSD 118  
 |||||  
 DB 129 CSPGWSGKS-----CQADPCASNPFCANGGQCLPFESSYICRCPGPHGPTCRQD 178  
 |||||  
 QY 119 VDSCARRGSCQP--RCVNTAGSYWCQWEGH-----SLSADGTLCPVKG 161  
 |||||  
 DB 179 VNECSQNPGLCRHGHCHNEISYRCACCATHTGHCELPYVPCSPQNGATCRPTG 237  
 |||||

RESULT 15  
 FBNI\_MOUSE  
 ID FBNI\_MOUSE STANDARD; PRT; 2871 AA.  
 AC Q61554; Q60826; FBNI\_MOUSE  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Fibrillin 1 precursor.  
 GN FBNI OR FBNI-1.  
 OS Mus musculus (Mouse)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=95130561; PubMed=7829516;  
 RA Yin W., Gemmiller J., Sanguinetti C., Smiley E., Pangillan T.,  
 RA Pereira L., Ramirez F., Bonadio J.;  
 RT "Primary structure and developmental expression of Fbn-1, the mouse  
 RT fibrillin gene."  
 RL J. Biol. Chem. 270:1798-1806 (1995).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CD-1; TISSUE=Kidney;  
 RA Ota K., Kumar A., Wada J., Liu Z., Kanwar Y.S.;  
 RA Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: STRUCTURAL COMPONENT OF CONNECTIVE TISSUE MICROFIBRILS  
 CC THAT BINDS CALCIUM. FIBRILLIN-1-CONTAINING MICROFIBRILS PROVIDE  
 CC LONG-TERM FORCE BEARING STRUCTURAL SUPPORT.  
 CC -!- PTM: FORMS INTRAMOLECULAR DISULFIDE BONDS EITHER WITH OTHER  
 CC MICROFIBRILS (BY SIMILARITY).  
 CC -!- SIMILARITY: CONTAINS 47 EGF-LIKE DOMAINS.  
 CC -!- SIMILARITY: CONTAINS 7 TGF-BETA BINDING PROTEIN DOMAINS.  
 CC  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its

use by non-profit institutions as long as its content is in no way  
 modified and this statement is not removed. Usage by and for commercial  
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

-----  
 EMBL; L23454; AAA56840.1; -;  
 DR EMBL; U22493; AAA64217.1; -;  
 DR HSP; P35555; 1APJ.  
 DR MGD; MGI:95489; Fbn1.  
 DR InterPro; IPR000152; Asx hydroxyl.  
 DR InterPro; IPR000581; EGF-like.  
 DR InterPro; IPR001881; EGF-CA.  
 DR InterPro; IPR002212; Fibril-assoc.  
 DR Pfam; PF00008; EGF; 46.  
 DR Pfam; PF00683; TB; 9.  
 DR SMART; SM00179; EGF-CA; 42.  
 DR SMART; SM00001; EGF-like; 4.  
 DR PROSITE; PS00010; ASX-HYDROXYL; 43.  
 DR PROSITE; PS00022; EGF\_1; 2.  
 DR PROSITE; PS01186; EGF\_2; 38.  
 DR PROSITE; PS01187; EGF-CA; 43.  
 DR Extracellular matrix; Calcium-binding; Glycoprotein; EGF-like domain;  
 KW Repeat; Signal; Multigene family.  
 FT SIGNAL 1 27 POTENTIAL.  
 FT CHAIN 28 2871 FIBRILLIN 1.  
 FT DOMAIN 81 112 EGF-LIKE 1.  
 FT DOMAIN 115 146 EGF-LIKE 2.  
 FT DOMAIN 147 178 EGF-LIKE 3.  
 FT DOMAIN 246 287 EGF-LIKE 4. CALCIUM-BINDING.  
 FT DOMAIN 288 329 EGF-LIKE 5. CALCIUM-BINDING.  
 FT DOMAIN 330 401 TGFBP 1.  
 FT DOMAIN 402 446 PRO-RICH.  
 FT DOMAIN 449 489 EGF-LIKE 6.  
 FT DOMAIN 490 529 EGF-LIKE 7. CALCIUM-BINDING.  
 FT DOMAIN 530 571 EGF-LIKE 8. CALCIUM-BINDING.  
 FT DOMAIN 572 612 EGF-LIKE 9. CALCIUM-BINDING.  
 FT DOMAIN 613 653 EGF-LIKE 10. CALCIUM-BINDING.  
 FT DOMAIN 656 721 TGFBP 2.  
 FT DOMAIN 723 764 EGF-LIKE 11. CALCIUM-BINDING.  
 FT DOMAIN 765 806 EGF-LIKE 12. CALCIUM-BINDING.  
 FT DOMAIN 807 846 EGF-LIKE 13. CALCIUM-BINDING.  
 FT DOMAIN 910 951 EGF-LIKE 14. CALCIUM-BINDING.  
 FT DOMAIN 952 1018 TGFBP 3.  
 FT DOMAIN 1028 1069 EGF-LIKE 15. CALCIUM-BINDING.  
 FT DOMAIN 1070 1112 EGF-LIKE 16. CALCIUM-BINDING.  
 FT DOMAIN 1113 1154 EGF-LIKE 17. CALCIUM-BINDING.  
 FT DOMAIN 1155 1196 EGF-LIKE 18. CALCIUM-BINDING.  
 FT DOMAIN 1197 1237 EGF-LIKE 19. CALCIUM-BINDING.  
 FT DOMAIN 1238 1279 EGF-LIKE 20. CALCIUM-BINDING.  
 FT DOMAIN 1280 1321 EGF-LIKE 21. CALCIUM-BINDING.  
 FT DOMAIN 1322 1362 EGF-LIKE 22. CALCIUM-BINDING.  
 FT DOMAIN 1363 1403 EGF-LIKE 23. CALCIUM-BINDING.  
 FT DOMAIN 1404 1445 EGF-LIKE 24. CALCIUM-BINDING.  
 FT DOMAIN 1446 1486 EGF-LIKE 25. CALCIUM-BINDING.  
 FT DOMAIN 1487 1527 EGF-LIKE 26. CALCIUM-BINDING.  
 FT DOMAIN 1528 1599 TGFBP 4.  
 FT DOMAIN 1606 1647 EGF-LIKE 27. CALCIUM-BINDING.  
 FT DOMAIN 1648 1688 EGF-LIKE 28. CALCIUM-BINDING.  
 FT DOMAIN 1689 1758 TGFBP 5.  
 FT DOMAIN 1766 1807 EGF-LIKE 29. CALCIUM-BINDING.  
 FT DOMAIN 1808 1848 EGF-LIKE 30. CALCIUM-BINDING.  
 FT DOMAIN 1849 1890 EGF-LIKE 31. CALCIUM-BINDING.  
 FT DOMAIN 1891 1929 EGF-LIKE 32. CALCIUM-BINDING.  
 FT DOMAIN 1930 1972 EGF-LIKE 33. CALCIUM-BINDING.  
 FT DOMAIN 1973 2012 EGF-LIKE 34. CALCIUM-BINDING.  
 FT DOMAIN 2013 2054 EGF-LIKE 35. CALCIUM-BINDING.  
 FT DOMAIN 2055 2121 TGFBP 6.  
 FT DOMAIN 2127 2165 EGF-LIKE 36. CALCIUM-BINDING.  
 FT DOMAIN 2166 2205 EGF-LIKE 37. CALCIUM-BINDING.  
 FT DOMAIN 2206 2246 EGF-LIKE 38. CALCIUM-BINDING.  
 FT DOMAIN 2247 2290 EGF-LIKE 39. CALCIUM-BINDING.  
 FT DOMAIN 2291 2332 EGF-LIKE 40. CALCIUM-BINDING.  
 FT DOMAIN 2333 2400 TGFBP 7.

FT	DOMAIN	2402	2443	EGF-LIKE 41, CALCIUM-BINDING.
FT	DOMAIN	2444	2484	EGF-LIKE 42, CALCIUM-BINDING.
FT	DOMAIN	2485	2523	EGF-LIKE 43, CALCIUM-BINDING.
FT	DOMAIN	2524	2566	EGF-LIKE 44, CALCIUM-BINDING.
FT	DOMAIN	2567	2606	EGF-LIKE 45, CALCIUM-BINDING.
FT	DOMAIN	2607	2647	EGF-LIKE 46, CALCIUM-BINDING.
FT	DOMAIN	2648	2687	EGF-LIKE 47, CALCIUM-BINDING.
FT	DISULFID	85	94	BY SIMILARITY.
FT	DISULFID	89	100	BY SIMILARITY.
FT	DISULFID	102	111	BY SIMILARITY.
FT	DISULFID	119	129	BY SIMILARITY.
FT	DISULFID	123	134	BY SIMILARITY.
FT	DISULFID	136	145	BY SIMILARITY.
FT	DISULFID	150	160	BY SIMILARITY.
FT	DISULFID	154	166	BY SIMILARITY.
FT	DISULFID	168	177	BY SIMILARITY.
FT	DISULFID	250	262	BY SIMILARITY.
FT	DISULFID	257	271	BY SIMILARITY.
FT	DISULFID	273	286	BY SIMILARITY.
FT	DISULFID	292	304	BY SIMILARITY.
FT	DISULFID	299	313	BY SIMILARITY.
FT	DISULFID	315	328	BY SIMILARITY.
FT	DISULFID	453	465	BY SIMILARITY.
FT	DISULFID	460	474	BY SIMILARITY.
FT	DISULFID	476	488	BY SIMILARITY.
FT	DISULFID	494	504	BY SIMILARITY.
FT	DISULFID	499	513	BY SIMILARITY.
FT	DISULFID	515	528	BY SIMILARITY.
FT	DISULFID	534	546	BY SIMILARITY.
FT	DISULFID	541	555	BY SIMILARITY.
FT	DISULFID	557	570	BY SIMILARITY.
FT	DISULFID	576	587	BY SIMILARITY.
FT	DISULFID	582	596	BY SIMILARITY.
FT	DISULFID	598	611	BY SIMILARITY.
FT	DISULFID	617	628	BY SIMILARITY.
FT	DISULFID	623	637	BY SIMILARITY.
FT	DISULFID	639	652	BY SIMILARITY.
FT	DISULFID	727	739	BY SIMILARITY.
FT	DISULFID	734	748	BY SIMILARITY.
FT	DISULFID	750	763	BY SIMILARITY.
FT	DISULFID	769	781	BY SIMILARITY.
FT	DISULFID	776	790	BY SIMILARITY.
FT	DISULFID	792	805	BY SIMILARITY.
FT	DISULFID	811	821	BY SIMILARITY.
FT	DISULFID	816	830	BY SIMILARITY.
FT	DISULFID	832	845	BY SIMILARITY.
FT	DISULFID	914	926	BY SIMILARITY.
FT	DISULFID	921	935	BY SIMILARITY.
FT	DISULFID	937	950	BY SIMILARITY.
FT	DISULFID	1032	1044	BY SIMILARITY.
FT	DISULFID	1039	1053	BY SIMILARITY.
FT	DISULFID	1055	1068	BY SIMILARITY.
FT	DISULFID	1074	1086	BY SIMILARITY.
FT	DISULFID	1081	1095	BY SIMILARITY.
FT	DISULFID	1097	1111	BY SIMILARITY.
FT	DISULFID	1117	1129	BY SIMILARITY.
FT	DISULFID	1124	1138	BY SIMILARITY.
FT	DISULFID	1140	1153	BY SIMILARITY.
FT	DISULFID	1159	1171	BY SIMILARITY.
FT	DISULFID	1166	1180	BY SIMILARITY.
FT	DISULFID	1182	1195	BY SIMILARITY.
FT	DISULFID	1201	1212	BY SIMILARITY.
FT	DISULFID	1208	1221	BY SIMILARITY.
FT	DISULFID	1223	1236	BY SIMILARITY.
FT	DISULFID	1242	1254	BY SIMILARITY.
FT	DISULFID	1249	1263	BY SIMILARITY.
FT	DISULFID	1265	1278	BY SIMILARITY.
FT	DISULFID	1284	1296	BY SIMILARITY.
FT	DISULFID	1291	1305	BY SIMILARITY.
FT	DISULFID	1307	1320	BY SIMILARITY.
FT	DISULFID	1326	1339	BY SIMILARITY.
FT	DISULFID	1333	1348	BY SIMILARITY.
FT	DISULFID	1350	1361	BY SIMILARITY.

FT	DISULFID	1367	1380	BY SIMILARITY.
FT	DISULFID	1374	1389	BY SIMILARITY.
FT	DISULFID	1391	1402	BY SIMILARITY.
FT	DISULFID	1408	1420	BY SIMILARITY.
FT	DISULFID	1415	1429	BY SIMILARITY.
FT	DISULFID	1431	1444	BY SIMILARITY.
FT	DISULFID	1450	1461	BY SIMILARITY.
FT	DISULFID	1456	1470	BY SIMILARITY.
FT	DISULFID	1472	1485	BY SIMILARITY.
FT	DISULFID	1491	1502	BY SIMILARITY.
FT	DISULFID	1497	1511	BY SIMILARITY.
FT	DISULFID	1513	1526	BY SIMILARITY.
FT	DISULFID	1610	1622	BY SIMILARITY.
FT	DISULFID	1617	1631	BY SIMILARITY.
FT	DISULFID	1633	1646	BY SIMILARITY.
FT	DISULFID	1652	1663	BY SIMILARITY.
FT	DISULFID	1658	1672	BY SIMILARITY.
FT	DISULFID	1674	1687	BY SIMILARITY.

Query Match 12.2%; Score 171.5; DB 1; Length 2871;  
 Best Local Similarity 18.9%; Pred. No. 2, 1e-05;  
 Matches 52; Conservative 12; Mismatches 50; Indels 161; Gaps 6;

QY	56	RSPGLAPRPRVACCPGKRTSLPGA	82
DB	54	KGPVCGSRVYVACCPGKRTSLPGA	110
QY	83	CGAICQPPCRNGSGCYQPRCKCPA	108
DB	111	CGSRIOHCNIRCMNGSGSDHCLCKQGYIGTHGQPVCSGCLNGRCVAFNRCACTY	170
QY	109	GWRGDTQ	116
DB	171	GFTGQCRDRTRTGCTFVSNQMCQGLSGIVCTKLCCATVGRANGHPCMCAPQPHR	230
QY	117	SDVDECSARRGCEP-ORCVNTAGSYWCQWEGHSLADGTLG	157
DB	231	CRGFTPIRIRGACQVDVCOAIPMCGGNCINTVGSFECKCPAGHKFNEVSSQKCDID	290
QY	158	YPKG	172
DB	291	ECSTIPGVCDGCECTNTVSYFCKCPGFTSPDG	325

Search completed: December 17, 2002, 10:02:01  
 Job time : 11.1935 secs



GenCore version 5.1.3  
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 17, 2002, 09:58:37 ; Search time 26.5085 Seconds  
(without alignments)  
1974.306 Million cell updates/sec

Title: US-09-852-472-3

Perfect score: 1411  
Sequence: 1 TEHAYRPGRRVCARAHGDP.....SEQISFILEEQUGSCCKKDS 254

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phase:\*
- 10: sp\_plant:\*
- 11: sp\_protein:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_virus:\*
- 16: sp\_bacteriap:\*
- 17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query Length	DB ID	Description
1	1411	100.0	273	4 Q9UHF1	Q9UHF1 homo sapien
2	1410	99.9	273	4 Q9E8G0	Q9E8G0 homo sapien
3	1139.5	80.8	278	11 Q9QX15	Q9QX15 mus musculu
4	1063	75.3	265	11 Q9DCP5	Q9DCP5 mus musculu
5	728.5	51.6	190	11 Q9JW3	Q9JW3 ratu mus
6	425	30.1	293	11 Q35447	Q35447 mus musculu
7	415.5	29.4	293	4 Q99944	Q99944 homo sapien
8	276.5	19.6	509	5 Q9VZD0	Q9VZD0 homo sapien
9	276.5	19.6	512	5 Q9SRQ1	Q9SRQ1 drosophila
10	257	18.2	1574	11 Q88281	Q88281 ratu mus
11	253.5	18.0	558	4 Q9UFG6	Q9UFG6 homo sapien
12	252.5	17.9	553	4 Q9NZL7	Q9NZL7 homo sapien
13	252.5	17.9	554	4 Q9N67	Q9N67 homo sapien
14	246.5	17.5	550	11 Q9J3Z5	Q9J3Z5 mus musculu
15	223	15.8	561	11 Q91V88	Q91V88 mus musculu
16	219	15.5	1664	5 Q9TVQ2	Q9TVQ2 caenorhabdi

17	218.5	15.5	578	11 Q91ZD3	Q91ZD3 mus musculu
18	217.5	15.4	528	11 Q9CXD8	Q9CXD8 mus musculu
19	197.5	14.0	592	11 Q91XLS	Q91XLS mus musculu
20	193	13.7	609	11 Q923T5	Q923T5 mus musculu
21	189	13.4	678	4 Q14393	Q14393 homo sapien
22	185.5	13.1	747	11 Q8VHP4	Q8VHP4 mus musculu
23	185.5	13.1	1034	11 Q8VHL7	Q8VHL7 mus musculu
24	184	13.0	673	11 Q61592	Q61592 mus musculu
25	184	13.0	674	11 Q99K57	Q99K57 mus musculu
26	183.5	13.0	1034	11 Q8VIX5	Q8VIX5 mus musculu
27	182.5	12.9	816	11 Q8R417	Q8R417 ratu mus
28	182	12.9	1764	11 Q35806	Q35806 ratu mus
29	181.5	12.9	815	4 Q96J52	Q96J52 homo sapien
30	180	12.8	2809	4 Q96JP8	Q96JP8 homo sapien
31	178.5	12.7	4555	11 Q8R508	Q8R508 ratu mus
32	178	12.6	648	5 Q9NND7	Q9NND7 drosophila
33	178	12.6	674	11 Q63772	Q63772 ratu mus
34	178	12.6	701	5 Q9VU4	Q9VU4 drosophila
35	177.5	12.6	3138	5 Q9VTP0	Q9VTP0 drosophila
36	177	12.5	4215	5 Q9W332	Q9W332 ratu mus
37	176.5	12.5	2906	11 Q9WUH9	Q9WUH9 ratu mus
38	176	12.5	1511	4 Q75412	Q75412 homo sapien
39	175	12.4	1587	4 Q00508	Q00508 homo sapien
40	174.5	12.4	1095	11 Q60784	Q60784 mus musculu
41	174.5	12.4	3857	11 Q88840	Q88840 mus musculu
42	173.5	12.3	2872	11 Q9WUH8	Q9WUH8 ratu mus
43	172	12.2	418	4 Q8TF19	Q8TF19 homo sapien
44	172	12.2	1212	13 Q42347	Q42347 gallu
45	172	12.2	1833	11 Q08999	Q08999 mus musculu

ALIGNMENTS

RESULT 1

Q9UHF1 ID Q9UHF1 PRELIMINARY; PRT; 273 AA.  
AC Q9UHF1; 01-MAY-2000 (TREMURel. 13, Created)  
DT 01-MAY-2000 (TREMURel. 13, Last sequence update)  
DT 01-DEC-2001 (TREMURel. 19, Last annotation update)  
DE NOTCH4-like protein (Hypothetical 29.6 kDa protein).  
GN ZNFUI OR DKFZP586L2317.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
CX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Sheppard P., Jelinek L., Whitmore T., Blumberg H., Lehner J.,  
O'Hara P.;  
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=UTERUS;  
RA Koehler K., Beyer A., Mewes H.W., Gassenhuber J., Wiemann S.;  
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AL512735; CAC21666.1; -.  
DR HSSP; P08709; IFAX.  
DR InterPro; IPR00152; Asx\_hydroxyl.  
DR InterPro; IPR000561; EGF-like.  
DR InterPro; IPR001881; EGF\_Ca.  
DR Pfam; PF00008; EGF\_2.  
DR SMART; SM00179; EGF\_CA; 1.  
DR SMART; SM00001; EGF\_Like; 1.  
DR PROSITE; PS00010; ASX\_HYDROXYL; 1.  
DR PROSITE; PS00022; EGF\_1; UNKNOWN\_1.  
DR PROSITE; PS01186; EGF\_2; UNKNOWN\_1.  
DR PROSITE; PS01187; EGF\_CA; 1.  
KW Calcium-binding; EGF-like domain; Glycoprotein; Hydroxylation; Repeat.  
SQ SEQUENCE 273 AA; 29617 MW; 5740BB845ED5A988 CRC64;

Query Match 100.0%; Score 1411; DB 4; Length 273;  
 Best Local Similarity 100.0%; Pred. No. 8.1e-122;  
 Matches 254; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TEHAYRPGRRCAVRAHGDVPSEFVQRYQVQFLTTCDGHRACSTYRTIYRTAYRRSPGL 60  
 DB 20 TEHAYRPGRRCAVRAHGDVPSEFVQRYQVQFLTTCDGHRACSTYRTIYRTAYRRSPGL 79

QY 61 APAPRYACCPGKRTSLGPGACGAAICQPPCRNGGSCVQPGRCPCAGWRGDTCCSDVD 120  
 DB 80 APAPRYACCPGKRTSLGPGACGAAICQPPCRNGGSCVQPGRCPCAGWRGDTCCSDVD 139

QY 121 ECSARRGCGPCRCVNTAGSYWCQWEGHSLSDAGTLCVPKGGPRVAPNPTGVDSAMKEE 180  
 DB 140 ECSARRGCGPCRCVNTAGSYWCQWEGHSLSDAGTLCVPKGGPRVAPNPTGVDSAMKEE 199

QY 181 VQRQSRVDLLEELQLVLAPLHSLASQALEHGLPDPGSLLVHVSFOQLGRIDSLSSEQISF 240  
 DB 200 VQRQSRVDLLEELQLVLAPLHSLASQALEHGLPDPGSLLVHVSFOQLGRIDSLSSEQISF 259

QY 241 LEEQLGSCCKKDS 254  
 DB 260 LEEQLGSCCKKDS 273

## RESULT 2

Q96EGO PRELIMINARY; PRT; 273 AA.  
 AC Q96EGO;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
 DE Similar to NEU1 protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=OVARY;  
 RA Strausberg R.;  
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC012377; AAH12377.1; -;  
 DR InterPro; IPR000152; Asx\_hydroxyl.  
 DR InterPro; IPR000561; EGF-like.  
 DR InterPro; IPR001881; EGF\_Ca.  
 DR Pfam; PF00008; EGF; 2.  
 DR PROSITE; PS00010; ASX\_HYDROXYL; UNKNOWN\_1.  
 DR PROSITE; PS00022; EGF\_1; UNKNOWN\_1.  
 DR PROSITE; PS01186; EGF\_2; UNKNOWN\_1.  
 DR PROSITE; PS01187; EGF\_Ca; UNKNOWN\_1.  
 SQ SEQUENCE 273 AA; 29631 MW; 5AD0A4845ED5B688 CRC64;

Query Match 99.9%; Score 1410; DB 4; Length 273;  
 Best Local Similarity 99.6%; Pred. No. 1e-121;  
 Matches 253; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TEHAYRPGRRCAVRAHGDVPSEFVQRYQVQFLTTCDGHRACSTYRTIYRTAYRRSPGL 60  
 DB 20 TEHAYRPGRRCAVRAHGDVPSEFVQRYQVQFLTTCDGHRACSTYRTIYRTAYRRSPGL 79

QY 61 APAPRYACCPGKRTSLGPGACGAAICQPPCRNGGSCVQPGRCPCAGWRGDTCCSDVD 120  
 DB 80 APAPRYACCPGKRTSLGPGACGAAICQPPCRNGGSCVQPGRCPCAGWRGDTCCSDVD 139

QY 121 ECSARRGCGPCRCVNTAGSYWCQWEGHSLSDAGTLCVPKGGPRVAPNPTGVDSAMKEE 180  
 DB 140 ECSARRGCGPCRCVNTAGSYWCQWEGHSLSDAGTLCVPKGGPRVAPNPTGVDSAMKEE 199

QY 181 VQRQSRVDLLEELQLVLAPLHSLASQALEHGLPDPGSLLVHVSFOQLGRIDSLSSEQISF 240  
 DB 200 VQRQSRVDLLEELQLVLAPLHSLASQALEHGLPDPGSLLVHVSFOQLGRIDSLSSEQISF 259

QY 241 LEEQLGSCCKKDS 254  
 DB 260 LEEQLGSCCKKDS 273

RESULT 3  
 Q9QXT5 PRELIMINARY; PRT; 278 AA.  
 ID Q9QXT5  
 AC Q9QXT5;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE NOTCH4-like protein (Vascular endothelial zinc finger 1).  
 GN VEZF1 OR ZNEU1.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 OX NCI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Sheppard P., Jelinek L., Whitmore T., Blumberg H., Lehner J.,  
 RA O'Hara P.;  
 RT "Mus musculus homolog of HLA class III region containing NOTCH4  
 gene.";  
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Presnell S., Gilbert T., Whitmore T., Foster D., Hart C., Lehner J.,  
 RA Martinez T., Hoffman R., O'Hara P.;  
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=LIVER;  
 RA Strausberg R.;  
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF184973; AAF01322.1; -;  
 DR EMBL; BC024610; AAH24610.1; -;  
 DR HSPF; P00740; IEDM.  
 DR MGI; MGI:1313291; Vezfl.  
 DR InterPro; IPR000561; EGF-like.  
 DR InterPro; IPR001881; EGF\_Ca.  
 DR Pfam; PF00008; EGF; 2.  
 DR SMART; SM00181; EGF; 1.  
 DR SMART; SM00001; EGF\_like; 1.  
 DR PROSITE; PS00022; EGF\_1; UNKNOWN\_1.  
 DR PROSITE; PS01186; EGF\_2; UNKNOWN\_1.  
 DR PROSITE; PS01187; EGF\_Ca; 1.  
 KW Calcium-binding; EGF-Like domain; Glycoprotein; Repeat.  
 SQ SEQUENCE 278 AA; 30125 MW; 863159F567102FA7 CRC64;

Query Match 80.8%; Score 1139.5; DB 11; Length 278;  
 Best Local Similarity 79.9%; Pred. No. 7.6e-97;  
 Matches 203; Conservative 16; Mismatches 34; Indels 1; Gaps 1;

QY 1 TEHAYRPGRRCAVRAHGDVPSEFVQRYQVQFLTTCDGHRACSTYRTIYRTAYRRSPGL 60  
 DB 24 TEHAYRPGRRCAVRAHGDVPSEFVQRYQVQFLTTCDGHRACSTYRTIYRTAYRRSPGL 83

QY 61 APAPRYACCPGKRTSLGPGACGAAICQPPCRNGGSCVQPGRCPCAGWRGDTCCSDVD 120  
 DB 84 TPAPRYACCPGKRTSLGPGACGAAICQPPCGNGGSCIRFGHCPCPVGWGDTCCSDVD 143

QY 121 ECSARRGCGPCRCVNTAGSYWCQWEGHSLSDAGTLCVPKGGPRVAPNPTGVDSAMKEE 179  
 DB 144 ECSTGEASCPQRCVNTAGSYWCQWEGHSLSDAGTLCVKEGSPVAPNPTAGVDSMARE 203

QY 180 EVQRQSRVDLLEELQLVLAPLHSLASQALEHGLPDPGSLLVHVSFOQLGRIDSLSSEQIS 239  
 DB 204 EVYRQARVDVLEELQLVLAPLHSLASRSTEHGLQDPGSLLAHSFQQLDRIDSLSSEQIS 263

QY 240 FLEEQLGSCCKKD 253  
 DB 264 FLEEHLGSCCKKD 277



RESULT 4

09DCPS PRELIMINARY; PRT; 265 AA.  
 AC 09DCPS: 17, Created)  
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)  
 DT 01-JUN-2001 (TREMBlrel. 21, Last sequence update)  
 DE Vascular endothelial zinc finger 1.  
 GN VEZF1.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_Taxid=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=KIDNEY;  
 RA MEDLINE=21085660; PubMed=11217851;  
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
 RA Aitawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,  
 RA Saito T., Okazaki Y., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,  
 RA Kadota K., Matsuda H.A., Ashburner T., Bono H., Kasukawa T., Saito R.,  
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Koehne H.,  
 RA Kiehl P., Lewis S., Matsuo Y., Nakado I., Pesole G., Quackenbush J.,  
 RA Schirni L.M., Staubli F., Suzuki K., Tomita M., Wagner L., Washio L.,  
 RA Sakai K., Okido T., Furuno M., Kono H., Balderelli R., Barin G.,  
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
 RA Brownstein S., Hill D., Hofmann M., Hume D.A., Gariboldi M.,  
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Gariboldi M.,  
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombauts P.,  
 RA Norone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
 RA Suzuki H., Sato K., Schoenbach C., Seza T., Shibata Y., Storch K.-F.,  
 RA Hayashizaki Y., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,  
 RA Hayashizaki Y., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,  
 RA "Functional annotation of a full-length mouse cDNA collection."  
 RL Nature 409:685-690 (2001).  
 DR EMBL: AK002601; BAB22222.1;  
 DR HSSP: P00740; 1EDM.  
 DR MGD: MG11313291; Vefel.  
 DR InterPro: IPR000561; EGF-like.  
 DR InterPro: IPR001881; EGF\_Ca.  
 DR Pfam: PFO0008; EGF\_2.  
 DR SMART: SM00181; EGF\_2.  
 DR SMART: SM00001; EGF-like; 2.  
 DR PROSITE: PS00022; EGF\_1; UNKNOWN\_1.  
 DR PROSITE: PS01186; EGF\_2; UNKNOWN\_1.  
 DR PROSITE: PS01187; EGF\_Ca; 1.  
 SQ SEQUENCE 265 AA; 28665 MW; D81EC3DA848FF97E CRC64;

Query Match

Best Local Similarity 75.3%; Score 1063; DB 11; Length 265;  
 Matches 192; Conservative 15; Mismatches 33; Indels 14; Gaps 2;

QY 1 TEHAYRPGRCVCAVRAHGDVSESVFQVOPRLTTDGRACSTRTTYTAYRRSGT 60  
 DB 24 TEHAYRPGRCVCAVRAHGDVSESVFQVOPRLTTDGRACSTRTTYTAYRRSGT 60  
 QY 61 AAPRRVACCPGKRTSGLPAGCAATCOPPCNNGSCVQPRGRCPCPGMGCTGCGDVA 120  
 DB 84 TARRRYVACCPGKRTSGLPAGCAATCOPPCNNGSCVQPRGRCPCPGMGCTGCGDVA 120  
 QY 121 EESARRGCGPCRCVNTAGSYWCOCWEGHSLADGTLCPKGGPRVAPNPT-GVDSAMKE 179  
 DB 144 EESARRGCGPCRCVNTAGSYWCOCWEGHSLADGTLCPKGGPRVAPNPT-GVDSAMKE 179  
 QY 180 EVAPRLGSRVLLLEKQLVLAFLASLQALHGLPPGSLVHVSFOQGRIDSLSEQIS 203  
 DB 204 EVAPRLGSRVLLLEKQLVLAFLASLQALHGLPPGSLVHVSFOQGRIDSLSEQIS 203  
 QY 240 FLEBQJGSCCKRD 253

DB 260 -----SCKD 264

RESULT 5

09JMW3 PRELIMINARY; PRT; 190 AA.  
 AC 09JMW3: 15, Created)  
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
 DT 01-OCT-2000 (TREMBlrel. 21, Last sequence update)  
 DE Rattus norvegicus (Rat).  
 GN R20.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_Taxid=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=SPLEEN;  
 RA Chan M.T.W., Ng C.C.Y., Lim E.K.B., Huynh H.T.;  
 RA "Cloning and characterization of a novel 20.4kd Estrogen-regulated  
 protein in the Rat Spleen."  
 RL Submitted (Feb-2000) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=SPLEEN;  
 RA Marcantonio D., Huynh H.T.;  
 RA Submitted (Jan-2000) to the EMBL/GenBank/DBJ databases.  
 RL EMBL: AF23678; AAF5352.1;  
 DR InterPro: IPR000152; Asx hydroxyl.  
 DR InterPro: IPR000561; EGF-like.  
 DR InterPro: IPR001881; EGF\_Ca.  
 DR Pfam: PFO0008; EGF\_2.  
 DR SMART: SM00179; EGF\_2.  
 DR SMART: SM00001; EGF-like; 1.  
 DR PROSITE: PS00010; Asx hydroxyl; 1.  
 DR PROSITE: PS00022; EGF\_1; UNKNOWN\_1.  
 DR PROSITE: PS01186; EGF\_2; UNKNOWN\_1.  
 DR PROSITE: PS01187; EGF\_Ca; 1.  
 KW Calcium-binding; EGF-like domain; Glycoprotein; Hydroxylation; Repeat.  
 SQ SEQUENCE 190 AA; 20527 MW; C540EF0687F1E998 CRC64;

Query Match

Best Local Similarity 51.6%; Score 728.5; DB 11; Length 190;  
 Matches 131; Conservative 14; Mismatches 23; Indels 1; Gaps 1;

QY 86 AICOPPCNNGSCVQPRGRCPCPGMGCTGCGDVADEGARRGCGPCRCVNTAGSYWCOCW 145  
 DB 21 AICOPPCNNGSCVQPRGRCPCPGMGCTGCGDVADEGARRGCGPCRCVNTAGSYWCOCW 145  
 QY 146 EGHSLADGTLCPKGGPRVAPNPT-GVDSAMKEEYORLQSVLDLEKQLVLAFLHS 204  
 DB 81 EGHSLADGTLCPKGGPRVAPNPT-GVDSAMKEEYORLQSVLDLEKQLVLAFLHS 204  
 QY 205 LMSQALHGLPPGSLVHVSFOQGRIDSLSEQISFLEBQJGSCCKRD 253  
 DB 141 LMSQALHGLPPGSLVHVSFOQGRIDSLSEQISFLEBQJGSCCKRD 253

RESULT 6

035447 PRELIMINARY; PRT; 293 AA.  
 AC 035447:  
 DT 01-JAN-1998 (TREMBlrel. 05, Created)  
 DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)  
 DE Hypothetical 32.1 kDa protein.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_Taxid=10090;  
 RN [1]

SMART; SMO0001; EGF like; 1.  
PROSITE; PS00010; ASX\_HYDROXYL; 1.  
DR PROSITE; PS00022; EGF\_1; UNKNOWN\_1.  
DR PROSITE; PS01186; EGF\_2; 1.  
DR PROSITE; PS01187; EGF\_CA; 1.  
DR PROSITE; PS01187; EGF-like domain; Glycoprotein; Hydroxylation; Repeat.  
DR Calcium-binding; EGF-like domain; Glycoprotein; Hydroxylation; Repeat.  
KW SMART; SMO0001; EGF like; 1.  
SQ SEQUENCE 293 AA; 32262 MW; 6519CA254FB23FD0 CRC64;

Query Match  
Best Local Similarity 37.2%; Pred. No. 3e-30;  
Matches 100; Conservative 35; Mismatches 99; Indels 35; Gaps 10;

QY	6	RGRVRCACVAHGDVP--SESFVQRVYQPFLTTCGHRACSTYRTIYRVARRRSPGLA 63
D	32	RESQGVCSKQTLLVLPLRYNESISQPVYKYLTLTGAGRICSTYRTIYRVARRRSPGLA 63
D	64	PRIYACCPGWKRTSLPGA--CGAICQPCRNCGSCVQPGRCRCAPAGRGDTCCSDVD 121
QY	64	PRIYACCPGWKRTSLPGA--CGAICQPCRNCGSCVQPGRCRCAPAGRGDTCCSDVD 121
D	91	QTHAVCCQGNKKRH--PGALTC-EAICAKPCLNGVCVRPDCECAPGKGKHCHVDVD 147
D	122	CSARRGGCPCORCVNTAGSYWCQCWEGHSLSADGTLCVPGKGPVRVAPNPTGV----- 173
QY	122	CSARRGGCPCORCVNTAGSYWCQCWEGHSLSADGTLCVPGKGPVRVAPNPTGV----- 173
D	148	CRTSITLCSHHCFNTAGSTCCGPHDLVLGVDGTRCMESPEPTTSASILSVAREAKD 207
D	174	DSAMKEEVQRLQSRVDLLEKLQLVLAFLHLSAQO---LEHGLP-DPGSLLVHVSFQOL- 228
QY	174	DSAMKEEVQRLQSRVDLLEKLQLVLAFLHLSAQO---LEHGLP-DPGSLLVHVSFQOL- 228
D	208	EPAKAQETHELGRLELEQ-----WAGQAGWRAVLVPPEELQEQVAELW 256
QY	229	----GRIDSLSQI1SFLEEQLGSCCKKDS 254
D	257	GRDIIESLSQVLLLEERLGACSDNS 285

RESULT 8  
Q9VZD0 PRELIMINARY; PRT; 509 AA.

ID	Q9VZD0	Created
AC	01-MAY-2000 (TrEMBLrel. 13, Last sequence update)	
DT	01-MAY-2000 (TrEMBLrel. 13, Last annotation update)	
DT	01-JUN-2001 (TrEMBLrel. 17, Last annotation update)	
DE	CG1447 protein.	
OS	Drosophila melanogaster (fruit fly).	
GN	Drosophila melanogaster (fruit fly).	
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;	
OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;	
OC	Ephydroidea; Drosophilidae; Drosophila.	
OX	NCBI_Taxid=7227;	
EN	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=BERKELEY;	
RA	MEDLINE=20196006; PubMed=10731132;	
RA	Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,	
RA	Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galante R.F.,	
RA	George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,	
RA	Sutton G.C., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,	
RA	Burton R.C., Rogers Y.-H.C., Blazer E.G., Helt G., Pfeiffer B.D.,	
RA	Wan K.H., Doyle C., Baxter E.G., Nelson C.R., Miklos G.T.G.,	
RA	Abriel J.F., Agbayani A., An H.-J., Andrews-Pfankuch C., Baldwin D.,	
RA	Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,	
RA	Benson K.Y., Benos P.V., Bernier B.P., Brokstein P., Brotter P.,	
RA	Borkova D., Botchan M.R., Bouck J.J., Brokstein P., Center A., Chandra I.,	
RA	Burtis K.C., Busam D.A., Butler H., Cadieu E.L., Davies P.,	
RA	Cherry J.M., Cavley S., Dahlke C., Davenport L.B., Dietz S.M.,	
RA	de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dunham P.,	
RA	Dodson K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,	
RA	Fowler C., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,	
RA	Glocke A., Harve D., Heiman T.J., Hernandez J.R., Houck J.,	
RA	Harris N.H., Houston K.A., Howland T.J., Wei M.-H., Ibegwan K.A.,	
RA	Hoskins R.A., Karpman G.H., Ke Z., Kennison J.A., Ketchum K.A.,	
RA	Jalali M., Kalush F., Karpen G.H., Kravitz S., Kulp D., Lai Z.,	
RA	Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lin X.,	
RA	Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,	

---

SEQUENCE FROM N.A.  
Rowen L., Mahaitas G., Qin S., Ahern M.E., Dankers C., Lasky S.,  
A Rowen L., Mahaitas G., Qin S., Traicoff R., Zackrone K., Hood L.,  
Loretz C., Schmidt S., Tibbon S., major histocompatibility locus class III  
"sequence of the mouse major histocompatibility locus class III  
region".  
(ICT-1997) to the EMBL/GenBank/DBJ databases.

Submitted: AAB82010.1; --  
EMBL; AF030001; AAB82010.1; --  
HSP; P35555; 1EMN.  
InterPro; IPRO00152; Asx hydroxyl.  
InterPro; IPRO00561; EGF-like.  
InterPro; IPRO01881; EGF\_Ca.  
InterPro; IPRO01881; 2.  
Pfam; PF00008; EGF; CA; 1.  
SMART; SMO0179; EGF-like; 1.  
SMART; SMO0001; ASX\_HYDROXYL; 1.  
PROSITE; PS00010; ASX\_HYDROXYL; 1.  
PROSITE; PS00022; EGF\_1; UNKNOWN\_1.  
PROSITE; PS01186; EGF\_2; 1.  
PROSITE; PS01187; EGF\_CA; 1.  
PROSITE; PS01187; EGF-like domain; Glycoprotein; Hydroxylation;  
Calcium-binding; EGF-like domain; Glycoprotein; Hydroxylation;  
Calcium-binding; EGF-like domain; Glycoprotein; Hydroxylation;  
Hypochemical protein; Repeat.  
KW SMART; SMO0001; EGF like; 1.  
SQ SEQUENCE 293 AA; 32066 MW; 8A99ASEC000A2C62 CRC64;

Query Match  
Best Local Similarity 30.1%; Score 425; DB 11; Length 293;  
Matches 103; Conservative 34; Mismatches 95; Indels 44; Gaps 11;

QY	4	AVPRGRYCAVRAHGDVP--SESFVQRVYQPFLTTCGHRACSTYRTIYRVARRRSPGLA 61
D	30	SKESLGSQKTLVLPLRYNESISQPVYKYLTLTGAGRICSTYRTIYRVARRRSPGLA 61
QY	62	PARIYACCPGWKRTSLPGA--CGAICQPCRNCGSCVQPGRCRCAPAGRGDTCCSDVD 120
D	90	P-QTHVCCQGNKKRH--PGALTC-EAICAKPCLNGVCVRPDCECAPGKGKHCHVDVD 146
D	121	ECASARRGGCPCORCVNTAGSYWCQCWEGHSLSADGTLCVPGKGPVRVAPNPTGV----- 173
D	147	ECRASLTCSHGCLNTLGSFLCSPPHLVLGIDGTCA--GGPPE---SPTSASILSVAV 201
D	174	DSAMKEEVQRLQSRVDLLEKLQLVLAFLHLSAQO---LEHGLP-DPGSLLV 222
QY	174	DSAMKEEVQRLQSRVDLLEKLQLVLAFLHLSAQO---LEHGLP-DPGSLLV 222
D	202	READSEERALLRWAEIRGLEKLEQ-----WATQAGWRAVLVPPEELRP 250
QY	223	HSFQOL----GRIDSLSQI1SFLEEQLGSCCKKDS 254
D	251	EQVAELWGDRISLSDQVLLLEERLGACSDNS 286

RESULT 7  
Q99944 PRELIMINARY; PRT; 293 AA.

ID	Q99944	Created
AC	01-MAY-1997 (TrEMBLrel. 03, Last sequence update)	
DT	01-MAY-1997 (TrEMBLrel. 03, Last annotation update)	
DT	01-DEC-2001 (TrEMBLrel. 19, Last annotation update)	
DE	Ng3.	
OS	Homo sapiens (Human).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.	
OX	NCBI_Taxid=9606;	

Query Match	Best Local Similarity
... FE4782E4A6E121F0, hydroxylation; Repeat	19.6%
... CRC64;	

## RESULT 9

RP SEQUENCE ERROR: [1] --value=1227; --name=Dirosophila. --name=Dirosophila, Dirosophila, Muscomorpha;

Query Match	Best Local	Similarity	Score
4DD3/2E4A6FE7627	CRC64;	19.6%	Score

4/8 RLQTNLYKTESRTNKL EGM LNL 500

DR	SMART;	SM00179;	EGF-CA;	4.
SMART;	SM00001;	EGF-141		

138

9

6

10

2;

•

CONTR.

mg.

[illegible]

```

RN Submitted (Aug-1999) to the EMBL/GenBank/DBJ databases.
RP SEQUENCE FROM N.A.
RX MEDLINE=20241927; PubMed=10777661;
RA Buchner G., Orfanelli U., Quadrelli N., Bassi M.T., Andolfi G.,
RT "Identification of a new EGF-repeat-containing gene from human Xp22:
RL Genomics 65:16-23(2000).
CC - SIMILARITY: CONTAINS 1 MAM DOMAIN.
DR EMBL; AJ245672; CB92138.1;
DR HSSP; P3555; 1EMN.
DR MGD; MGI:185859; Bgf16.
DR InterPro; IPR000152; Asx_Hydroxyl.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR001881; EGF Ca.
DR Pfam; PF00068; EGF; 1.
DR SMART; SM00179; EGF_CA; 3.
DR SMART; SM00137; MAM_1.
DR PROSITE; PS001010; ASX_HYDROXYL; 3.
DR PROSITE; PS000022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_CA; 3.
DR Calcium-binding; EGF-like domain; Glycoprotein; Hydroxylation;
KW Hypothetical protein; Repeat
SV SEQUENCE 550 AA; 61520 MW; DEF36325C9F31B3 CRC64;

Query Match 17.5%; Score 246.5; DB 11; Length 550;
Best Local Similarity 36.9%; Freq. No. 2.1e-14;
Matches 52; Conservative 12; Mismatches 50; Indels 27; Gaps

QY 52 TVRRSPGLAARRYACCGWRTSGLGACGAATCOPEPRNAGSCVOPGRCPAGWR 111
DB 30 SALAHQGVDCVGYTKRMACCYGWKRRNN--KGVC-EMAEPRCK-FGECVGNKRCRCPGT 85
QY 112 GDTQSGVDGCSARRGQCPQRCVNTAGSYWCQCEHSLSDGTL----- 156
DB 86 GKTQDVNMGCVKRPQCHRCVNHSGYKCFCLSGHMLLPDATCSNRTCARLMQYGC 145
QY 157 -----CVPKGCPPVAPN 169
DB 146 EDTEGPRCVCPCSSGLRGN 166

RESULT 15
Q91V88 PRELIMINARY; PRT; 561 AA.
AC Q91V88;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE P0M (NEPHRONECTIN short isoform).
GN NPNP OR P0M OR NEPH.
OS Mus musculus (Mouse).
OC Mus musculus (Mouse).
OC Eus musculus (Mouse).
OC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Neumalli; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6;
RX MEDLINE=21551216; PubMed=11546798;
RA Morimura N., Tezuka Y., Watanabe N., Yasuda M., Miyatani S.,
RT "Molecular cloning of P0M. A novel adhesion molecule that interacts
RL with alpha2beta1 integrin.";
J. Biol. Chem. 276:42172-42181(2001).
RP [2]
RP SEQUENCE FROM N.A.
RX STRAIN=N1H SWISS; TISSUE=KIDNEY;
RX MEDLINE=21363579; PubMed=11470831;

```

US-09-852-472-3.rspt

Tue Dec 17 14:03:59 2002

Brandenberger R., Schmidt A., Linton J., Wang D., Backus C., Denda S.,

Muller U., Reichardt L.F.;

"Identification and characterization of a novel extracellular matrix

protein nephronectin that is associated with integrin alpha8beta1 in

the embryonic kidney.";

J. Cell Biol. 154:447-458 (2001).

-!- SIMILARITY: CONTAINS 1 MAM DOMAIN.

EMBL; AB059656; BAB69692.1; -

EMBL; AF035838; AAK96010.1; -

MGI; 2148811; Npnt.

InterPro; IPR000152; Asx hydroxyl.

InterPro; IPR000561; EGF-like.

InterPro; IPR001881; EGF\_Ca.

InterPro; IPR000998; MAM\_domain.

Pfam; PF00008; EGF; 4.

Pfam; PF00629; MAM; 1.

PROSITE; PS00010; ASX\_HYDROXYL; UNKNOWN\_3.

PROSITE; PS00022; EGF\_1; UNKNOWN\_1.

PROSITE; PS01186; EGF\_2; UNKNOWN\_3.

PROSITE; PS01187; EGF\_CA; UNKNOWN\_3.

PROSITE; PS00060; MAM\_2; 1.

Glycoprotein.

KW Glycoprotein.

SEQUENCE 561 AA; 61490 MW; 69ETACAA0EE3F506 CRC64;

Query Match 15.8%; Score 223; DB 11; Length 561;

Best Local Similarity 43.4%; Pred. No. 3.1e-12; Indels 4; Gaps 3;

Matches 43; Conservative 12; Mismatches 40; QY 57 SPGLAPARPRYACCPGWKRTSLGLGACGAICOPPCRNNGSCVQPGRCPCAGWRGDTCC 116

Db 32 SIGLCRYGGRIDCCMGWQSW--GQC--QPVCPQCKH-GEVGNPKCKCHPGFAGKTCN 87

QY 117 SDVDECSARRGGCPQRCVNTAGSYWCQCEGHSLSDGT 155

Db 88 QDLNECGKLPKPCPKHRCMNTFGSYKCYCLNGYMLLPDGS 126

Search completed: December 17, 2002, 10:03:02

Job time : 27.5085 secs